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(54) Title: METHODS OF IDENTIFYING PUTATIVE GENE PRODUCTS BY INTERSPECIES SEQUENCE COMPARISON AND BIOMOLECULAR SEQUENCES UNCOVERED THEREBY

(57) Abstract: A method of identifying alternatively spliced exons is provided. The method comprising, scoring each of a plurality of exon sequences derived from genes of a species according to at least one sequence parameter, wherein exon sequences of the plurality of exon sequences scoring above a predetermined threshold represent alternatively spliced exons, thereby identifying the alternatively spliced exons.

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METHODS OF IDENTIFYING PUTATIVE GENE PRODUCTS BY
INTERSPECIES SEQUENCE COMPARISON AND
BIOMOLECULAR SEQUENCES UNCOVERED THEREBY

FIELD OF THE INVENTION

The present invention relates to methods of identifying putative gene products by interspecies sequence comparison and, more particularly, to biomolecular sequences uncovered using these methodologies.

BACKGROUND OF THE INVENTION

Alternative splicing of eukaryotic pre-mRNAs is a mechanism for generating many transcript isoforms from a single gene. It is known to play important regulatory functions. A classic example is the *Drosophila* sex-determination pathway, in which alternative splicing acts as a sex-specific genetic switch that forms the basis of a regulatory hierarchy [Boggs et al. (1987) Cell 50:739-747; Baker (1989) Nature 340:521-524; Lopez (1999) Annu. Rev. Genet. 32:279-305]. Another intriguing example was found in the inner ear of the chicken, where differential distribution of splice variants for the calcium-activated potassium channel gene *slo* may form a tonotopic gradient and attune sensory hair cells to the detection of different sound frequencies [Black (1998) Neuron 20:165-168; Ramanathan et al. (1999) Science 283:215-217; Graveley (2001) Trends Genet. 17:100-107]. Alternative splicing is also implicated in human diseases. For example, the neurodegenerative disease FTDP-17 has been associated with mutations that affect the alternative splicing of *tau* pre-mRNAs [Goedert et al. (2000) Ann. NY Acad. Sci. 920:74-83; Jiang et al. (2000) Mol. Cell. Biol. 20:4036-4048].

Initial sequencing and analysis of the human genome has placed further attention on the role of alternative splicing. The surprising finding that the genome contains about 30,000 protein-coding genes, significantly less than previously estimated, led to the proposal that alternative splicing contributes greatly to functional diversity [Ewing and Green (2000) Nat. Genet. 25:232-234; Lander et al. (2001) Nature 409:860-921; Venter et al. (2001) Science 291:1304-1351].

Expressed sequence tags (ESTs) provide a primary resource for analyzing gene products and predicting alternative splicing events. More than 5 million human

ESTs are available to date, which provide a comprehensive sample of the transcriptome. In recent years, numerous studies attempted to computationally assess the extent of alternative splicing in the human genome. With the availability of a nearly complete sequence of the human genome, aligning ESTs to the genome has become a common strategy.

A number of methods based on this strategy have been developed, to enable large-scale analysis of alternative splicing [Brett (2000) FEBS Lett. 47:83-86; Kan (2002) Genome Res. 12:1837-1845; Kan (2001) Genome Res. 11:875-888; Lander (2001) Nature 409:860-921; Mironov (1999) Genome Res. 9:1288-1293; Modrek (2001) Nucleic Acids Res. 29:2850-2859; Hide (2001) Genome Res. 11:1848-1853]. Some of these are summarized infra.

Mironov et al. have developed an algorithm for predicting exon-intron structure of genomic DNA fragments using EST data. This algorithm (Procrustes-EST) is based on the previously published spliced alignment algorithm [Gelfand et al. (1996) Proc. Natl. Acad. Sci. USA 93:9061-9066], which explores all possible exon assemblies in polynomial time and finds the multiexon structure with the best fit to a related protein. When applied to known human genes and TIGR EST assemblies, the software found a large number of alternatively spliced genes (~35%). Most of the alternative splicing events occurred in 5'-untranslated regions. In many cases the use of this software allowed for linking and merging multiple existing assemblies into single contigs [Mironov (1999) Genome Research 9:1288-1293].

Kan et al. have developed a software tool, Transcript Assembly Program (TAP), that infers the predominant gene structure and reports alternative splicing events using genomic EST alignments [Kan (2001) Genome Research 11:889-900. The gene structure is assembled from individual splice junction pairs using connectivity information encoded in the ESTs. A method called PASS (Polyadenylation Site Scan) is used to infer poly-A sites from 3' EST clusters. The gene boundaries are identified using the poly-A site predictions. Reconstructing about one thousand known transcripts, TAP scored a sensitivity of 60 % and a specificity of 92 % at the exon level. The gene boundary identification process was found to be accurate 78 % of the time. TAP also reports alternative splicing patterns in EST alignments. An analysis of alternative splicing in 1124 genomic regions suggested that more than half of human genes undergo alternative splicing. Furthermore, the

evolutionary conservation of alternative splicing between human and mouse was analyzed using an EST-based approach.

Modrek et al. have performed a genome-wide analysis of alternative splicing based on human EST data. Tens of thousands of splices and thousands of alternative splices were identified in thousands of human genes. These were mapped onto the human genome sequence to verify that the putative splice junctions detected in the expressed sequences map onto genomic exon intron junctions that match the known splice site consensus [Modrek (2001) Nucleic Acids Research, 29:2850-2859].

As mentioned, the above-described approaches use EST data or full-length cDNA sequences to detect alternative splicing. However, expressed sequences present a problematic source of information, as they are merely a sample of the transcriptome. Thus, the detection of a splice variant is possible only if it is expressed above a certain expression level, or if there is an EST library prepared from the tissue type in which the variant is expressed. In addition, ESTs are very noisy and contain numerous erroneous sequences [Sorek (2003) Nucleic Acids Res. 31: 1067-1074]. For example, many wrongly termed splice events represent incompletely spliced heteronuclear RNA (hnRNA) or oligo(dT)-primed genomic DNA contaminants of cDNA library constructions. Furthermore, the splicing apparatus is known to make errors, resulting in aberrant transcripts that are degraded by the mRNA surveillance system and amount to little that is functionally important [Maquat and Charmichael (2001) Cell 104:173-176; Modrek and Lee (2001) Nat. Genet. 30:13-19]. Consequently the mere presence of a transcript isoform in the ESTs cannot establish a functional role for it. Thus, the use of expressed sequence data allows only very general estimates regarding the number of genes that have splice variants (currently running between 35% and 75%), but does not allow specific estimation regarding the actual number of exons that can be alternatively spliced.

SUMMARY OF THE INVENTION

The background art fails to teach or suggest a method for large-scale prediction of alternative splicing events, which is devoid of the previously described limitations.

According to one aspect of the present invention there is provided a method of identifying alternatively spliced exons, the method comprising, scoring each of a

plurality of exon sequences derived from genes of a species according to at least one sequence parameter, wherein exon sequences of the plurality of exon sequences scoring above a predetermined threshold represent alternatively spliced exons, thereby identifying the alternatively spliced exons.

According to another aspect of the present invention there is provided a system for generating a database of alternatively spliced exons, the system comprising a processing unit, the processing unit executing a software application configured for: (a) scoring each of a plurality of exon sequences derived from genes of a species according to at least one sequence parameter, wherein exon sequences of the plurality of exon sequences scoring above a predetermined threshold represent alternatively spliced exons, to thereby identify the alternatively spliced exons; and (b) storing the identified alternatively spliced exons to thereby generate the database of alternatively spliced exons.

According to yet another aspect of the present invention there is provided a computer readable storage medium comprising data stored in a retrievable manner, the data including sequence information as set forth in the files "transcripts.fasta" and "proteins.fasta" of enclosed CD-ROM1 and in the files "transcripts" and "proteins" of enclosed CD-ROM2 and sequence annotations as set forth in the file "AnnotationForPatent.txt" of enclosed CD-ROM1.

According to still another aspect of the present invention there is provided a method of predicting expression products of a gene of interest, the method comprising: (a) scoring exon sequences of the gene of interest according to at least one sequence parameter and identifying exon sequences scoring above a predetermined threshold as alternatively spliced exons of the gene of interest; and (b) analyzing chromosomal location of each of the alternatively spliced exons with respect to coding sequence of the gene of interest to thereby predict expression products of the gene of interest.

According to an additional aspect of the present invention there is provided a method of predicting expression products of a gene of interest in a given species, the method comprising: (a) providing a contig of exon sequences of the gene of interest of a first species; (b) identifying exon sequences of an orthologue of the gene of interest of the first species which align to a genome of the first species; (c) assembling the exon sequences of the orthologue of the gene of interest in the contig, thereby

generating a hybrid contig; (d) identifying in the hybrid contig, exon sequences of the orthologue of the gene of interest, which do not align with the exon sequences of the gene of interest of the first species, thereby uncovering non-overlapping exon sequences of the gene of interest; and (e) analyzing chromosomal location of non-overlapping exon sequences of the gene of interest with respect to the chromosomal location of the gene of interest to thereby predict expression products of the gene of interest in a given species.

According to further features in preferred embodiments of the invention described below, at least a portion of the exon sequences are alternatively spliced sequences.

According to still further features in the described preferred embodiments the alternatively spliced sequences are identified by scoring exon sequences of the gene of interest according to at least one sequence parameter, wherein exon sequences scoring above a predetermined threshold represent the alternatively spliced exons of the gene of interest.

According to still further features in the described preferred embodiments the at least one sequence parameter is selected from the group consisting of: (i) exon length; (ii) division by 3; (iii) conservation level between the plurality of exon sequences of genes of a species and corresponding exon sequences of genes of an orthologous species; (iv) length of conserved intron sequences upstream of each of the plurality of exon sequences; (v) length of conserved intron sequences downstream of each of the plurality of exon sequences ; (vi) conservation level of the intron sequences upstream of each of the plurality of exon sequences ; and (vii) conservation level of the intron sequences downstream of each of the plurality of exon sequences;

According to still further features in the described preferred embodiments the exon length does not exceed 1000 bp.

According to still further features in the described preferred embodiments the conservation level is at least 95 %.

According to still further features in the described preferred embodiments the length of conserved intron sequences upstream of each of the plurality of exon sequences is at least 12.

According to still further features in the described preferred embodiments the length of conserved intron sequences downstream of each of the plurality of exon sequences is at least 15.

According to still further features in the described preferred embodiments the conservation level of the intron sequences upstream of each of the plurality of exon sequences is at least 85 %.

According to still further features in the described preferred embodiments the conservation level of the intron sequences downstream of each of the plurality of exon sequences is at least 60 %.

According to yet an additional aspect of the present invention there is provided an isolated polynucleotide comprising a nucleic acid sequence being at least 70 % identical to a nucleic acid sequence of the sequences set forth in file "transcripts.fasta" of CD-ROM1 or in the file "transcripts" of CD-ROM2.

According to still further features in the described preferred embodiments the nucleic acid sequence is set forth in the file "transcripts.fasta" of enclosed CD-ROM1 or in the file "transcripts" of enclosed CD-ROM 2.

According to still an additional aspect of the present invention there is provided an isolated polynucleotide comprising a nucleic acid sequence encoding a polypeptide having an amino acid sequence at least 70 % homologous to a sequence set forth in the file "proteins.fasta" of enclosed CD-ROM1 or in the file "proteins" of enclosed CD-ROM2.

According to a further aspect of the present invention there is provided an isolated polypeptide having an amino acid sequence at least 80 % homologous to a sequence set forth in the file "proteins.fasta" of enclosed CD-ROM1 or in the file "proteins" of enclosed CD-ROM2.

According to yet a further aspect of the present invention there is provided use of a polynucleotide or polypeptide set forth in the file "transcripts.fasta" of CD-ROM1 or in the file "transcripts" of CD-ROM2 or in the file "proteins.fasta" of enclosed CD-ROM1 or in the file "proteins" of enclosed CD-ROM2 for the diagnosis and/or treatment of the diseases listed in Example 8.

In addition, a brief description of exemplary, non-limiting embodiments of the present invention related to the proteins listed in Table 3 is given below, with regard to the amino acid sequences of the splice variants as compared to the wild type

sequences. As is further described hereinbelow, the present invention encompasses both nucleic acid and amino acid sequences, as well as homologs, analogs and derivatives thereof. The present invention also encompasses the exemplary protein (amino acid) sequences as described below.

The below description is given as follows. Each sequence is described with regard to the name of the splice variant as given in the included file. For example, for the first sequence below, the name of the splice variant is "ANGPT1_Skippingexon_5 #PEP_NUM_117", which is a variant of the wild type protein "ANGPT1". The splice variant sequence for this variant is described with reference to the wild type amino acid sequence: the amino acid sequence of the splice variant ANGPT1_Skippingexon_5 #PEP_NUM_117 is comprised of a first amino acid sequence that is at least about 90% homologous to amino acids 1-269 of the amino acid sequence of the wild type protein ANGPT1; and a second amino acid sequence that is at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GVLQYGCQWGRLCDNTTS (SEQ ID NO: 205), which corresponds to the unique "tail" sequence. Therefore, the splice variant has a first portion having at least about 90% homology to the specified part of the wild type amino acid sequence, and a second portion with the described homology to the unique tail sequence.

The phrase "contiguous and in a sequential order" indicates that these two portions are part of the same polypeptide (are contiguous) and are in the order given (in a sequential order), as described above with regard to the example.

Also as described above, the term "tail" refers to a portion at the C-terminus of the splice variant protein. An "edge portion" occurs at the junction of two exons that are now contiguous in the splice variant, but were not contiguous in the corresponding wild type protein. A "bridging polypeptide" is a unique sequence (of the splice variant) located between two amino acid sequences that correspond to portions of the wild type protein. Any of the tail, the edge portion or the bridging polypeptide may be at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90%, and most preferably at least about 95% homologous to the sequences given below. A "bridging amino acid" is an amino acid in the splice

variant that is located between two amino acid sequences that correspond to portions of the wild type protein.

Optionally and preferably, the edge portion, the bridging polypeptide or the tail may optionally be used as a peptide therapeutic, and/or in an assay (such as a diagnostic assay for example), and/or or as partial or complete antibody epitope that is capable of being specifically bound by and/or elicited by an antibody, preferably a monoclonal antibody and/or a fragment of an antibody. For example, a splice variant may be differentially expressed as compared to the wild type protein with regard to

Optionally, although the percent homology of the portion(s) of a splice variant that correspond to a wild type sequence is preferably at least about 90%, optionally the percent homology is at least about 70%, also optionally at least about 80%, preferably at least about 85%, and most preferably at least about 95% homologous to the corresponding part of the wild type sequence.

It should also be noted that although the edge portions are described as being 22 amino acids in length (11 on either side of the join that is present in the splice variant between two portions of the wild type protein), or 23 amino acids in length if a bridge amino acid is present, the length of an edge portion can also optionally be any number of amino acids from about 10 to about 50, or any number within this range, optionally from about 15 to about 30, preferably from about 20 to about 25 amino acids.

The exemplary embodiments of the present invention are given below with regard to the described sequences.

An isolated ANGPT1_Skippingexon_5 #PEP_NUM_117 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-269 of ANGPT1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GVLQYGCQWGRLCDNTTS (SEQ ID NO: 205), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of ANGPT1_Skippingexon_5 #PEP_NUM_117, comprising a polypeptide having the sequence GVLQYGCQWGRLCDNTTS (SEQ ID NO: 205).

An isolated ANGPT1_Skipping exon_6 #PEP_NUM_118 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-312 of ANGPT1, and a second amino acid sequence being at least about 90 % homologous to amino acids 347-498 of ANGPT1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of ANGPT1_Skipping exon_6 #PEP_NUM_118, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 302-312 of ANGPT1, and a second amino acid sequence being at least about 90 % homologous to amino acids 347-357 of ANGPT1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated ANGPT1_Skipping exon_8 #PEP_NUM_119 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-401 of ANGPT1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence MW, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of ANGPT1_Skipping exon_8 #PEP_NUM_119, comprising a polypeptide having the sequence MW.

An isolated APBB1_Skipping exon_10 #PEP_NUM_159 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-501 of APBB1, and a second amino acid sequence being at least about about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence WNSQRLRMSWSRSSKSITWGMYLLLNL LG (SEQ ID NO: 206), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of APBB1_Skipping exon_10 #PEP_NUM_159, comprising a polypeptide having the sequence WNSQRLRMSWSRSSKSITWGMYLLLNL LG (SEQ ID NO: 206).

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An isolated APBB1_Skipping exon_12_#PEP_NUM_160 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-557 of APBB1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence DRGSAGRSGAFPLLPGRGQRCPHVCIHGCRPSLLLLPHVLVRAQCCQPLR GCAGCVHASLPEVSGCPFPGLHLLPPSTPC (SEQ ID NO: 207), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of APBB1_Skipping exon_12_#PEP_NUM_160, comprising a polypeptide having the sequence DRGSAGRSGAFPLLPGRGQRCPHVCIHGCRPSLLLLPHVLVRAQCCQPLR GCAGCVHASLPEVSGCPFPGLHLLPPSTPC (SEQ ID NO: 207).

An isolated APBB1_Skipping exon_3_#PEP_NUM_156 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-240 of APBB1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence AHLDRFC SWRRL (SEQ ID NO: 208), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of APBB1_Skipping exon_3_#PEP_NUM_156, comprising a polypeptide having the sequence AHLDRFC SWRRL (SEQ ID NO: 208).

An isolated APBB1_Skipping exon_7_#PEP_NUM_157 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-368 of APBB1, and a second amino acid sequence being at least about 90 % homologous to amino acids 414-710 of APBB1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of APBB1_Skipping exon_7_#PEP_NUM_157, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 358-368 of APBB1, and a second amino acid sequence being at least about 90 % homologous to amino acids

414-424 of APBB1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated APBB1_Skipping exon_9 #PEP_NUM_158 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-462 of APBB1, and a second amino acid sequence being at least about 90 % homologous to amino acids 502-710 of APBB1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of APBB1_Skipping exon_9 #PEP_NUM_158, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 452-462 of APBB1, and a second amino acid sequence being at least about 90 % homologous to amino acids 502-512 of APBB1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated CUL5_Skipping exon_2 #PEP_NUM_137 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-8 of CUL5, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GCACSLSLG (SEQ ID NO: 209), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of CUL5_Skipping exon_2 #PEP_NUM_137, comprising a polypeptide having the sequence GCACSLSLG (SEQ ID NO: 209).

An isolated CUL5_Skipping exon_2 #PEP_NUM_138 polypeptide, consisting essentially of an amino acid sequence being at least about 90 % homologous to amino acids 119-780 of CUL5.

An isolated CUL5_Skipping exon_8 #PEP_NUM_139 polypeptide, comprising a first amino acid sequence being at least 90 % homologous to amino acids 1-260 of CUL5, and a second amino acid sequence being at least 70%, optionally at least 80%, preferably at least 85%, more preferably at least 90% and most preferably at least 95% homologous to a polypeptide having the sequence NYI, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

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An isolated polypeptide corresponding to a tail of CUL5_Skippingexon_8 #PEP_NUM_139, comprising a polypeptide having the sequence NYI.

An isolated ECE1_Skippingexon_2 #PEP_NUM_129 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-17 of ECE1, and a second amino acid sequence being at least about 90 % homologous to amino acids 47-770 of ECE1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of ECE1_Skippingexon_2 #PEP_NUM_129, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 7-17 of ECE1, and a second amino acid sequence being at least about 90 % homologous to amino acids 47-57 of ECE1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated ECE2_Skippingexon_12 #PEP_NUM_132 polypeptide, comprising a first amino acid sequence being at least 90 % homologous to amino acids 1-458 of ECE2, and a second amino acid sequence being at least 90 % homologous to amino acids 492-765 of ECE2 or a portion thereof, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of ECE2_Skippingexon_12 #PEP_NUM_132, comprising a first amino acid sequence being at least 90 % homologous to amino acids 448-458 of ECE2 or a portion thereof, and a second amino acid sequence being at least 90 % homologous to amino acids 492-502 of ECE2 or a portion thereof, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated ECE2_Skippingexon_13 #PEP_NUM_133 polypeptide, comprising a first amino acid sequence being at least 90 % homologous to amino acids 1-491 of ECE2, and a second amino acid sequence being at least 90 % homologous to amino acids 518-765 of ECE2 or a portion thereof, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of ECE2_Skippingexon_13 #PEP_NUM_133, comprising a first amino acid sequence being at least 90 % homologous to amino acids 481-491 of ECE2 or a portion thereof,

and a second amino acid sequence being at least 90 % homologous to amino acids 518-528 of ECE2 or a portion thereof, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated ECE2_Skippingexon_15_#PEP_NUM_134 polypeptide, comprising a first amino acid sequence being at least 90 % homologous to amino acids 1-552 of ECE2, and a second amino acid sequence being at least 90 % homologous to amino acids 590-765 of ECE2 or a portion thereof, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of ECE2_Skippingexon_15_#PEP_NUM_134, comprising a first amino acid sequence being at least 90 % homologous to amino acids 542-552 of ECE2 or a portion thereof, and a second amino acid sequence being at least 90 % homologous to amino acids 590-600 of ECE2 or a portion thereof, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated ECE2_Skippingexon_2_#PEP_NUM_130 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-13 of ECE2, and a second amino acid sequence being at least about 90 % homologous to amino acids 43-765 of ECE2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of ECE2_Skippingexon_2_#PEP_NUM_130, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 3-13 of ECE2, and a second amino acid sequence being at least about 90 % homologous to amino acids 43-53 of ECE2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated ECE2_Skippingexon_8_#PEP_NUM_131 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-272 of ECE2, and a second amino acid sequence being at least about 90 % homologous to amino acids 336-765 of ECE2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of ECE2_Skippingexon_8_#PEP_NUM_131, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 262-272 of ECE2, and a second

amino acid sequence being at least about 90 % homologous to amino acids 336-346 of ECE2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated EDNRB_Skippingexon_4 #PEP_NUM_128 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-198 of EDNRB, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence SFTRQQKIGGYSVSISACHWPSLHFFIH (SEQ ID NO: 210), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of EDNRB_Skippingexon_4 #PEP_NUM_128, comprising a polypeptide having the sequence SFTRQQKIGGYSVSISACHWPSLHFFIH (SEQ ID NO: 210).

An isolated EFNA1_Skipping_exon_3 #PEP_NUM_42 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-130 of EFNA1, and a second amino acid sequence being at least about 90 % homologous to amino acids 153-205 of EFNA1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of EFNA1_Skipping_exon_3 #PEP_NUM_42, comprising a first amino acid sequence being at least 90 % homologous to amino acids 120-130 of EFNA1, and a second amino acid sequence being at least about 90 % homologous to amino acids 153-163 of EFNA1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated EFNA3_Skippingexon_3 #PEP_NUM_43 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-148 of EFNA3, and a second amino acid sequence being at least about 90 % homologous to amino acids 171-238 of EFNA3, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of EFNA3_Skippingexon_3 #PEP_NUM_43, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 138-148 of EFNA3, and a

second amino acid sequence being at least about 90 % homologous to amino acids 171-181 of EFNA3, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated EFNA3_Skippingexon_4_#PEP_NUM_44 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-169 of EFNA3, a bridging amino acid K and a second amino acid sequence being at least about 90 % homologous to amino acids 197-238 of EFNA3, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of EFNA3_Skippingexon_4_#PEP_NUM_44, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 159-169 of EFNA3, a bridging amino acid K and a second amino acid sequence being at least about 90 % homologous to amino acids 197-207 of EFNA3, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated EFNA5_Skipping_exon_3_#PEP_NUM_45 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-139 of EFNA5, a bridging amino acid Y and a second amino acid sequence being at least 90 % homologous to amino acids 163-228 of EFNA5, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of EFNA5_Skipping_exon_3_#PEP_NUM_45, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 129-139 of EFNA5, a bridging amino acid Y and a second amino acid sequence being at least about 90 % homologous to amino acids 163-173 of EFNA5, wherein said first amino acid

sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated EFNA5_Skipping_exon_4 #PEP_NUM_46 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-162 of EFNA5, and a second amino acid sequence being at least about 90 % homologous to amino acids 189-228 of EFNA5, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of EFNA5_Skipping_exon_4 #PEP_NUM_46, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 152-162 of EFNA5, and a second amino acid sequence being at least about 90 % homologous to amino acids 189-199 of EFNA5, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated EFNB2_Skipping_exon_2 #PEP_NUM_47 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-40 of EFNB2, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least 90% and most preferably at least about 95% homologous to a polypeptide having the sequence NYIKWVFGGPG (SEQ ID NO: 211), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of EFNB2_Skipping_exon_2 #PEP_NUM_47, comprising a polypeptide having the sequence NYIKWVFGGPG (SEQ ID NO: 211).

An isolated EFNB2_Skipping_exon_3 #PEP_NUM_48 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-135 of EFNB2, a bridging amino acid Y and a second amino acid sequence being at least about 90 % homologous to amino acids 169-333 of EFNB2, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of EFNB2_Skipping_exon_3 #PEP_NUM_48, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 125-135 of EFNB2, a bridging amino acid Y and a second amino acid sequence being at least about 90 % homologous to amino acids 169-179 of EFNB2, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated EFNB2_Skipping_exon_4 #PEP_NUM_49 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-166 of EFNB2, and a second amino acid sequence being at least about 90 % homologous to amino acids 205-333 of EFNB2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of EFNB2_Skipping_exon_4 #PEP_NUM_49, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 156-166 of EFNB2, and a second amino acid sequence being at least about 90 % homologous to amino acids 205-215 of EFNB2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated EPHA4_Skipping_exon_12 #PEP_NUM_53 polypeptide, consisting essentially of an amino acid sequence being at least about 90 % homologous to amino acids 1-691 of EPHA4.

An isolated EPHA4_Skipping_exon_2 #PEP_NUM_50 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-31 of EPHA4, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GGSEYHG (SEQ ID NO: 212), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of EPHA4_Skipping_exon_2 #PEP_NUM_50, comprising a polypeptide having the sequence GGSEYHG (SEQ ID NO: 212).

An isolated EPHA4_Skipping_exon_3_#PEP_NUM_51 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-53 of EPHA4, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence LAKLDITRLSPRMPPVPSAHPTATLSGKEPPRAPVTEAFSELTTMLPLCPAPVH HLLP (SEQ ID NO: 213), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of EPHA4_Skipping_exon_3_#PEP_NUM_51, comprising a polypeptide having the sequence LAKLDITRLSPRMPPVPSAHPTATLSGKEPPRAPVTEAFSELTTMLPLCPAPVH HLLP (SEQ ID NO: 213).

An isolated EPHA4_Skipping_exon_4_#PEP_NUM_52 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-274 of EPHA4, a bridging amino acid G and a second amino acid sequence being at least about 90 % homologous to amino acids 328-986 of EPHA4, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of EPHA4_Skipping_exon_4_#PEP_NUM_52, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 264-274 of EPHA4, a bridging amino acid G and a second amino acid sequence being at least about 90 % homologous to amino acids 328-338 of EPHA4, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated EPHA5_Skipping_exon_10_#PEP_NUM_57 polypeptide, consisting essentially of an amino acid sequence being at least about 90 % homologous to amino acids 1-618 of EPHA5, followed by C.

An isolated EPHA5_Skipping_exon_14_#PEP_NUM_58 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-766 of EPHA5, and a second amino acid sequence being at least about 90 % homologous to amino acids 837-1037 of EPHA5, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of EPHA5_Skipping_exon_14_#PEP_NUM_58, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 756-766 of EPHA5, and a second amino acid sequence being at least about 90 % homologous to amino acids 837-847 of EPHA5, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated EPHA5_Skipping_exon_16_#PEP_NUM_59 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-886 of EPHA5, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence SI, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of EPHA5_Skipping_exon_16_#PEP_NUM_59, comprising a polypeptide having the sequence SI.

An isolated EPHA5_Skipping_exon_4_#PEP_NUM_54 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-303 of EPHA5, a bridging amino acid G and a second amino acid sequence being at least about 90 % homologous to amino acids 357-1037 of EPHA5, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

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An isolated polypeptide of an edge portion of EPHA5_Skipping_exon_4 #PEP_NUM_54, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 293-303 of EPHA5, a bridging amino acid G and a second amino acid sequence being at least about 90 % homologous to amino acids 357-367 of EPHA5, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated EPHA5_Skipping_exon_5 #PEP_NUM_55 polypeptide, comprising a first amino acid sequence being at least 90 % homologous to amino acids 1-355 of EPHA5, bridged by T and a second amino acid sequence being at least 90 % homologous to amino acids 469-1037 of EPHA5, wherein said first amino acid is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of EPHA5_Skipping_exon_5 #PEP_NUM_55, comprising a first amino acid sequence being at least 90 % homologous to amino acids 345-355 of EPHA5, bridged by T and a second amino acid sequence being at least 90 % homologous to amino acids 469-479 of EPHA5, wherein said first amino acid is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of EPHA5_Skipping_exon_5 #PEP_NUM_55, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 345-355 of EPHA5, a bridging amino acid T and a second amino acid sequence being at least about 90 % homologous to amino acids 469-479 of EPHA5, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated EPHAS_Skipping_exon_8_#PEP_NUM_56 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-565 of EPHAS, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence IVAVGGLLPCALLPIQA (SEQ ID NO: 214), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of EPHAS_Skipping_exon_8_#PEP_NUM_56, comprising a polypeptide having the sequence IVAVGGLLPCALLPIQA (SEQ ID NO: 214).

An isolated EPHAS_Skippingexon_17_#PEP_NUM_60 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-951 of EPHAS, and a second amino acid sequence being at least about 90 % homologous to amino acids 1004-1037 of EPHAS, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of EPHAS_Skippingexon_17_#PEP_NUM_60, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 941-951 of EPHAS, and a second amino acid sequence being at least about 90 % homologous to amino acids 1004-1014 of EPHAS, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated EPHA7_Skippingexon_10_#PEP_NUM_61 polypeptide, consisting essentially of an amino acid sequence being at least about 90 % homologous to amino acids 1-599 of EPHA7.

An isolated EPHA7_Skippingexon_15_#PEP_NUM_62 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-844 of EPHA7, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence ANKPSSGSKHS (SEQ ID NO: 215), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

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An isolated polypeptide corresponding to a tail of EPHA7_Skippingexon_15 #PEP_NUM_62, comprising a polypeptide having the sequence ANKPSSGSKHS (SEQ ID NO: 215).

An isolated EPHB1_Skippingexon_10 #PEP_NUM_65 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-586 of EPHB1, and a second amino acid sequence being at least about 90 % homologous to amino acids 628-984 of EPHB1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of EPHB1_Skippingexon_10 #PEP_NUM_65, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 576-586 of EPHB1, and a second amino acid sequence being at least about 90 % homologous to amino acids 628-638 of EPHB1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated EPHB1_Skippingexon_6 #PEP_NUM_63 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-432 of EPHB1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GTG, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of EPHB1_Skippingexon_6 #PEP_NUM_63, comprising a polypeptide having the sequence GTG.

An isolated EPHB1_Skippingexon_8 #PEP_NUM_64 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-528 of EPHB1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GNGLIAKRLCTAISSSITAQAEGLSLEKCTRGV (SEQ ID NO: 216), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of EPHB1_Skippingexon_8 #PEP_NUM_64, comprising a polypeptide having the sequence GNGLIAKRLCTAISSSITAQAEGSLEKCTRGV (SEQ ID NO: 216).

An isolated ErbB2_Skippingexon_6 #PEP_NUM_76 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-214 of ErbB2, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence RLPPLQPQWHL (SEQ ID NO: 217), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of ErbB2_Skippingexon_6 #PEP_NUM_76, comprising a polypeptide having the sequence RLPPLQPQWHL (SEQ ID NO: 217).

An isolated ErbB3_Skippingexon_15 #PEP_NUM_78 polypeptide, consisting essentially of an amino acid sequence being at least about 90 % homologous to amino acids 1-468 of ErbB3, followed by V.

An isolated ErbB3_Skippingexon_18 #PEP_NUM_79 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-685 of ErbB3, and a second amino acid sequence being at least about 90 % homologous to amino acids 726-1342 of ErbB3, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of ErbB3_Skippingexon_18 #PEP_NUM_79, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 675-685 of ErbB3, and a second amino acid sequence being at least about 90 % homologous to amino acids 726-736 of ErbB3, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated ErbB3_Skippingexon_4 #PEP_NUM_77 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-140 of ErbB3, a bridging amino acid G and a second amino acid sequence being at least about 90 % homologous to amino acids 174-1342 of ErbB3, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino

acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of ErbB3_Skippingexon_4 #PEP_NUM_77, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 130-140 of ErbB3, a bridging amino acid G and a second amino acid sequence being at least about 90 % homologous to amino acids 174-184 of ErbB3, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated ErbB4_Skippingexon_14 #PEP_NUM_80 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-541 of ErbB4, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence VLTTVQSALILKMAQTVWKNVQMAYRGQTVSFSSMLIQIGSATHAIQTAPKG VTVPLVMTAFTHGRAIPLYHNMLELP (SEQ ID NO: 218), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of ErbB4_Skippingexon_14 #PEP_NUM_80, comprising a polypeptide having the sequence

VLTTVQSALILKMAQTVWKNVQMAYRGQTVSFSSMLIQIGSATHAIQTAPKG VTVPLVMTAFTHGRAIPLYHNMLELP (SEQ ID NO: 218).

An isolated ErbB4_Skippingexon_16 #PEP_NUM_81 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-624 of ErbB4, and a second amino acid sequence being at least about 90 % homologous to amino acids 650-1308 of ErbB4, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of ErbB4_Skippingexon_16 #PEP_NUM_81, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 614-624 of ErbB4, and a second

amino acid sequence being at least about 90 % homologous to amino acids 650-660 of ErbB4, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated FGF10_Skippingexon_2 #PEP_NUM_114 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-108 of FGF10, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence KRI, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of FGF10_Skippingexon_2 #PEP_NUM_114, comprising a polypeptide having the sequence KRI.

An isolated FGF11_Skipping_exon_2 #PEP_NUM_37 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-64 of FGF11, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 101-225 of FGF11, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of FGF11_Skipping_exon_2 #PEP_NUM_37, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 54-64 of FGF11, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 101-111 of FGF11, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated FGF12_Skipping_exon_2_Short_isoform #PEP_NUM_39 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-4 of FGF12_Short_isoform, a bridging amino acid A

and a second amino acid sequence being at least about 90 % homologous to amino acids 43-181 of FGF12_Short_isoform, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of FGF12_Skipping_exon_2_Short_isoform #PEP_NUM_39, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-4 of FGF12_Short_isoform, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 43-53 of FGF12_Short_isoform, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated FGF12_Skipping_exon_2_long_isoform #PEP_NUM_38 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-66 of FGF12_Long_isoform, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 105-243 of FGF12_Long_isoform, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of FGF12_Skipping_exon_2_long_isoform #PEP_NUM_38, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 56-66 of FGF12_Long_isoform, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 105-115 of FGF12_Long_isoform, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated FGF13_Skipping_exon_2_Long_isoform #PEP_NUM_40 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-62 of FGF13_Long_isoform, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 101-245 of FGF13_Long_isoform, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of FGF13_Skipping_exon_2_Long_isoform #PEP_NUM_40, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 52-62 of FGF13_Long_isoform, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 101-111 of FGF13_Long_isoform, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated FGF13_Skipping_exon_3_Long_isoform #PEP_NUM_41 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-99 of FGF13_Long_isoform, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence RTFHT, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of FGF13_Skipping_exon_3_Long_isoform #PEP_NUM_41, comprising a polypeptide having the sequence RTFHT.

An isolated FGF13_Skipping_exon_2_Short_isoform #PEP_NUM_40a polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-9 of FGF13_Short_isoform, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 48-192 of FGF13_Short_isoform, wherein said first amino acid sequence is

contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of FGF13_Skipping_exon_2_Short_isoform #PEP_NUM_40a, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-9 of FGF13_Short_isoform, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 48-58 of FGF13_Short_isoform, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated FGF13_Skipping_exon_3_Short_isoform #PEP_NUM_41a polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-46 of FGF13_Short_isoform, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence RTFHT (SEQ ID NO: 219), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of FGF13_Skipping_exon_3_Short_isoform #PEP_NUM_41a, comprising a polypeptide having the sequence RTFHT (SEQ ID NO: 219).

An isolated FGF18_Skippingexon_2 #PEP_NUM_115 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-12 of FGF18, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence WLPRRTWTSAASTWRTRRGLGTM (SEQ ID NO: 220), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of FGF18_Skippingexon_2 #PEP_NUM_115, comprising a polypeptide having the sequence WLPRRRTWTSAASTWRTRRGLGTM (SEQ ID NO: 220).

An isolated FGF18_Skippingexon_4 #PEP_NUM_116 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-84 of FGF18, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence RWHQQGVVWVHREGSGEQLHGPDVG (SEQ ID NO: 221), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of FGF18_Skippingexon_4 #PEP_NUM_116, comprising a polypeptide having the sequence RWHQQGVVWVHREGSGEQLHGPDVG (SEQ ID NO: 221).

An isolated FGF9_Skippingexon_2 #PEP_NUM_113 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-93 of FGF9, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence KTNPRVCIQRTVRRKLV (SEQ ID NO: 222), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of FGF9_Skippingexon_2 #PEP_NUM_113, comprising a polypeptide having the sequence KTNPRVCIQRTVRRKLV (SEQ ID NO: 222).

An isolated FSHR_Intron_7_retention #PEP_NUM_28 polypeptide, consisting essentially of an amino acid sequence being at least about 90 % homologous to amino acids 1-198 of FSHR.

An isolated FSHR_Skipping_exon_7 #PEP_NUM_26 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-174 of FSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 198-695 of FSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

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An isolated polypeptide of an edge portion of FSHR_Skipping_exon_7 #PEP_NUM_26, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 164-174 of FSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 198-208 of FSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated FSHR_Skipping_exon_8 #PEP_NUM_27 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-197 of FSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 223-695 of FSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of FSHR_Skipping_exon_8 #PEP_NUM_27, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 187-197 of FSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 223-233 of FSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated FSHR_with_Novel_exon_8A #PEP_NUM_29 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-223 of FSHR, an amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a bridging polypeptide having the sequence NRRTRTPTEPNVLLAKYPSGQGVLEEPESLSSSI (SEQ ID NO: 223), and a second amino acid sequence being at least about 90 % homologous to amino acids 224-695 of FSHR, wherein said first amino acid sequence is contiguous to said bridging polypeptide and said second amino acid sequence is contiguous to said bridging polypeptide, and wherein said first amino acid, said bridging polypeptide and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of FSHR_with_Novel_exon_8A #PEP_NUM_29, comprising an amino acid sequence of NRRTRTPTEPNVLLAKYPSGQGVLEEPESLSSSI (SEQ ID NO: 223).

An isolated GFRA1_Skippingexon_4_#PEP_NUM_107 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-111 of GFRA1, and a second amino acid sequence being at least about 90 % homologous to amino acids 140-465 of GFRA1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of GFRA1_Skippingexon_4_#PEP_NUM_107, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 101-111 of GFRA1, and a second amino acid sequence being at least about 90 % homologous to amino acids 140-150 of GFRA1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated GFRA2_Skippingexon_3_#PEP_NUM_108 polypeptide, consisting essentially of an amino acid sequence being at least about 90 % homologous to amino acids 1-60 of GFRA2.

An isolated HSFLT_Skipping_exon_19_#PEP_NUM_8 polypeptide, comprising a first amino acid sequence being at least 90 % homologous to amino acids 1-864 of HSFLT, and a second amino acid sequence being at least 90 % homologous to amino acids 903-1338 of HSFLT or a portion thereof, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of HSFLT_Skipping_exon_19_#PEP_NUM_8, comprising a first amino acid sequence being at least 90 % homologous to amino acids 854-864 of HSFLT or a portion thereof, and a second amino acid sequence being at least 90 % homologous to amino acids 903-913 of HSFLT or a portion thereof, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated Heparanase2_Skippingexon_10_#PEP_NUM_146 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-440 of Heparanase2, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence PQLRSWVHYTFYHQLASIKKENQAGWDSQRQAGSPVPAAALWAGGPKVQV SATEWPALSDGGRRDPPIEAPPSGRPDIGHPSSHGLLCGQECQCFGGLPLPIS

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YPHTHGYQWACWAASTPPLQ (SEQ ID NO: 224), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of Heparanase2_Skipping exon_10 #PEP_NUM_146, comprising a polypeptide having the sequence
PQLRSWVHYTFYHQLASIKKENQAGWDSQRQAGSPVPAAALWAGGPKVQV
SATEWPALSDDGGRDPPRIEAPPSGRPDIGHPSSHIGLLCGQECQCFGGLPLPIS
YPHTHGYQWACWAASTPPLQ (SEQ ID NO: 224).

An isolated Heparanase2_Skipping exon_11 #PEP_NUM_147 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-489 of Heparanase2, and a second amino acid sequence being at least about 90 % homologous to amino acids 538-592 of Heparanase2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of Heparanase2_Skipping exon_11 #PEP_NUM_147, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 479-489 of Heparanase2, and a second amino acid sequence being at least about 90 % homologous to amino acids 538-548 of Heparanase2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated Heparanase2_Skipping exon_5 #PEP_NUM_141 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-261 of Heparanase2, and a second amino acid sequence being at least about 90 % homologous to amino acids 395-396 of Heparanase2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of Heparanase2_Skipping exon_5 #PEP_NUM_141, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 251-261 of Heparanase2, and a second amino acid sequence being at least about 90 % homologous to amino acids 395-396 of Heparanase2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated Heparanase2_Skipping exon_6 #PEP_NUM_142 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-319 of Heparanase2, and a second amino acid sequence being at least

about 90 % homologous to amino acids 335-592 of Heparanase2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of Heparanase2_Skippingexon_6 #PEP_NUM_142, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 309-319 of Heparanase2, and a second amino acid sequence being at least about 90 % homologous to amino acids 335-345 of Heparanase2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated Heparanase2_Skippingexon_7 #PEP_NUM_143 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-334 of Heparanase2, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence QWLIHTLQERRFGLKVV (SEQ ID NO: 225), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of Heparanase2_Skippingexon_7 #PEP_NUM_143, comprising a polypeptide having the sequence QWLIHTLQERRFGLKVV (SEQ ID NO: 225).

An isolated Heparanase2_Skippingexon_8 #PEP_NUM_144 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-366 of Heparanase2, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence MVEHFRIAGQSGH (SEQ ID NO: 226), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of Heparanase2_Skippingexon_8 #PEP_NUM_144, comprising a polypeptide having the sequence MVEHFRIAGQSGH (SEQ ID NO: 226).

An isolated Heparanase2_Skippingexon_9 #PEP_NUM_145 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-401 of Heparanase2, and a second amino acid sequence being at least

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about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence TTGSLSSSTA (SEQ ID NO: 227), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of Heparanase2_Skippingexon_9 #PEP_NUM_145, comprising a polypeptide having the sequence TTGSLSSSTA (SEQ ID NO: 227).

An isolated Heparanase_Skipping_exon_10 #PEP_NUM_140 polypeptide, comprising a first amino acid sequence being at least 90 % homologous to amino acids 1-364 of Heparanase, and a second amino acid sequence being at least 70%, optionally at least 80%, preferably at least 85%, more preferably at least 90% and most preferably at least 95% homologous to a polypeptide having the sequence IIGYLFCRSRNWWAPRC, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of Heparanase_Skipping_exon_10 #PEP_NUM_140, comprising a polypeptide having the sequence IIGYLFCRSRNWWAPRC.

An isolated IGFBP4_Skippingexon_3 #PEP_NUM_111 polypeptide, comprising a first amino acid sequence being at least 90 % homologous to amino acids 1-169 of IGFBP4, and a second amino acid sequence being at least 90 % homologous to amino acids 215-258 of IGFBP4 or a portion thereof, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of IGFBP4_Skippingexon_3 #PEP_NUM_111, comprising a first amino acid sequence being at least 90 % homologous to amino acids 159-169 of IGFBP4 or a portion thereof, and a second amino acid sequence being at least 90 % homologous to amino acids 215-225 of IGFBP4 or a portion thereof, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated IL16_Long_Skippingexon_18 #PEP_NUM_110 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1060 of IL16, and a second amino acid sequence being at least about 90 % homologous to amino acids 1095-1244 of IL16, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of IL16_Long_Skippingexon_18_#PEP_NUM_110, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1050-1060 of IL16, and a second amino acid sequence being at least about 90 % homologous to amino acids 1095-1105 of IL16, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated IL16_Long_Skippingexon_5_#PEP_NUM_109 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-103 of IL16, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence VLPIAQEKLIFQ (SEQ ID NO: 228), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of IL16_Long_Skippingexon_5_#PEP_NUM_109, comprising a polypeptide having the sequence VLPIAQEKLIFQ (SEQ ID NO: 228).

An isolated IL18R_Skippingexon_9_#PEP_NUM_164 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-370 of IL18R, and a second amino acid sequence being at least about 90 % homologous to amino acids 424-541 of IL18R, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of IL18R_Skippingexon_9_#PEP_NUM_164, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 360-370 of IL18R, and a second amino acid sequence being at least about 90 % homologous to amino acids 424-434 of IL18R, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated IL1RAPL1_Skippingexon_4_#PEP_NUM_170 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-122 of IL1RAPL1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence AGQKHGGQVLYSKEILCL (SEQ ID NO: 229),

wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of IL1RAPL1_Skippingexon_4 #PEP_NUM_170, comprising a polypeptide having the sequence AGQKHGGQVLYSKEILCL (SEQ ID NO: 229).

An isolated IL1RAPL1_Skippingexon_5 #PEP_NUM_171 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-183 of IL1RAPL1, and a second amino acid sequence being at least about 90 % homologous to amino acids 236-237 of IL1RAPL1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of IL1RAPL1_Skippingexon_5 #PEP_NUM_171, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 173-183 of IL1RAPL1, and a second amino acid sequence being at least about 90 % homologous to amino acids 236-246 of IL1RAPL1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated IL1RAPL1_Skippingexon_6 #PEP_NUM_172 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-234 of IL1RAPL1, and a second amino acid sequence being at least about 90 % homologous to amino acids 260-696 of IL1RAPL1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of IL1RAPL1_Skippingexon_6 #PEP_NUM_172, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 224-234 of IL1RAPL1, and a second amino acid sequence being at least about 90 % homologous to amino acids 260-270 of IL1RAPL1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated IL1RAPL1_Skippingexon_7 #PEP_NUM_173 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-259 of IL1RAPL1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence EFLRSILGNRKFPSH (SEQ ID NO: 230), wherein

said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of IL1RAPL1_Skippingexon_7 #PEP_NUM_173, comprising a polypeptide having the sequence EFLRSILGNRKFPSH (SEQ ID NO: 230).

An isolated IL1RAPL1_Skippingexon_8 #PEP_NUM_174 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-304 of IL1RAPL1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence ANVHSGTCCRCCYSCCLYVW (SEQ ID NO: 231), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of IL1RAPL1_Skippingexon_8 #PEP_NUM_174, comprising a polypeptide having the sequence ANVHSGTCCRCCYSCCLYVW. (SEQ ID NO: 231).

An isolated IL1RAPL2_Skippingexon_4 #PEP_NUM_175 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-120 of IL1RAPL2, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence ASQKCGEA (SEQ ID NO: 232), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of IL1RAPL2_Skippingexon_4 #PEP_NUM_175, comprising a polypeptide having the sequence ASQKCGEA (SEQ ID NO: 232).

An isolated IL1RAPL2_Skippingexon_5 #PEP_NUM_176 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-181 of IL1RAPL2, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence LYSQTSLPSHCSPWRISQVL (SEQ ID NO: 233),

wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of IL1RAPL2_Skippingexon_5 #PEP_NUM_176, comprising a polypeptide having the sequence LYSQTSLPSHCSPWRISQVL (SEQ ID NO: 233).

An isolated IL1RAPL2_Skippingexon_6 #PEP_NUM_177 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-232 of IL1RAPL2, and a second amino acid sequence being at least about 90 % homologous to amino acids 258-686 of IL1RAPL2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of IL1RAPL2_Skippingexon_6 #PEP_NUM_177, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 222-232 of IL1RAPL2, and a second amino acid sequence being at least about 90 % homologous to amino acids 258-268 of IL1RAPL2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated IL1RAPL2_Skippingexon_7 #PEP_NUM_178 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-258 of IL1RAPL2, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence FSKSILEKKKLNWHSSLTQLWKLTWRIIPAMLKTEMDGNMPVFCCVKRI (SEQ ID NO: 234), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of IL1RAPL2_Skippingexon_7 #PEP_NUM_178, comprising a polypeptide having the sequence FSKSILEKKKLNWHSSLTQLWKLTWRIIPAMLKTEMDGNMPVFCCVKRI

(SEQ ID NO: 234).

An isolated IL1RAPL2_Skippingexon_8 #PEP_NUM_179 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-301 of IL1RAPL2, and a second amino acid sequence being at least

about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence FNL, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of IL1RAPL2_Skippingexon_8 #PEP_NUM_179, comprising a polypeptide having the sequence FNL.

An isolated IL1RAP_Skippingexon_11 #PEP_NUM_169 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-400 of IL1RAP, a bridging amino acid V and a second amino acid sequence being at least about 90 % homologous to amino acids 450-570 of IL1RAP, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of IL1RAP_Skippingexon_11 #PEP_NUM_169, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 390-400 of IL1RAP, a bridging amino acid V and a second amino acid sequence being at least about 90 % homologous to amino acids 450-460 of IL1RAP, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated ITAV_Skipping_exon_11 #PEP_NUM_14 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-301 of ITAV, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence LCRCVYWSTSLHGSWL (SEQ ID NO: 235), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

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An isolated polypeptide corresponding to a tail of ITAV_Skipping_exon_11 #PEP_NUM_14, comprising a polypeptide having the sequence LCRCVYWSTSLHGSWL (SEQ ID NO: 235).

An isolated ITAV_Skipping_exon_20 #PEP_NUM_15 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-641 of ITAV, and a second amino acid sequence being at least about 90 % homologous to amino acids 1025-1026 of ITAV, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of ITAV_Skipping_exon_20 #PEP_NUM_15, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 631-641 of ITAV, and a second amino acid sequence being at least about 90 % homologous to amino acids 1025-1026 of ITAV, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated ITAV_Skipping_exon_21 #PEP_NUM_16 polypeptide, comprising a first amino acid sequence being at least 90 % homologous to amino acids 1-691 of ITAV, and a second amino acid sequence being at least 90 % homologous to amino acids 723-1048 of ITAV or a portion thereof, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of ITAV_Skipping_exon_21 #PEP_NUM_16, comprising a first amino acid sequence being at least 90 % homologous to amino acids 681-691 of ITAV or a portion thereof, and a second amino acid sequence being at least 90 % homologous to amino acids 723-733 of ITAV or a portion thereof, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated ITAV_Skipping_exon_25 #PEP_NUM_17 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-811 of ITAV, and a second amino acid sequence being at least about 90 % homologous to amino acids 865-1048 of ITAV, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of ITAV_Skipping_exon_25 #PEP_NUM_17, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 801-811 of ITAV, and a second

amino acid sequence being at least about 90 % homologous to amino acids 865-875 of ITAV, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated ITGA2B_Skippingexon_3 #PEP_NUM_135 polypeptide, comprising a first amino acid sequence being at least 90 % homologous to amino acids 1-104 of ITGA2B, and a second amino acid sequence being at least 70%, optionally at least 80%, preferably at least 85%, more preferably at least 90% and most preferably at least 95% homologous to a polypeptide having the sequence LRPLAALERPRKD, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of ITGA2B_Skippingexon_3 #PEP_NUM_135, comprising a polypeptide having the sequence LRPLAALERPRKD.

An isolated JAG1_Skippingexon_10 #PEP_NUM_96 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-412 of JAG1, and a second amino acid sequence being at least about 90 % homologous to amino acids 451-1218 of JAG1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of JAG1_Skippingexon_10 #PEP_NUM_96, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 402-412 of JAG1, and a second amino acid sequence being at least about 90 % homologous to amino acids 451-461 of JAG1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated JAG1_Skippingexon_12 #PEP_NUM_97 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-465 of JAG1, and a second amino acid sequence being at least about 90 % homologous to amino acids 524-1218 of JAG1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of JAG1_Skippingexon_12 #PEP_NUM_97, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 455-465 of JAG1, and a second amino acid sequence being at least about 90 % homologous to amino acids 524-534

of JAG1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated JAG1_Skippingexon_18_#PEP_NUM_98 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-742 of JAG1, a bridging amino acid D and a second amino acid sequence being at least about 90 % homologous to amino acids 783-1218 of JAG1, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of JAG1_Skippingexon_18_#PEP_NUM_98, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 732-742 of JAG1, a bridging amino acid D and a second amino acid sequence being at least about 90 % homologous to amino acids 783-793 of JAG1, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated JAG1_Skippingexon_22_#PEP_NUM_99 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-857 of JAG1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GLVPSILPAPQRAQRVPQRAELHPHPGRPVLRPPLHWCGRVSVFQSPAGEDK VHL (SEQ ID NO: 236), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of JAG1_Skippingexon_22_#PEP_NUM_99, comprising a polypeptide having the sequence

GLVPSILPAPQRAQRVPQRAELHPHPGRPVLRPPLHWCGRVSVFQSPAGEDK VHL (SEQ ID NO: 236).

An isolated KDR_Skipping_exon_16_#PEP_NUM_9 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-756 of KDR, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence QWRGTEDRLLVHRHGSR (SEQ ID NO: 237), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of KDR_Skipping_exon_16_#PEP_NUM_9, comprising a polypeptide having the sequence QWRGTEDRLLVHRHGSR (SEQ ID NO: 237).

An isolated KDR_Skipping_exon_17_#PEP_NUM_10 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-791 of KDR, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence VSLLAVVPLAK (SEQ ID NO: 238), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of KDR_Skipping_exon_17_#PEP_NUM_10, comprising a polypeptide having the sequence VSLLAVVPLAK (SEQ ID NO: 238).

An isolated KDR_Skipping_exon_27_#PEP_NUM_11 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1171 of KDR, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence SVSAEQ (SEQ ID NO: 239), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of KDR_Skipping_exon_27_#PEP_NUM_11, comprising a polypeptide having the sequence SVSAEQ (SEQ ID NO: 239).

An isolated KDR_Skipping_exon_28_#PEP_NUM_12 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1220 of KDR, and a second amino acid sequence being at least about

70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence RTTRRTVVWFLPQKS (SEQ ID NO: 240), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of KDR_Skipping_exon_28 #PEP_NUM_12, comprising a polypeptide having the sequence RTTRRTVVWFLPQKS (SEQ ID NO: 240).

An isolated KDR_Skipping_exon_29 #PEP_NUM_13 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1254 of KDR, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence WNGAQQQKQGVCGI (SEQ ID NO: 241), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of KDR_Skipping_exon_29 #PEP_NUM_13, comprising a polypeptide having the sequence WNGAQQQKQGVCGI (SEQ ID NO: 241).

An isolated KITLG_Skippingexon_8 #PEP_NUM_73 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-238 of KITLG, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence YVARERERVSRSVIVACINTVTFVHWLVTVHVCFINEAALNKFIFCLE (SEQ ID NO: 242), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of KITLG_Skippingexon_8 #PEP_NUM_73, comprising a polypeptide having the sequence YVARERERVSRSVIVACINTVTFVHWLVTVHVCFINEAALNKFIFCLE (SEQ ID NO: 242).

An isolated KIT_Skippingexon_14 #PEP_NUM_75 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-

663 of KIT, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence AAIVLNSTWT (SEQ ID NO: 243), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of KIT_Skippingexon_14 #PEP_NUM_75, comprising a polypeptide having the sequence AAIVLNSTWT (SEQ ID NO: 243).

An isolated KIT_Skippingexon_8 #PEP_NUM_74 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-410 of KIT, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence NALLLYCQWMCRH (SEQ ID NO: 244), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of KIT_Skippingexon_8 #PEP_NUM_74, comprising a polypeptide having the sequence NALLLYCQWMCRH (SEQ ID NO: 244).

An isolated LSHR_Intron_5_retention #PEP_NUM_36 polypeptide, consisting essentially of an amino acid sequence being at least about 90 % homologous to amino acids 1-153 of LSHR.

An isolated LSHR_Skipping_exon_10 #PEP_NUM_35 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-289 of LSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 317-699 of LSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of LSHR_Skipping_exon_10 #PEP_NUM_35, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 279-289 of LSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 317-327 of LSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated LSHR_Skipping_exon_2 #PEP_NUM_30 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-54 of LSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 79-699 of LSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of LSHR_Skipping_exon_2 #PEP_NUM_30, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 44-54 of LSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 79-89 of LSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated LSHR_Skipping_exon_3 #PEP_NUM_31 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-78 of LSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 101-699 of LSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of LSHR_Skipping_exon_3 #PEP_NUM_31, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 68-78 of LSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 101-111 of LSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated LSHR_Skipping_exon_5 #PEP_NUM_32 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-128 of LSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 151-699 of LSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of LSHR_Skipping_exon_5 #PEP_NUM_32, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 118-128 of LSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 151-161 of LSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated LSHR_Skipping_exon_6 #PEP_NUM_33 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-152 of LSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 179-699 of LSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of LSHR_Skipping_exon_6 #PEP_NUM_33, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 142-152 of LSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 179-189 of LSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated LSHR_Skipping_exon_7 #PEP_NUM_34 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-179 of LSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 201-699 of LSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of LSHR_Skipping_exon_7 #PEP_NUM_34, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 169-179 of LSHR, and a second amino acid sequence being at least about 90 % homologous to amino acids 201-211 of LSHR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated M17S2_Skippingexon_14 #PEP_NUM_189 polypeptide, consisting essentially of an amino acid sequence being at least about 90 % homologous to amino acids 1-558 of M17S2, followed by M.

An isolated M17S2_Skippingexon_15 #PEP_NUM_190 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-583 of M17S2, and a second amino acid sequence being at least about 90 % homologous to amino acids 621-966 of M17S2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of M17S2_Skippingexon_15 #PEP_NUM_190, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 573-583 of M17S2, and a

second amino acid sequence being at least about 90 % homologous to amino acids 621-631 of M17S2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated M17S2_Skippingexon_20_#PEP_NUM_191 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-873 of M17S2, and a second amino acid sequence being at least about 90 % homologous to amino acids 963-964 of M17S2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of M17S2_Skippingexon_20_#PEP_NUM_191, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 863-873 of M17S2, and a second amino acid sequence being at least about 90 % homologous to amino acids 963-964 of M17S2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated MET_Skipping_exon_12_#PEP_NUM_18 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-861 of MET, and a second amino acid sequence being at least about 90 % homologous to amino acids 911-1390 of MET, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of MET_Skipping_exon_12_#PEP_NUM_18, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 851-861 of MET, and a second amino acid sequence being at least about 90 % homologous to amino acids 911-921 of MET, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated MET_Skipping_exon_14_#PEP_NUM_19 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-962 of MET, and a second amino acid sequence being at least about 90 % homologous to amino acids 1010-1390 of MET, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of MET_Skipping_exon_14_#PEP_NUM_19, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 952-962 of MET, and a second

amino acid sequence being at least about 90 % homologous to amino acids 1010-1020 of MET, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated MET_Skipping_exon_18_#PEP_NUM_20 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1174 of MET, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence AG, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of MET_Skipping_exon_18_#PEP_NUM_20, comprising a polypeptide having the sequence AG.

An isolated MME_Skippingexon_11_#PEP_NUM_153 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-318 of MME, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence
RSSKFNVLEIHNGSCKQPQPNLQGVQKCFPQGPLWYNLRNSNLETLCQW
EYGKCCGEALCGSSICWRE (SEQ ID NO: 245), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of MME_Skippingexon_11_#PEP_NUM_153, comprising a polypeptide having the sequence
RSSKFNVLEIHNGSCKQPQPNLQGVQKCFPQGPLWYNLRNSNLETLCQW
EYGKCCGEALCGSSICWRE (SEQ ID NO: 245).

An isolated MME_Skippingexon_12_#PEP_NUM_154 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-364 of MME, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence

PFMVQPQKQQQLGDDVVQTMSMGIWKMLWGGFMWKQHLLERVNMWSRI
(SEQ ID NO: 246), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of MME_Skipping exon_12_#PEP_NUM_154, comprising a polypeptide having the sequence

PFMVQPQKQQQLGDDVVQTMSMGIWKMLWGGFMWKQHLLERVNMWSRI
(SEQ ID NO: 246).

An isolated MME_Skipping exon_16_#PEP_NUM_155 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-498 of MME, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence VDKWSSCSQCILLFRKKSDSLPSRHSAAPELL (SEQ ID NO: 247), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of MME_Skipping exon_16_#PEP_NUM_155, comprising a polypeptide having the sequence VDKWSSCSQCILLFRKKSDSLPSRHSAAPELL (SEQ ID NO: 247).

An isolated MME_Skipping exon_4_#PEP_NUM_150 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-64 of MME, and a second amino acid sequence being at least about 90 % homologous to amino acids 119-749 of MME, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of MME_Skipping exon_4_#PEP_NUM_150, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 54-64 of MME, and a second amino acid sequence being at least about 90 % homologous to amino acids 119-129 of MME, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated MME_Skipping exon_7_#PEP_NUM_151 polypeptide, consisting essentially of an amino acid sequence being at least about 90 % homologous to amino acids 1-177 of MME, followed by D.

An isolated MME_Skippingexon_9 #PEP_NUM_152 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-239 of MME, and a second amino acid sequence being at least about 90 % homologous to amino acids 285-749 of MME, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of MME_Skippingexon_9 #PEP_NUM_152, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 229-239 of MME, and a second amino acid sequence being at least about 90 % homologous to amino acids 285-295 of MME, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated MPL_Skippingexon_2 #PEP_NUM_136 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-26 of MPL, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GRSPVLAP (SEQ ID NO: 248), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of MPL_Skippingexon_2 #PEP_NUM_136, comprising a polypeptide having the sequence GRSPVLAP (SEQ ID NO: 248).

An isolated NOTCH2_Skipping_exon_12 #PEP_NUM_101 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-638 of NOTCH2, and a second amino acid sequence being at least about 90 % homologous to amino acids 676-2471 of NOTCH2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of NOTCH2_Skipping_exon_12 #PEP_NUM_101, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 628-638 of NOTCH2, and a second amino acid sequence being at least about 90 % homologous to amino acids 676-686 of NOTCH2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

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An isolated NOTCH2_Skippingexon_9 #PEP_NUM_100 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-483 of NOTCH2, and a second amino acid sequence being at least about 90 % homologous to amino acids 522-2471 of NOTCH2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of NOTCH2_Skippingexon_9 #PEP_NUM_100, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 473-483 of NOTCH2, and a second amino acid sequence being at least about 90 % homologous to amino acids 522-532 of NOTCH2, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated NOTCH3_Skippingexon_2 #PEP_NUM_102 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-39 of NOTCH3, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GARLAGWVSGVSWRTPVTQAPVLAVVSARVQWWLAPPDSHAGAPVASEAL TAPCQIPASAALVPTVPAAQWGPMDASSAPAHLATRAAAAATWMSAGWV SPAAMVAPASTHLAPSAASVQLATQGHYVRTPRCPVPHHAVTGANAGRVA TSLTTVPVFLGLRVRIVK (SEQ ID NO: 249), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of NOTCH3_Skippingexon_2 #PEP_NUM_102, comprising a polypeptide having the sequence

GARLAGWVSGVSWRTPVTQAPVLAVVSARVQWWLAPPDSHAGAPVASEAL TAPCQIPASAALVPTVPAAQWGPMDASSAPAHLATRAAAAATWMSAGWV SPAAMVAPASTHLAPSAASVQLATQGHYVRTPRCPVPHHAVTGANAGRVA TSLTTVPVFLGLRVRIVK (SEQ ID NO: 249).

An isolated NOTCH4_Skipping_exon_8 #PEP_NUM_103 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-438 of NOTCH4, and a second amino acid sequence being at least

about 90 % homologous to amino acids 504-2003 of NOTCH4, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of NOTCH4_Skipping_exon_8_#PEP_NUM_103, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 428-438 of NOTCH4, and a second amino acid sequence being at least about 90 % homologous to amino acids 504-514 of NOTCH4, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated NRG1_HGR-ALPHA_skippingexon_5_#PEP_NUM_82 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-150 of NRG1-HRG-ALPHA, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-640 of NRG1-HRG-ALPHA, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of NRG1_HGR-ALPHA_skippingexon_5_#PEP_NUM_82, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 140-150 of NRG1-HRG-ALPHA, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-179 of NRG1-HRG-ALPHA, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated NRG1_HGR-ALPHA_skippingexon_7_#PEP_NUM_83 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-211 of NRG1-HRG-ALPHA, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GGGAVPEESADHNRHLHRPPCGRHHVCGGLLQNQETAKEAA (SEQ ID NO:

250), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of NRG1_HGR-ALPHA_skipping exon_7 #PEP_NUM_83, comprising a polypeptide having the sequence GGGAVPEESADHNRHLHRPPCGRHHVCGGLLQNQETAKAA (SEQ ID NO: 250).

An isolated NRG1_HGR-BETA1_skipping exon_5 #PEP_NUM_84 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-150 of NRG1-HRG-BETA1, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-645 of NRG1-HRG-BETA1, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of NRG1_HGR-BETA1_skipping exon_5 #PEP_NUM_84, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 140-150 of NRG1-HRG-BETA1, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-179 of NRG1-HRG-BETA1, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated NRG1_HGR-BETA1_skipping exon_7 #PEP_NUM_85 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-211 of NRG1-HRG-BETA1 NRG1-HRG-BETA2 NRG1-HRG-BETA3, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence
GGGAVPEESADHNRHLHRPPCGRHHVCGGLLQNQETAKAA (SEQ ID NO:

251), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of NRG1_HGR-BETA1_skipping exon_7 #PEP_NUM_85, comprising a polypeptide having the sequence GGGAVPEESADHNRHLHRPPCGRHHVCGGLLQNQETAKEAA (SEQ ID NO: 251).

An isolated NRG1_HGR-BETA1_skipping exon_8 #PEP_NUM_86 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-231 of NRG1-HRG-BETA1, and a second amino acid sequence being at least about 90 % homologous to amino acids 240-645 of NRG1-HRG-BETA1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of NRG1_HGR-BETA1_skipping exon_8 #PEP_NUM_86, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 221-231 of NRG1-HRG-BETA1, and a second amino acid sequence being at least about 90 % homologous to amino acids 240-250 of NRG1-HRG-BETA1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated NRG1_HGR-BETA1_skipping exon_9 #PEP_NUM_87 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-230 of NRG1-HRG-BETA1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence RNSGKSCMTVFGRAFGLNETI (SEQ ID NO: 252), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of NRG1_HGR-BETA1_skipping exon_9 #PEP_NUM_87, comprising a polypeptide having the sequence RNSGKSCMTVFGRAFGLNETI (SEQ ID NO: 252).

An isolated NRG1_HGR-BETA2_skipping exon_5 #PEP_NUM_88 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-150 of NRG1_HRG-BETA2, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino

acids 169-636 of NRG1-HRG-BETA2, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of NRG1_HGR-BETA2_skippingexon_5 #PEP_NUM_88, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 140-150 of NRG1-HRG-BETA2, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-179 of NRG1-HRG-BETA2, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated NRG1_HGR-BETA2_skippingexon_8 #PEP_NUM_89 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-230 of NRG1-HRG-BETA2 NRG1-HRG-BETA3, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence RNSGKSCMTVFGRAFGLNETI (SEQ ID NO: 253), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of NRG1_HGR-BETA2_skippingexon_8 #PEP_NUM_89, comprising a polypeptide having the sequence RNSGKSCMTVFGRAFGLNETI (SEQ ID NO: 253).

An isolated NRG1_HGR-BETA3_skippingexon_5 #PEP_NUM_90 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-150 of NRG1-HRG-BETA3, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-241 of NRG1-HRG-BETA3, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence,

said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of NRG1_HGR-BETA3_skippingexon_5_#PEP_NUM_90, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 140-150 of NRG1-HRG-BETA3, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-179 of NRG1-HRG-BETA3, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated NRG1_HGR-GAMMA_skippingexon_5_#PEP_NUM_91 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-150 of NRG1-HRG-GAMMA, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-211 of NRG1-HRG-GAMMA, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of NRG1_HGR-GAMMA_skippingexon_5_#PEP_NUM_91, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 140-150 of NRG1-HRG-GAMMA, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-179 of NRG1-HRG-GAMMA, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated NRG1_HGR-GGF_skippingexon_5_#PEP_NUM_92 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-150 of NRG1-HRG-GGF, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-241 of

NRG1-HRG-GGF, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of NRG1_HGR-GGF_skipping exon_5 #PEP_NUM_92, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 140-150 of NRG1-HRG-GGF, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-179 of NRG1-HRG-GGF, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated NRG1_NDF43_skipping exon_12 #PEP_NUM_95 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-423 of NRG1-NDF43, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence YVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPNSMAVSPFMEEER PLLLVTPPRLREKKFDHHPQQFSSFHNPAAHDSNSLPASPLRIVEDEEYETTQE YEPAQEPVK (SEQ ID NO: 254), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of NRG1_NDF43_skipping exon_12 #PEP_NUM_95, comprising a polypeptide having the sequence YVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPNSMAVSPFMEEER PLLLVTPPRLREKKFDHHPQQFSSFHNPAAHDSNSLPASPLRIVEDEEYETTQE YEPAQEPVK (SEQ ID NO: 254).

An isolated NRG1_NDF43_skipping exon_5 #PEP_NUM_93 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-150 of NRG1-NDF43, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-462 of

NRG1-NDF43, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of NRG1_NDF43_skippingexon_5 #PEP_NUM_93, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 140-150 of NRG1-NDF43, a bridging amino acid A and a second amino acid sequence being at least about 90 % homologous to amino acids 169-179 of NRG1-NDF43, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated NRG1_NDF43_skippingexon_7 #PEP_NUM_94 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-211 of NRG1-NDF43, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GGGAVPEESADHNRHLHRPPCGRHHVCGLLQNQETAKEAA (SEQ ID NO: 255), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of NRG1_NDF43_skippingexon_7 #PEP_NUM_94, comprising a polypeptide having the sequence GGGAVPEESADHNRHLHRPPCGRHHVCGLLQNQETAKEAA (SEQ ID NO: 255).

An isolated NRP1_Skippingexon_5 #PEP_NUM_112 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-219 of NRP1, and a second amino acid sequence being at least about 90 % homologous to amino acids 272-923 of NRP1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of NRP1_Skippingexon_5 #PEP_NUM_112, comprising a first amino acid sequence

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being at least about 90 % homologous to amino acids 209-219 of NRP1, and a second amino acid sequence being at least about 90 % homologous to amino acids 272-282 of NRP1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated NTRK2_Skipping exon_14_#PEP_NUM_104 polypeptide, consisting essentially of an amino acid sequence being at least about 90 % homologous to amino acids 1-240 of NTRK2.

An isolated NTRK3_Skipping exon_16_#PEP_NUM_106 polypeptide, comprising a first amino acid sequence being at least 90 % homologous to amino acids 1-630 of NTRK3, and a second amino acid sequence being at least 70%, optionally at least 80%, preferably at least 85%, more preferably at least 90% and most preferably at least 95% homologous to a polypeptide having the sequence WEDTPCSPFAGCLLKASCTGSSLQRVMYGASG, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of NTRK3_Skipping exon_16_#PEP_NUM_106, comprising a polypeptide having the sequence WEDTPCSPFAGCLLKASCTGSSLQRVMYGASG.

An isolated NTRK3_Skipping exon_5_#PEP_NUM_105 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-131 of NTRK3, and a second amino acid sequence being at least about 90 % homologous to amino acids 156-839 of NTRK3, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of NTRK3_Skipping exon_5_#PEP_NUM_105, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 121-131 of NTRK3, and a second amino acid sequence being at least about 90 % homologous to amino acids 156-166 of NTRK3, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated PROS1_Skipping exon_3_#PEP_NUM_185 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-78 of PROS1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide

having the sequence FVFALFKLGYSLHVSQMLILT (SEQ ID NO: 256), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of PROS1_Skipping exon_3 #PEP_NUM_185, comprising a polypeptide having the sequence FVFALFKLGYSLHVSQMLILT (SEQ ID NO: 256).

An isolated PTPRB_Skipping exon_26 #PEP_NUM_72 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1738 of PTPRB, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence WQQLQKRIHCHSGTASWHQG (SEQ ID NO: 257), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of PTPRB_Skipping exon_26 #PEP_NUM_72, comprising a polypeptide having the sequence WQQLQKRIHCHSGTASWHQG (SEQ ID NO: 257).

An isolated PTPRZ1_Skipping exon_11 #PEP_NUM_67 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-413 of PTPRZ1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GGGRGKRH (SEQ ID NO: 258), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of PTPRZ1_Skipping exon_11 #PEP_NUM_67, comprising a polypeptide having the sequence GGGRGKRH (SEQ ID NO: 258).

An isolated PTPRZ1_Skipping exon_13 #PEP_NUM_68 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1613 of PTPRZ1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a

polypeptide having the sequence GNASRLHTFT (SEQ ID NO: 258), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of PTPRZ1_Skippingexon_13 #PEP_NUM_68, comprising a polypeptide having the sequence GNASRLHTFT (SEQ ID NO: 259).

An isolated PTPRZ1_Skippingexon_15 #PEP_NUM_69 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1693 of PTPRZ1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence TEEVLPGRLYYDEQLQPPEQQAQESIHKYRCL (SEQ ID NO: 260), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of PTPRZ1_Skippingexon_15 #PEP_NUM_69, comprising a polypeptide having the sequence TEEVLPGRLYYDEQLQPPEQQAQESIHKYRCL (SEQ ID NO: 260).

An isolated PTPRZ1_Skippingexon_16 #PEP_NUM_70 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1721 of PTPRZ1, and a second amino acid sequence being at least about 90 % homologous to amino acids 1729-2314 of PTPRZ1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of PTPRZ1_Skippingexon_16 #PEP_NUM_70, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1711-1721 of PTPRZ1, and a second amino acid sequence being at least about 90 % homologous to amino acids 1729-1739 of PTPRZ1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated PTPRZ1_Skippingexon_22 #PEP_NUM_71 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1932 of PTPRZ1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a

polypeptide having the sequence RSNMSSFMIHWLRPYLVKKLRCWTVIFMPMLMHSSFLDQQAKQ (SEQ ID NO: 261), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of PTPRZ1_Skipping exon_22 #PEP_NUM_71, comprising a polypeptide having the sequence RSNMSSFMIHWLRPYLVKKLRCWTVIFMPMLMHSSFLDQQAKQ (SEQ ID NO: 261).

An isolated PTPRZ1_Skipping exon_7 #PEP_NUM_66 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-206 of PTPRZ1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence VGCFCVELTCNNLVMSC (SEQ ID NO: 262), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of PTPRZ1_Skipping exon_7 #PEP_NUM_66, comprising a polypeptide having the sequence VGCFCVELTCNNLVMSC (SEQ ID NO: 262).

An isolated RSU1_Skipping exon_6 #PEP_NUM_163 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-134 of RSU1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence QP, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of RSU1_Skipping exon_6 #PEP_NUM_163, comprising a polypeptide having the sequence QP.

An isolated SCTR_Skipping exon_10 #PEP_NUM_162 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-307 of SCTR, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide

having the sequence APGQVHSPADPPLWHPLHRLRLLPRGRYGDPAVF (SEQ ID NO: 263), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of SCTR_Skipping exon_10 #PEP_NUM_162, comprising a polypeptide having the sequence APGQVHSPADPPLWHPLHRLRLLPRGRYGDPAVF (SEQ ID NO: 263).

An isolated TGFB2_Skipping exon_5 #PEP_NUM_165 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-251 of TGFB2, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence EMCRIIAAYVHFTLISRGI (SEQ ID NO: 264), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of TGFB2_Skipping exon_5 #PEP_NUM_165, comprising a polypeptide having the sequence EMCRIIAAYVHFTLISRGI (SEQ ID NO: 264).

An isolated THBS1_Skipping exon_12 #PEP_NUM_183 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-591 of THBS1, and a second amino acid sequence being at least about 90 % homologous to amino acids 643-1170 of THBS1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of THBS1_Skipping exon_12 #PEP_NUM_183, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 581-591 of THBS1, and a second amino acid sequence being at least about 90 % homologous to amino acids 643-653 of THBS1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated THBS1_Skipping exon_4 #PEP_NUM_180 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-209 of THBS1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide

having the sequence LPVSSSPLTTTW (SEQ ID NO: 265), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of THBS1_Skipping exon_4 #PEP_NUM_180, comprising a polypeptide having the sequence LPVSSSPLTTTW (SEQ ID NO: 265).

An isolated THBS1_Skipping exon_7 #PEP_NUM_181 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-342 of THBS1, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence PATLRTMAGLHGPGPPVLRNAVAMEFSSAAAPAIASTTDVRAPRSRHGPAIFR SVTRDLNRMVAGATGPRGHLVL (SEQ ID NO: 266), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of THBS1_Skipping exon_7 #PEP_NUM_181, comprising a polypeptide having the sequence PATLRTMAGLHGPGPPVLRNAVAMEFSSAAAPAIASTTDVRAPRSRHGPAIFR SVTRDLNRMVAGATGPRGHLVL (SEQ ID NO: 266).

An isolated THBS1_Skipping exon_9 #PEP_NUM_182 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-373 of THBS1, and a second amino acid sequence being at least about 90 % homologous to amino acids 432-1170 of THBS1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of THBS1_Skipping exon_9 #PEP_NUM_182, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 363-373 of THBS1, and a second amino acid sequence being at least about 90 % homologous to amino acids 432-442 of THBS1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated THBS4_Skipping exon_15 #PEP_NUM_184 polypeptide, consisting essentially of an amino acid sequence being at least about 90 % homologous to amino acids 1-613 of THBS4.

An isolated TIAF1_Skipping exon_11_#PEP_NUM_166 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-679 of TIAF1, and a second amino acid sequence being at least about 90 % homologous to amino acids 674-2054 of TIAF1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of TIAF1_Skipping exon_11_#PEP_NUM_166, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 669-679 of TIAF1, and a second amino acid sequence being at least about 90 % homologous to amino acids 674-684 of TIAF1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated TIAF1_Skipping exon_25_#PEP_NUM_167 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1290 of TIAF1, and a second amino acid sequence being at least about 90 % homologous to amino acids 1331-2054 of TIAF1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of TIAF1_Skipping exon_25_#PEP_NUM_167, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1280-1290 of TIAF1, and a second amino acid sequence being at least about 90 % homologous to amino acids 1331-1341 of TIAF1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated TIAF1_Skipping exon_34_#PEP_NUM_168 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1691 of TIAF1, and a second amino acid sequence being at least about 90 % homologous to amino acids 1730-2054 of TIAF1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of TIAF1_Skipping exon_34_#PEP_NUM_168, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1681-1691 of TIAF1, and a second amino acid sequence being at least about 90 % homologous to amino acids 1730-1740 of TIAF1, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated VEGFC_Skipping_exon_4 #PEP_NUM_7 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-184 of VEGFC, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence VSGSEQDLPQLHVE (SEQ ID NO: 267), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of VEGFC_Skipping_exon_4 #PEP_NUM_7, comprising a polypeptide having the sequence VSGSEQDLPQLHVE (SEQ ID NO: 267).

An isolated VLDLR_Skipping_exon_14 #PEP_NUM_4 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-654 of VLDLR, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence VKIGVKKTWRMEDVNTYACQHHRLMITLQNIPVPVPVGT M (SEQ ID NO: 268), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of VLDLR_Skipping_exon_14 #PEP_NUM_4, comprising a polypeptide having the sequence VKIGVKKTWRMEDVNTYACQHHRLMITLQNIPVPVPVGT M (SEQ ID NO: 268).

An isolated VLDLR_Skipping_exon_15 #PEP_NUM_5 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-702 of VLDLR, and a second amino acid sequence being at least about 90 % homologous to amino acids 752-873 of VLDLR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of VLDLR_Skipping_exon_15 #PEP_NUM_5, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 692-702 of VLDLR, and a second amino acid sequence being at least about 90 % homologous to amino acids

752-762 of VLDLR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated VLDLR_Skipping_exon_8_#PEP_NUM_1 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-356 of VLDLR, and a second amino acid sequence being at least about 90 % homologous to amino acids 357-873 of VLDLR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of VLDLR_Skipping_exon_8_#PEP_NUM_1, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 346-356 of VLDLR, and a second amino acid sequence being at least about 90 % homologous to amino acids 357-367 of VLDLR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated VLDLR_Skipping_exon_9_#PEP_NUM_2 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-395 of VLDLR, and a second amino acid sequence being at least about 90 % homologous to amino acids 438-873 of VLDLR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide of an edge portion of VLDLR_Skipping_exon_9_#PEP_NUM_2, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 385-395 of VLDLR, and a second amino acid sequence being at least about 90 % homologous to amino acids 438-448 of VLDLR, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated VLDLR_intron_8_retention_#PEP_NUM_6 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-395 of VLDLR, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence GESKKKTWTLQVMGKDMSMYLVRYRSSKTNSDFPPRY (SEQ ID NO: 269), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of VLDLR_intron_8_retention_#PEP_NUM_6, comprising a polypeptide having the sequence GESKKKTWTLQVMGKDSMYLVRYRSSKTNSDFPPRY (SEQ ID NO: 269).

An isolated VLDLR_skipping_exon_12_#PEP_NUM_3 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-568 of VLDLR, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence PYKKSPILLA (SEQ ID NO: 270), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of VLDLR_skipping_exon_12_#PEP_NUM_3, comprising a polypeptide having the sequence PYKKSPILLA (SEQ ID NO: 270).

An isolated VWF_Skippingexon_13_#PEP_NUM_187 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-477 of VWF, and a second amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence AGPRLCREDLRPVWELQWQPGRGLPYPLWAGGAPGGGLRERLEAARGLPGP AEAAQRSLRPQPAHEGSPRRRARS (SEQ ID NO: 271), wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated polypeptide corresponding to a tail of VWF_Skippingexon_13_#PEP_NUM_187, comprising a polypeptide having the sequence AGPRLCREDLRPVWELQWQPGRGLPYPLWAGGAPGGGLRERLEAARGLPGP AEAAQRSLRPQPAHEGSPRRRARS (SEQ ID NO: 271).

An isolated VWF_Skippingexon_29_#PEP_NUM_188 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-1684 of VWF, and a second amino acid sequence being at least about 90 % homologous to amino acids 1724-2813 of VWF, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

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An isolated polypeptide of an edge portion of VWF_Skippingexon_29_#PEP_NUM_188, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1674-1684 of VWF, and a second amino acid sequence being at least about 90 % homologous to amino acids 1724-1734 of VWF, wherein said first and said second amino acid sequences are contiguous and in a sequential order.

An isolated VWF_Skippingexon_8_#PEP_NUM_186 polypeptide, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 1-291 of VWF, a bridging amino acid K and a second amino acid sequence being at least about 90 % homologous to amino acids 334-2813 of VWF, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated polypeptide of an edge portion of VWF_Skippingexon_8_#PEP_NUM_186, comprising a first amino acid sequence being at least about 90 % homologous to amino acids 281-291 of VWF, a bridging amino acid K and a second amino acid sequence being at least about 90 % homologous to amino acids 334-344 of VWF, wherein said first amino acid sequence is contiguous to said bridging amino acid and said second amino acid sequence is contiguous to said bridging amino acid, and wherein said first amino acid sequence, said bridging amino acid and said second amino acid sequence are in a sequential order.

An isolated FGF12_Skipping_exon_2_long_isoform #PEP_NUM 38 polypeptide, comprising a first amino acid sequence being at least about 70%, optionally at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95% homologous to a polypeptide having the sequence MAAAIASSLIRQKRQARENSDRVSAASKRRSSPSKDGRSLCERHVLGVFSKVR FCSGRKRPVRRRPA (SEQ ID NO: 272), and a second amino acid sequence being at least about 90% homologous to amino acids 43- 181 of FGF12, wherein said first and second amino acid sequences are contiguous and in a sequential order.

The present invention successfully addresses the shortcomings of the presently known configurations by providing a method for large-scale prediction of alternative splicing events.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. In case of conflict, the patent specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

BRIEF DESCRIPTION OF THE DRAWINGS

The invention is herein described, by way of example only, with reference to the accompanying drawings. With specific reference now to the drawings in detail, it is stressed that the particulars shown are by way of example and for purposes of illustrative discussion of the preferred embodiments of the present invention only, and are presented in the cause of providing what is believed to be the most useful and readily understood description of the principles and conceptual aspects of the invention. In this regard, no attempt is made to show structural details of the invention in more detail than is necessary for a fundamental understanding of the invention, the description taken with the drawings making apparent to those skilled in the art how the several forms of the invention may be embodied in practice.

In the drawings:

FIGs. 1a-e are graphs depicting the differences between alternative and constitutive exons as determined by analyzing human exon datasets (Figures 1a-c) and comparing human-mouse exon datasets (Figures 1d-e). For each of the curves, constitutive exons are denoted by squares, and alternative exons are denoted by diamond shapes. Figure 1a - Length of conserved region in the last 100 nucleotides of an upstream intron flanking the exon. X axis, length of conserved region; Y axis, percent exons with upstream conserved region greater or equal to the value in X. Conservation was detected using local alignment with the mouse 100 counterpart intronic nucleotides. A minimum hit was 12 consecutive perfectly matching nucleotides. Figure 1b - Length of conserved region in the first 100 nucleotides of a

flanking intron downstream of the exon. Axes as in A. Figure 1c shows human-mouse exon identity for percent exons. X axis, percent identity in the alignment of the human and the mouse exons; Y axis, percent exons with identity greater or equal to the value in X. Figure 1d shows exon size distribution. X axis, exon size; Y axis, percent exons having size lesser or equal to the size in X. Figure 1e shows human-mouse exon identity, for exons having a size that is a multiple of 3. X axis, percent identity in the alignment of the human and the mouse exons; Y axis, percent exons with identity greater or equal to the value in X.

FIG. 2a is a photograph depicting RT-PCR detection of a splice variant featuring skipping of exon 10 in Ephrine receptor B1 (GenBank Accession No. NM_004441, SEQ ID Nos. 452, 453). Primers were taken from exon 9 (f, SEQ ID NO: 3) and 11 (r, SEQ ID NO: 4) of Ephrine receptor B1. Predicted size of full-length product was 324 bp, which was found in all samples but Placenta (lane 4). Skipping exon 10 variant (predicted size 201bp) was detected in Testis (lane 11 - Arrow) and slightly in Kidney (lane 12). A larger band was also found in Testis, and sequencing confirmed it was a novel exon upstream of exon 10 (9A - Arrowhead, sequence of 3' of exon 9a is set forth in SEQ ID NO: 201). All sequences were confirmed by sequencing. Tissue type cDNA pools: 1-Cervix+HeLa; 2-Uterus; 3-Ovary; 4-Placenta; 5-Breast; 6-Colon; 7-Pancreas; 8-Liver + Spleen; 9-Brain; 10-Prostate; 11-Testis; 12-Kidney; 13-Thyroid; 14-Assorted Cell-lines. M denotes a 1 kb ladder marker; H denotes H₂O negative control.

Figure 2b is a photograph depicting RT-PCR detection of a splice variant featuring skipping of exon 4 in VEGFC (GenBank Accession No. NM_005429, SEQ ID Nos. 466, 467). Primers were taken from exon 3 (f, SEQ ID NO: 17) and 6 (r, SEQ ID NO: 18). Predicted size of full-length product was 351 bp, which was found in all samples. Skipping exon 4 variant (predicted size 199 bp) was detected in all samples excluding Pancreas (lane 7) and a very weak expression in Breast and Colon (lanes 5 and 6). All sequences were confirmed by sequencing. A larger band was apparent in the testis and may represent a novel variant of VEGFC which sequence is yet to be determined. Tissue type cDNA pools: 1-Cervix+HeLa; 2-Uterus; 3-Ovary; 4-Placenta; 5-Breast; 6-Colon; 7-Pancreas; 8-Liver + Spleen; 9-Brain; 10-Prostate; 11-Testis; 12-Kidney; 13-Thyroid; 14-Assorted Cell-lines. M denotes a 1 kb ladder marker; H denotes H₂O negative control.

Figure 2c is a photograph depicting RT-PCR detection of a splice variant featuring skipping of exon 4 in EphrinA5 (GenBank Accession No. NM_001962, SEQ ID Nos. 450, 451) and a second splice variant featuring skipping of exon 11 in Heparanase 2 (GenBank Accession No. NM_021828, SEQ ID Nos. 468, 469). Primers were taken from exon 1 (f, SEQ ID NO: 1) and 5 (r, SEQ ID NO: 2) for EFNA5 and exon 9 (f, SEQ ID NO: 19) and 12 (r, SEQ ID NO: 20) for HPA2. Predicted size of full length EFNA5 product was 287 bp, which was found in all samples (samples 1-8 not shown). Skipping exon 4 variant (predicted size 199 bp) was detected in all samples. Predicted size of full length HPA2 product (357 bp) was detected in all samples, excluding Breast and Pancreas (lanes 5 and 7). Skipping exon 11 variant of HPA2 (199 bp) was found in Cervix (lane 1), Uterus (2), Prostate (10), Testis (11) and Kidney (12). In testis, two Novel exons were found and confirmed by sequencing (exons 11A and 11B, partial sequences are set forth in SEQ ID Nos: 203 and 204, respectively). All sequences were confirmed by sequencing.

Figure 2d is a photograph depicting RT-PCR detection of a splice variant featuring skipping of exon 2 in FGF11 (GenBank Accession No. NM_004112, SEQ ID Nos. 456, 457). Primers were taken from exon 1 (f, SEQ ID NO: 5) and 4 (r, SEQ ID NO: 6). Predicted full-length product was 344 bp, which was found in all samples. Skipping exon 2 variant (predicted size 233bp) was detected in all samples excluding Uterus (lane 2), Placenta (lane 4), Colon (lane 6), Pancreas (lane 7), Brain (lane 9), Cell-lines (Lane 14) and very weakly in Breast and Liver and Spleen (lanes 5 and 8). All sequences were validated by sequencing. Tissue type cDNA pools: 1-Cervix+HeLa; 2-Uterus; 3-Ovary; 4-Placenta; 5-Breast; 6-Colon; 7-Pancreas; 8-Liver + Spleen; 9-Brain; 10-Prostate; 11-Testis; 12-Kidney; 13-Thyroid; 14-Assorted Cell-lines. M denotes a 1\kb ladder marker; H denotes H₂O negative control.

Figure 2e is a photograph depicting RT-PCR detection of a splice variant featuring skipping of exon 9 in NOTCH2 (GenBank Accession No. NM_024408, SEQ ID Nos. 460, 461). Primers were taken from exon 8 (f, SEQ ID NO: 11) and 10 (r, SEQ ID NO: 12). Predicted full-length product was 352 bp, which was found only in Cervix and Breast. Skipping exon 9 variant (predicted size 169 bp) was detected in Testis (Lane 11 – Marked by Arrow). Tissue type cDNA pools: 1-Cervix+HeLa; 2-Uterus; 3-Ovary; 4-Placenta; 5-Breast; 6-Colon; 7-Pancreas; 8-Liver + Spleen; 9-

Brain; 10-Prostate; 11-Testis; 12-Kidney; 13-Thyroid; 14-Assorted Cell-lines. M denotes a 1 kb ladder marker; H denotes H₂O negative control.

Figure 2f is a photograph depicting RT-PCR detection of a splice variant featuring skipping of exon 13 in PTPRZ1 (GenBank Accession No. NM_002851, SEQ ID Nos. 464, 465). Primers were taken from the junction of exons 12-13 (f, SEQ ID NO: 15) and exons 14-15 junction (r, SEQ ID NO: 16). Predicted size of full-length product was 283 bp, which was found in Cervix (lane 1), Uterus (lane 2), Ovary (lane 3), Brain (lane 9), Prostate (lane 10) and Testis (lane 11). Exon 13 skipping (138bp) was detected in Cervix (Lane 1), Ovary (lane 3), Brain (lane 9) and Testis (lane 11). All sequences were confirmed by sequencing. Tissue type cDNA pools: 1-Cervix+HeLa; 2-Uterus; 3-Ovary; 4-Placenta; 5-Breast; 6-Colon; 7-Pancreas; 8-Liver + Spleen; 9-Brain; 10-Prostate; 11-Testis; 12-Kidney; 13-Thyroid; 14-Assorted Cell-lines. M denotes 1 kb ladder marker; H denotes H₂O negative control.

Figure 2g is a photograph depicting RT-PCR detection of splice variants featuring skipping of exons 13 and 14 in NTRK2 (GenBank Accession No. NM_006180, SEQ ID Nos. 462, 463). Primers were taken from exon 11-12 junction (f, SEQ ID NO: 13) and 15 (r, SEQ ID NO: 14). Predicted product of full-length product was 400 bp, which was found in all tissue samples excluding Placenta (lane 4), Breast (lane 5), Liver and Spleen (lane 8) and Cell-lines (lane 14). Exon 13 skipping (known - 352 bp) was detected in all tissue samples excluding Placenta (lane 4), Liver and Spleen (lane 8) and Cell-lines (lane 14). Skipping both exons 13 and 14 (139bp) was weakly found in Prostate (marked by an Arrow). All sequences were validated by sequencing. The sequence identity of the larger bands (e.g., 500bp in lane 11) was not determined. Tissue type cDNA pools: 1-Cervix+HeLa; 2-Uterus; 3-Ovary; 4-Placenta; 5-Breast; 6-Colon; 7-Pancreas; 8-Liver + Spleen; 9-Brain; 10-Prostate; 11-Testis; 12-Kidney; 13-Thyroid; 14-Assorted Cell-lines. M denotes 1 kb ladder marker; H denotes H₂O negative control.

Figure 2h is a photograph depicting RT-PCR detection of a splice variant featuring retention of intron 8 in Very Low Density Lipoprotein receptor (GenBank Accession No. NM_003383, SEQ ID Nos. 457, 458). Primers were taken from exon 7-8 junction (f, SEQ ID NO: 7) and 10 (r, SEQ ID NO: 8). Predicted size of full-length product was 324 bp, which was found in all tissue samples excluding Brain (lane 9). Retention of intron 8 (predicted size 427 bp) was detected in all tissue

samples excluding Placenta (lane 4), Colon (lane 6), and Brain (lane 9). All sequences were confirmed by sequencing. Tissue type cDNA pools: 1-Cervix+HeLa; 2-Uterus; 3-Ovary; 4-Placenta; 5-Breast; 6-Colon; 7-Pancreas; 8-Liver + Spleen; 9-Brain; 10-Prostate; 11-Testis; 12-Kidney; 13-Thyroid; 14-Assorted Cell-lines. M denotes 1 kb ladder marker; H denotes H₂O negative control.

Figure 2i is a photograph depicting RT-PCR detection of a first splice variant featuring skipping of exon 6 and a second splice variant featuring new exon 8a in FSH receptor (GenBank Accession No. NM_000145, SEQ ID Nos. 459, 460). Primers were taken from exon 5 (f, SEQ ID NO: 9) and 10 (r, SEQ ID NO: 10). Predicted size of full-length product was 394 bp, which was found in Ovary, Testis and Thyroid (lanes 3, 11 and 13 respectively). Skipping exon 6 variant (predicted size 316bp - arrowhead) was detected in Ovary and Testis (lanes 3, 11). A larger band was also found in Ovary and Testis, and sequencing approved it was a novel exon upstream to exon 9 (was called 8a, SEQ ID NO: 202). All sequences were confirmed by sequencing. Tissue type cDNA pools: 1-Cervix+HeLa; 2-Uterus; 3-Ovary; 4-Placenta; 5-Breast; 6-Colon; 7-Pancreas; 8-Liver + Spleen; 9-Brain; 10-Prostate; 11-Testis; 12-Kidney; 13-Thyroid; 14-Assorted Cell-lines. M denotes 1kb ladder marker; H denotes H₂O negative control.

Figure 2j is a photograph showing experimental validation for the existence of alternative splicing in selected predicted exons. RT-PCR for 15 exons (detailed in Table 8), for which no EST/cDNA indicating alternative splicing was found, was conducted over 14 different tissue types and cell lines (see Methods). Detected splice variants were confirmed by sequencing. For nine of these exons a splice isoform was detected in at least one of the tissues tested. Only a single tissue is shown here for each of these nine exons. Lane 1, DNA size marker. Lane 2, exon 2 skipping in FGF11 in ovary tissue (the 344nt and 233nt products are exon inclusion and skipping, respectively). Lane 3, exon 4 skipping in EFNA5 gene in ovary tissue (exon inclusion 287nt; skipping 199nt). Lane 4, exon 8 skipping in NCOA1 gene in placenta tissue (exon inclusion 377nt; skipping 275nt). Lane 5, exon 22 skipping in PAM gene in cervix tissue (exon inclusion 323nt; skipping 215nt). Additional upper band contains a novel exon in PAM. Lane 6, exon 9 skipping in GOLGA4 gene in uterus tissue (exon inclusion 288nt; skipping 213nt). Lane 7, exon 9 skipping of NPR2 gene in placenta tissue (282nt inclusion; 207nt skipping). Lane 8, intron 8 retention in

VLDLR gene in ovary tissue (wild type 324nt; intron retention 427nt). Lane 9, alternative acceptor site in exon 12 of BAZ1A in ovary tissue (wild type 351nt; alternative acceptor variant 265nt). The uppermost band represents a new exon in BAZ1A, inserted between exons 12 and 13. Lane 10, alternative acceptor site in exon 7 of SMARCD1 in uterus tissue (wild type 353nt; exon 7 extension 397nt).

FIGs. 3a-z are schematic presentations of the proteins encoded by the selected splice variants compared to full length wild type proteins. A full description of the new variants is provided in Table 3, below. The protein domains are based on Swissprot annotation. Figure 3a shows new alternatively spliced variants of VLDLR - Very low density Lipoprotein Receptor. The exon structure of the new variant is as follows: i. skipping exon 8 or 9; ii. extension of exon 8; iii. skipping exon 14; iv. skipping exon 15.

Figure 3b shows a new alternatively spliced variant of VEGFC - Vascular endothelial growth factor C. The new variant skips exon 4.

Figure 3c shows three new alternatively spliced variants of MET protooncogene (HGF receptor). Exon structure of the new variants is as follows: i. extension of exon 12; ii. skipping of exon 14; iii. skipping exon 18.

Figure 3d shows four new alternatively spliced variants of ITGAV, integrin, alpha V (vitronectin receptor, alpha polypeptide). The exon structure of the new variants is as follows: i. skipping exon 11; ii. skipping exon 20; iii. skipping exon 21; iv. skipping exon 25.

Figure 3e shows three new alternatively spliced variants of FSHR: follicle stimulating hormone receptor. The exon structure of the new variants is as follows: i. skipping exon 7; ii. skipping exon 8; iii. intron 7 retention.

Figure 3f shows new alternatively spliced variants of LHCGR: luteinizing hormone/choriogonadotropin receptor. The exon structure of the new variants is as follows: i. skipping either exon 2,3,5,6 or 7; ii. skipping exon 10; iii. intron 5 retention.

Figure 3g shows a new alternatively spliced variant of Fibroblast growth factor – FGF11. The exon structure of the new variant new variant skips exon 2.

Figure 3h shows two new alternatively spliced variants of Fibroblast growth factors – FGF12/13. The known FGF protein has two reported isoforms (isoform 1 and 2). The exon structure of the new splice variants is as follows: i. skipping exon 2

in both, isoform 1 and isoform 2; and ii. skipping exon 3 in both, isoform 1 and isoform 2.

Figure 3i shows new alternatively spliced variants of Ephrin ligand A family proteins, EFNA 1,3 and 5. The exon structure of the novel splice variants is as follows: i. skipping exon 3 in EFNA 1, 3 and 5; ii. skipping exon 4 in EFNA 3 and 5; iii. skipping both exons 3 and 4 in EFNA 1, 3 and 5.

Figure 3j shows three new alternatively spliced variants of Ephrin ligand B family (EFNB2). The exon structure of the new variants is as follows: i. skipping exon 2; ii. skipping exon 3; iii. skipping exon 4.

Figure 3k shows four new alternatively spliced variants of Ephrin type A receptor 4 (EPHA4). The exon structure of the new variants is as follows: i. skipping exon 2; ii. skipping exon 3; iii. skipping exon 4; iv. skipping exon 12.

Figure 3l shows seven new alternatively spliced variants of Ephrin type A receptor 5 (EPHAS5). The exon structure of the new variants is as follows: i. skipping exon 4; ii. skipping exon 5; iii. skipping exon 8; iv. skipping exon 10; v. skipping exon 14; vi. skipping exon 16; vii. skipping exon 17.

Figure 3m shows two new alternatively spliced variants of Ephrin type A receptor 7 (EPHA7). The exon structure of the new variants is as follows: i. skipping exon 10; ii. skipping exon 15.

Figure 3n shows three new alternatively spliced variants of Ephrin type B receptor 1 (EPHB1). The exon structure of the new variants is as follows: i. skipping exon 6; ii. skipping exon 8; iii. skipping exon 10.

Figure 3o shows five new alternatively spliced variants of PTPRZ1- protein tyrosine phosphatase zeta 1. The exon structure of the new variants is as follows: i. skipping exon 7; ii. skipping exon 11; iii. skipping exon 13; iv. skipping exon 15; v. skipping exon 22.

Figure 3p shows a new alternatively spliced variant of PTPRB1- protein tyrosine phosphatase beta 1. The new variant skips exon 26.

Figure 3q shows new splice variants of ErbB2 and ErbB3 receptor tyrosine kinases. The exon structure of the new variants is as follows. i. new splice variant of ErbB2, skipping exon 6; ii. new splice variant of ErbB3 skipping exon 4; iii. new splice variant of ErbB3 skipping exon 15; iv. new splice variant of ErbB3, skipping exon 18.

Figure 3r shows two new alternatively spliced variants of ErbB4 receptor tyrosine kinase. The exon structure of the new variants is as follows: i. skipping exon 14; ii. skipping exon 16.

Figure 3s shows a new alternatively spliced variant of Heparanase, skipping exon 10.

Figure 3t shows seven new alternatively spliced variants of Heparanase 2. The exon structure of the new variants is as follows: i. skipping exon 5; ii. skipping exon 6; iii. skipping exon 7; iv. skipping exon 8; v. skipping exon 9; vi. skipping exon 10; vii. skipping exon 11.

Figure 3u shows two new alternatively spliced variants of KIT oncogene (Tyrosine kinase receptor). The exon structure of the new variants is as follows: i. skipping exon 8; ii. skipping exon 14.

Figure 3v shows a new alternatively spliced variant of KIT ligand, skipping exon 8.

Figure 3w shows new alternatively spliced variants of JAG1. The exon structure of the new variants is as follows: i. skipping exon 10 or 18; ii. skipping exon 12; iii. skipping exon 22.

Figure 3x shows new alternatively spliced variants of Notch homologs NTC2, NTC3 and NTC4. The exon structure of the new variants is as follows: i. is a new variant of NTC2, skipping exon 9 or 12; ii. is a new variant of NTC3, skipping exon 3; iii. is a new variant of NTC4, skipping exon 8.

Figure 3y shows new alternatively spliced variants of BDNF/NT-3 growth factors receptors (NTRK2 and NTRK3). The exon structure of the new variants is as follows: i. is a new variant of NTRK2, skipping exon 14; ii. is a new variant of NTRK2, skipping exon 13 and 14; iii. is a new variant of NTRK3, skipping exon 5; iv. is a new variant of NTRK3, skipping exon 16.

Figure 3z shows new alternatively spliced variants of GDNF receptor alpha (GFRA1) and Neurturin receptor alpha (GFRA2)- RET ligands. The exon structure of the new variants is as follows: i. is a new variant of GFRA1, skipping exon 4; ii. is a new variant of GFRA2, skipping exon 4.

FIGs. 4a-m are schematic presentations of the proteins encoded by the selected splice variants compared to full length wild type proteins. A full description

of the new variants is provided in Table 3, below. The protein domains are based on Swissprot annotation.

Figure 4a shows new alternatively spliced variants of Interleukin 16. The exon structure of the new variants is as follows: i. skipping exon 5; ii. skipping exon 18.

Figure 4b shows new alternatively spliced variants of Insulin growth factor binding protein 4, IGFBP4, skipping exon 3.

Figure 4c shows new alternatively spliced variants of Angiopoietin 1. The exon structure of the new variants is as follows: i. skipping exon 5; ii. skipping exon 6; iii. skipping exon 8.

Figure 4d shows new alternatively spliced variants of long and short isoforms of Neuropilin 1. The exon structure of the new variants is as follows: i. is a new variant of a long isoform, skipping exon 5; ii. is a new variant of a short isoform, skipping exon 5.

Figure 4e shows new alternatively spliced variant of Endothelin converting enzyme 1, skipping exon 2.

Figure 4f shows new alternatively spliced variants of Endothelin converting enzyme 2. The exon structure of the new variants is as follows: i. skipping exon 8; ii. skipping exon 12; iii. skipping exon 13; iv. skipping exon 15.

Figure 4g shows new alternatively spliced variants of Enkephalinase, Neutral endopeptidase (NME). The exon structure of the new variants is as follows: i. skipping exon 4; ii. skipping exon 7; iii. skipping exon 9; iv. skipping exon 11; v. skipping exon 12; vi. skipping exon 16.

Figure 4h shows new alternatively spliced variants of APBB1- Alzheimer's disease amyloid A4 binding protein. The exon structure of the new variants is as follows: i. skipping exon 3; ii. skipping exon 7 or 9; iii. skipping exon 10; iv. skipping exon 12.

Figure 4i shows new alternatively spliced variant of Transforming growth factor beta 2 (TGFB2), skipping exon 5.

Figure 4j shows new alternatively spliced variant of IL1 receptor accessory protein (IL1RAP), skipping exon 11.

Figure 4k shows new alternatively spliced variants of IL1 receptor accessory protein like family members IL1RAPL1 and IL1RAPL2. The exon structure of the

new variants is as follows: i. skipping exon 4; ii. skipping exon 5; iii. skipping exon 6; iv. skipping exon 7; v. skipping exon 8. Figure 4l shows new alternatively spliced variant of Vitamin K dependent protein S precursor (PROS1), skipping exon 3. Figure 4m shows new alternatively spliced variants of Ovarian carcinoma antigen CA125 (M17S2). The exon structure of the new variants is as follows: i. skipping exon 14; ii. skipping exon 15; iii. skipping exon 20.

FIG. 5a is a black box diagram illustrating a system designed and configured for generating a database of putative gene products and generated according to the teachings of the present invention.

FIG. 5b is a black box diagram illustrating a remote configuration of the system of Figure 5a.

Figure 6 shows the ROC curve of classification rules in the experiments according to the present invention.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention is of methods of identifying putative gene products by interspecies sequence comparison and biomolecular sequences identified thereby, which can be used in a variety of therapeutic and diagnostic applications.

The principles and operation of the present invention may be better understood with reference to the drawings and accompanying descriptions.

Before explaining at least one embodiment of the invention in detail, it is to be understood that the invention is not limited in its application to the details set forth in the following description or exemplified by the Examples. The invention is capable of other embodiments or of being practiced or carried out in various ways. Also, it is to be understood that the phraseology and terminology employed herein is for the purpose of description and should not be regarded as limiting.

Alternative splicing is a mechanism by which multiple expression products are generated from a single gene. It is estimated that between 35 % to 60 % of all human genes can putatively undergo alternative splicing. Currently, the only approach available for the detection of alternatively spliced products relies on the use of expressed sequence data, such as, Expressed Sequence Tags (ESTs) and cDNAs.

However, expressed sequences present a problematic source of information, as they present only a sample of the transcriptome. Thus, the detection of a splice

variant is possible only if it is expressed above a certain expression level, or if there is an EST library prepared from the tissue type in which the variant is expressed. In addition, ESTs are very noisy and contain numerous sequence errors [Sorek (2003) Nucleic Acids Res. 31:1067-1074]. For example, many wrongly termed splice events, actually represent incompletely spliced heteronuclear RNA (hnRNA) or oligo(dT)-primed genomic DNA contaminants of cDNA library constructions. Furthermore, the splicing apparatus is known to make errors, resulting in aberrant transcripts that are degraded by the mRNA surveillance system and amount to little that is functionally important [Maquat and Charmichael (2001) Cell 104:173-176; Modrek and Lee (2001) Nat. Genet. 30:13-19]. Consequently the mere presence of a transcript isoform in the ESTs cannot establish a functional role for it.

Thus, the use of expressed sequence data allows only very general estimates regarding the number of genes that have splice variants (currently running between 35% and 75%), but does not allow specific estimation regarding the actual number and identity of exons that can be alternatively spliced.

While reducing the present invention to practice, the present inventors uncovered a combination of sequence features unique to alternatively spliced exons, which allow distinction thereof from constitutively spliced ones. These findings allow to computationally identify alternatively spliced exons even when no expressed sequence data is available, to thereby predict yet unknown gene expression products.

Thus, according to one aspect of the present invention there is provided a method of identifying alternatively spliced exons.

As used herein "alternatively spliced exons" refer to exons, which are spliced into an expression product only under specific conditions such as specific tissue environment, stress conditions or developmental state.

The method according to this aspect of the present invention is effected by scoring each of a plurality of exon sequences derived from genes of a species (i.e., a eukaryotic organism such as human) according to at least one sequence parameter. Exon sequences of the plurality of exon sequences scoring above a predetermined threshold represent alternatively spliced exons; thereby identifying the alternatively spliced exons.

Typically, exon sequences are identified by screening genomic data for reliable exons which require canonical splice sites and elimination of possible genomic contamination events [Sorek (2003) Nucleic Acids Res. 31:1067-1074].

As mentioned hereinabove, the present inventors uncovered a number of sequence parameters, which can serve for the identification of alternatively spliced exon sequences. Preferred examples of such are summarized infra.

Exon length – Typically, conserved alternatively spliced exons are much shorter than constitutively spliced exons, probably since the spliceosome typically recognizes exons that are between 50 and 200 bp.

Division by three – Since alternatively spliced exons are cassette exons, which may be incorporated in an expressed gene product or skipped, they should be divisible by three, such that the reading frame is maintained when they are skipped.

Conservation level between the exon sequences and corresponding exon sequences of orthologous species – Alternatively spliced exons are typically more conserved than constitutively spliced exons. This is probably since alternatively spliced exons contain sub-sequences that are important for inclusion/exclusion regulation [Exonic Splicing Enhancers and Silencers, Cartegni (2002) Nat. Rev. Genet. 3:285-298]. This requirement imposes additional conservation constraint on the sequence of the exon.

Length of conserved intron sequences upstream of each of the exon sequences – Alternatively spliced exons exhibit high level of conservation in an intronic sequence of about 100 bases upstream of the exon. This is only sparsely so for constitutively spliced exons. This is probably since these sequences are involved in regulation of inclusion/exclusion of the alternatively spliced exon. Alignment of intronic regions can be done using sim4 software. sim4 sources are available from <http://globin.cse.psu.edu/globin/html/software.html>. According to a presently known embodiment of the present invention the length of conserved intronic sequence is from about 12 to about 100 nucleotides.

Length of conserved intron sequences downstream of the exon sequences – Alternatively spliced exons exhibit high level of conservation in an intronic sequence of about 100 bases downstream of the exon. This is only sparsely so for constitutively spliced exons. This is probably since these sequences are involved in regulation of inclusion/exclusion of the alternatively spliced exon. Alignment of intronic regions

can be done using sim4 software. sim4 sources are available from <http://globin.cse.psu.edu/globin/html/software.html>. According to a presently known embodiment of the present invention the length of conserved intronic sequence is from about 12 to about 100 nucleotides.

Conservation level of intron sequences upstream of each of the exon sequences – For alternatively spliced exons, the intronic sequences in the 100 bases upstream of the exon are frequently conserved between species. This correlation is less strongly shown by constitutively spliced exons [Sorek and Ast (2003) Genome Res. 13(7):1631-7]. This is probably since these sequences are involved in regulation of inclusion/exclusion of the alternatively spliced exon. Therefore, conservation level of intron sequences upstream of exon sequences can be used to distinguish alternative from constitutive exons. Alignment of intronic regions can be done using sim4 software, which may be obtained from <http://globin.cse.psu.edu/globin/html/software.html>. The measured length of the conserved sequence was generally found to be between 12 to 100 nucleotides.

Conservation level of intron sequences downstream of each of the exon sequences – For alternatively spliced exons, the intronic sequences in the 100 bases downstream of the exon are frequently conserved between species. This correlation is less strongly shown by constitutively spliced exons. This is probably since these sequences are involved in regulation of inclusion/exclusion of the alternatively spliced exon. Therefore, conservation level of intron sequences downstream of exon sequences can be used to distinguish alternative from constitutive exons. Alignment of intronic regions can be done using sim4 software, which are available from <http://globin.cse.psu.edu/globin/html/software.html>.

Each of the above-described parameters can be considered separately according to predetermined criteria however a combination with other parameters used, is preferred. In this case, each parameter is preferably also weighted according to its importance and a scoring system e.g., a scoring matrix, is preferably applied.

Such a scoring matrix can list the various exons across the X-axis of the matrix while each parameter can be listed on the Y-axis of the matrix. Parameters include both a predetermined range of values from which a single value is selected from each exon, and a weight. Each exon is scored at each parameter according to its value and the weight of the parameter.

Finally, the scores of each parameter of a specific exon sequence are summed and the results are analyzed.

Exons which exhibit a total score greater than a particular stringency threshold are grouped as alternatively spliced exons.

According to presently known preferred embodiments of this aspect of the present invention the best scored exons share at least about 95 % identity with an orthologous exon; exon size is a multiple of 3; exon length of about 1000 bases; length of conserved intron sequences upstream of the exon sequence is at least about 12 bases; length of conserved intron sequences downstream of the exon sequence is at least about 15 bases; conservation level of the intron sequences upstream of the exon sequence is at least about 85 %; conservation level of the intron sequences downstream of the exon sequence is at least about 60 %.

As mentioned, the above-described methodology allows the prediction of yet unknown alternatively spliced exons, even in the absence of available expressed sequences. This allows the prediction of putative gene products of any known gene.

Thus in order to predict expression products of a gene of interest, alternatively spliced exons thereof are identified as described above. Thereafter, chromosomal location of the identified exons is analyzed with respect to the coding sequence of the gene of interest, to thereby predict expression products of the gene of interest.

Chromosomal location of the newly uncovered sequences may be done as described by aligning the new sequence to the genome, as described for example by Modrek (2001) Nucleic Acids Research, 29:2850-2859. Genomic sequences, which are found to include these exons, are then manipulated to exclude them to thereby generate the new isoforms.

For example, when the newly identified alternative exon is predicted to be skipped, all transcripts that are known to include it are computationally or manually manipulated to delete the sequence of the exon therefrom, thus creating a new transcript that represents the exon-skipping splice variant.

Once putative transcripts are identified using the above methodology, corresponding protein products can be predicted using any translation software known in the art [e.g., ORF-finder (<http://www.ncbi.nlm.nih.gov/gorf/gorf.html>)].

According to another aspect of the present invention there is provided a method of predicting expression products of a gene of interest in a given species (any

eukaryotic organism). The method according to this aspect of the present invention is effected by clustering expressed sequences of the given species to form a contig.

The term "contig" refers to a series of overlapping sequences with sufficient identity to create a longer contiguous sequence.

Expressed sequence clustering is effected using clustering methods which are well known in the art. Examples of clustering/assembly procedures with associated databases which are commercially available include, but are not limited to, UniGene (<http://www.ncbi.nlm.nih.gov/UniGene>), TIGR Gene Indices (<http://www.tigr.org/tdb/tgi.shtml>), STACK (<http://www.sanbi.ac.za/Dbases.html>), trEST (<ftp://ftp.isrec.isb.sib.ch/gub/databases/trest>) and LEADSTM (<http://www.cgen.com>).

Following contig construction, exon sequences of orthologues of the gene of interest which display homology with the contig sequence are aligned to a genome of interest (i.e., genome of the given species). Orthologous exon sequences which alignment overlaps the chromosomal location of the given contig are added to the set of sequences in the contig. This larger set of sequences is then assembled to form a hybrid multi-species contig.

Expression products that are unique to the hybrid contig and do not appear in the original contig are identified. It will be appreciated that such unique expression products could not have been identified using prior art methods, which do not utilize expressed sequences from other species.

The above-described methodology is further described in Example 4 of the Examples section.

Once novel transcripts of the gene of interest of the given species are identified, their corresponding protein products are predicted, as described above.

Biomolecular sequences uncovered as described herein can be experimentally validated using any method known in the art, such as northern blot, RT-PCR, western-blots and the like. For further details see Example 2 of the Examples section. Functional analysis of biomolecular sequences identified as described herein can be effected using biochemical, cell biology and molecular methods which are well known in the art.

Biomolecular sequences (i.e., nucleic acid and polypeptide sequences) uncovered using the above-described methodology can be functionally annotated to

discover their contribution to biological processes and physiological complexity. Numerous methods of automated gene annotation are known in the art (reviewed by Ashurst and Collins (2003) *Annu. Rev. Genomics Hum. Genet.* (2003) 4:69-88. Such automatic annotation approaches are summarized in Example 5 of the Examples section below and are also the subject of U.S. Pat. Appl. No. 60/539,129.

Alternatively spliced exons and/or expression products derived therefrom (i.e., including the exons thus identified or skipping same) can be stored in a database, which can be generated by a suitable computing platform.

Although the present methodology can be effected using prior art systems modified for such purposes, in order to process large amounts of sequence data, the present methodologies are preferably effected using a dedicated computational system.

Thus, according to another aspect of the present invention and as illustrated in Figures 5a-b, there is provided a system for generating a database of alternatively spliced sequences.

System 10 includes at least one central processing unit (CPU) 12, which executes a software application designed and configured for identifying alternatively spliced sequences. System 10 may also include a user input interface 14 [e.g., a keyboard and/or a cursor control device (e.g., a joy stick)] for inputting database or database related information, and a user output interface 16 (e.g., a monitor) for providing database information to a user 18.

System 10 may also include random access memory 24, ROM memory 26, a modem 28 and a graphic processing unit (GPU) 30.

System 10 preferably stores sequence information of the alternatively spliced sequences identified thereby on an internal and/or external storage device 20 such as a magnetic, optico-magnetic or optical disk as a database of alternatively spliced sequences. Such a database further includes information pertaining to database generation (e.g., source library), parameters used for selecting polynucleotide sequences, putative uses of the stored sequences, and various other annotations (as described below) and references which relate to the stored sequences and respective expression products.

The hardware elements of system 10 may be tied together by a common bus or several interlinked buses for transporting data between the various elements.

Examples of system 10 include but are not limited to, a personal computer, a work station, a mainframe and the like.

System 10 of the present invention may be used by a user to query the stored database of sequences, to retrieve nucleotide sequences stored therein or to generate polynucleotide sequences from user inputted sequences.

The methods of the present invention can be effected by any software application executable by system 10. The software application can be stored in random access memory 24, or internal and/or external data storage device 20 of system 10.

The database generated and stored by system 10 can be accessed by an on-site user of system 10, or by a remote user communicating with system 10, through for example, a terminal or thin client.

The latter configuration is best exemplified by the client-server system 50 which is shown in Figure 5b. System 50 is configured to perform similar functions to those performed by system 10. In system 50, communication between a remote client 34 (e.g., computer, PDA, cell phone etc) and CPU unit 12 of a local server or computer is typically effected via a communication network 32. Communication network 32 can be any private or public communication network including, but not limited to, a standard or cellular telephony network, a computer network such as the Internet or intranet, a satellite network or any combination thereof.

As illustrated in Figure 5b, communication network 32 can include one or more communication servers 22 (one shown in Figure 5b) which serve for communicating data pertaining to the sequence of interest between remote client 18 and processing unit 12. Thus, a request for data or processed data is communicated from remote client 18 to processing unit 12 through communication network 32 and processing unit 12 sends back a reply which includes data or processed data to remote client 18. Such a system configuration is advantageous since it enables users of system 50 to store and share gathered information and to collectively analyze gathered information.

Such a remote configuration can be implemented over a local area network (LAN) or a wide area network (WAN) using standard communication protocols.

It will be appreciated that existing computer networks such as the Internet can provide the infrastructure and technology necessary for supporting data communication between any number of users 18 and processors 12.

By applying the algorithms described hereinabove and in the Examples section, which follows, the present inventors collected sequence information which is presented in the files "transcripts.fasta" and "proteins.fasta" of enclosed CD-ROM1 and in the files "transcripts" and "proteins" of enclosed CD-ROM2. Annotations of these sequences are provided in the file "AnnotationForPatent.txt" of enclosed CD-ROM 1.

Novel polynucleotide sequences uncovered using the above-described methodology can be used in various clinical applications (e.g., therapeutic and diagnostic) as is further described hereinbelow.

A polynucleotide sequence of the present invention refers to a single or double stranded nucleic acid sequences which is isolated and provided in the form of an RNA sequence, a complementary polynucleotide sequence (cDNA), a genomic polynucleotide sequence and/or a composite polynucleotide sequences (e.g., a combination of the above).

As used herein the phrase "complementary polynucleotide sequence" refers to a sequence, which results from reverse transcription of messenger RNA using a reverse transcriptase or any other RNA dependent DNA polymerase. Such a sequence can be subsequently amplified *in vivo* or *in vitro* using a DNA dependent DNA polymerase.

As used herein the phrase "genomic polynucleotide sequence" refers to a sequence derived (isolated) from a chromosome and thus it represents a contiguous portion of a chromosome.

As used herein the phrase "composite polynucleotide sequence" refers to a sequence, which is composed of genomic and cDNA sequences. A composite sequence can include some exon sequences required to encode the polypeptide of the present invention, as well as some intronic sequences interposing therebetween. The intronic sequences can be of any source, including of other genes, and typically will include conserved splicing signal sequences. Such intronic sequences may further include cis acting expression regulatory elements.

Thus, the present invention encompasses nucleic acid sequences described hereinabove; fragments thereof, sequences hybridizable therewith, sequences homologous thereto [e.g., at least 50 %, at least 55 %, at least 60%, at least 65 %, at least 70 %, at least 75 %, at least 80 %, at least 85 %, at least 95 % or more say 100 % identical to the nucleic acid sequences set forth in the file "transcripts.fasta" of enclosed CD-ROM1 and in the file "transcripts" of enclosed CD-ROM2], sequences encoding similar polypeptides with different codon usage, altered sequences characterized by mutations, such as deletion, insertion or substitution of one or more nucleotides, either naturally occurring or man induced, either randomly or in a targeted fashion. The present invention also encompasses homologous nucleic acid sequences (i.e., which form a part of a polynucleotide sequence of the present invention) which include sequence regions unique to the polynucleotides of the present invention.

In cases where the polynucleotide sequences of the present invention encode previously unidentified polypeptides, the present invention also encompasses novel polypeptides or portions thereof, which are encoded by the isolated polynucleotide and respective nucleic acid fragments thereof described hereinabove.

Thus, the present invention also encompasses polypeptides encoded by the polynucleotide sequences of the present invention. The present invention also encompasses homologues of these polypeptides, such homologues can be at least 50 %, at least 55 %, at least 60%, at least 65 %, at least 70 %, at least 75 %, at least 80 %, at least 85 %, at least 95 % or more say 100 % homologous to the amino acid sequences set forth in the file "proteins.fasta" of enclosed CD-ROM1 and in the file "proteins" of enclosed CD-ROM2, as can be determined using BlastP software of the National Center of Biotechnology Information (NCBI) using default parameters. Finally, the present invention also encompasses fragments of the above described polypeptides and polypeptides having mutations, such as deletions, insertions or substitutions of one or more amino acids, either naturally occurring or man induced, either randomly or in a targeted fashion.

As mentioned hereinabove, biomolecular sequences uncovered using the methodology of the present invention can be efficiently utilized as tissue or pathological markers and as putative drugs or drug targets for treating or preventing a disease, according to their annotations (see Examples 6 and 7 of the Examples section).

For example, it is conceivable that the biomolecular sequences of the present invention may be functionally altered, by the addition or deletion of exons as described above.

As used herein the phrase "functionally altered biomolecular sequences" refers to expressed sequences, which protein products exhibit gain of function or loss of function or modification of the original function. Specific examples of functionally altered gene products identified using the teachings of the present invention are provided in Table 3, below:

As used herein the phrase "gain of function" when made in reference to a gene product (e.g., product of alternative splicing, product of RNA editing), indicates increased functionality as compared to the wild type gene product. Such a gain of function may have a dominant effect on the wild-type gene product. An alternatively spliced variant of Max, a binding partner of the Myc oncogene, provides a typical example for a "gain of function" alteration. This variant is truncated at the COOH-terminus and while is still capable of binding to the CACGTG motif of c-Myc, it lacks the nuclear localization signal and the putative regulatory domain of Max. When tested in a myc-ras cotransformation assay in rat embryo fibroblasts, wild-type Max suppressed cellular transformation, whereas the above-described Max splice variant enhanced transformation [Makela TP, Koskinen PJ, Vastrik I, Alitalo K., Science. 1992 Apr 17;256(5055):373-7]. Thus, it is envisaged that a protein product, which exhibits a gain of function contributing to disease onset or progression be down regulated to thereby treat the disease. Alternatively, when such a gain of function promotes positive biological processes such as enhanced wound-healing, it is highly desirable to up-regulate expression or activity of the protein product in the subject in need thereof. Methods of up-regulating or down-regulating expression or activity of gene products are summarized hereinbelow.

As used herein the phrase "loss of function" when made in reference to any gene product (mRNA or protein), indicates total or partial reduction in function as compared to the wild type gene product. Loss of function can also manifest itself through a dominant negative effect.

As used herein the phrase "dominant negative" refers to the dominant negative effect of a gene product (e.g., product of alternative splicing, product of RNA editing) on the activity of wild type protein. For example, a protein product of an altered

splice variant may bind a wild type target protein without enzymatically activating it (e.g., receptor dimers), thus blocking and preventing the active enzymes from binding and activating the target protein. This mode of action provides a mechanism to the dominant negative action of soluble receptors on wild-type membrane anchored receptors. Such soluble receptors may compete with wild-type receptors on ligand-binding and as such may be used as antagonists. For example, two splice variants of guanylyl cyclase-B receptor were recently described (GC-B1, Tamura N and Garbers DL, *J. Biol. Chem.* (2003) 278(49):48880-9). One form has a 25 amino acid deletion in the kinase homology domain. This variant binds the ligand but fails to activate the cyclase. A second variant includes only a portion of the extracellular domain. This form fails to bind the ligand. Both variants, when co-expressed with the wild-type receptor both act as dominant negative isoforms by virtue of blocking formation of active GC-B1 homodimers.

A dominant negative effect may also be exerted by miss-localization of the altered variant or by multiple modes of action. For example, the splice variants of wild-type mitogen activated protein kinase 5a, ERK5b and mERK5c act as dominant negative inhibitors based on inhibition of mERK5a kinase activity and mERK5a-mediated MEF2C transactivation. The C-terminal tail, which contains a putative nuclear localization signal, is not required for activation and kinase activity but is responsible for the activation of nuclear transcription factor MEF2C due to nuclear targeting. In addition, the N-terminal domain spanning amino acids (aa) 1-77 is important for cytoplasmic targeting; the domain from aa 78 to 139 is required for association with the upstream kinase MEK5; and the domain from aa 140-406 is necessary for oligomerization [Yan et al. *J Biol Chem.* (2001) 276(14):10870-8]. In the case of protein products which exhibit dominant negative effect, it may be highly desirable to up-regulate their expression when necessary. For example, in a malignant stage which is controlled by over-expression of a specific receptor tyrosine kinase it may be desirable to upregulate expression or activity of a dominant negative form thereof to thereby treat the disease. For example, the soluble isoform of ErbB-2 and/or ErbB-3 which were uncovered as described herein (further described in Table 3, below) may be exogenously upregulated so as to treat epithelial cancers. Alternatively, when a dominant negative form of a naturally occurring negative regulator of a biochemical proliferative pathway is expressed in cancer, it may be

highly desirable to down-regulate expression or activity of this altered form to thereby treat the disease. In such a case this dominant negative isoform also serves as a valuable diagnostic tool which may be also used for monitoring disease progression with or without treatment.

The phrase "modification of the original function" may be exemplified by a changing a receptor function to a ligand function. For example, a soluble secreted receptor may exhibit change in functionality as compared to a membrane-anchored wild-type receptor by acting as a ligand, activating parallel signaling pathways by trans-signaling [e.g., the signaling reported for soluble IL-6R, Kallen Biochim Biophys Acta. (2002) Nov 11;1592(3):323-43], stabilizing ligand-receptor interactions or protecting the ligand or the wild-type receptor from degradation and/or prolonging their half-life. In this case the soluble receptor will function as an agonist.

Thus, the biomolecular sequences of the present invention can be used as drugs or drug targets for treating a disease in a subject either by upregulating or downregulating expression thereof in the subject (i.e., a mammal, preferably a human subject).

As used herein the term "treating" refers to alleviating or diminishing a symptom associated with the disease or the condition. Preferably, treating cures, e.g., substantially eliminates, and/or substantially decreases, the symptoms associated with the diseases or conditions of the present invention.

Antibodies, oligonucleotides, polynucleotides, polypeptides (collectively termed herein "agents") and methods of utilizing same for upregulating or downregulating activity or expression of biomolecular sequences in a subject are summarized infra.

Upregulating

An agent capable of upregulating expression of a specific protein product may be an exogenous polynucleotide sequence designed and constructed to express at least a functional portion thereof (e.g., a catalytic domain, a protein-protein interaction domain, etc.). Accordingly, the exogenous polynucleotide sequence may be a DNA or RNA sequence encoding the protein.

The exogenous polynucleotide may be cloned from any animal origin which is suitable to provide the desired protein product or compatible homologs thereof. Methods of molecular cloning are described in the Example section which follows.

To express an exogenous protein in mammalian cells, a polynucleotide same is preferably ligated into a nucleic acid construct suitable for mammalian cell expression. Such a nucleic acid construct includes a promoter sequence for directing transcription of the polynucleotide sequence in the cell in a constitutive or inducible manner. Any suitable promoter sequence can be used by the nucleic acid construct of the present invention. Preferably, the promoter utilized by the nucleic acid construct of the present invention is active in the specific cell population transformed. Examples of cell type-specific and/or tissue-specific promoters include promoters such as albumin that is liver specific [Pinkert et al., (1987) Genes Dev. 1:268-277], lymphoid specific promoters [Calame et al., (1988) Adv. Immunol. 43:235-275]; in particular promoters of T-cell receptors [Winoto et al., (1989) EMBO J. 8:729-733] and immunoglobulins; [Banerji et al. (1983) Cell 33:729-740], neuron-specific promoters such as the neurofilament promoter [Byrne et al. (1989) Proc. Natl. Acad. Sci. USA 86:5473-5477], pancreas-specific promoters [Edlunch et al. (1985) Science 230:912-916] or mammary gland-specific promoters such as the milk whey promoter (U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). The nucleic acid construct of the present invention can further include an enhancer, which can be adjacent or distant to the promoter sequence and can function in up regulating the transcription therefrom.

The nucleic acid construct of the present invention preferably further includes an appropriate selectable marker and/or an origin of replication. Preferably, the nucleic acid construct utilized is a shuttle vector, which can propagate both in *E. coli* (wherein the construct comprises an appropriate selectable marker and origin of replication) and be compatible for propagation in cells, or integration in a gene and a tissue of choice. The construct according to the present invention can be, for example, a plasmid, a bacmid, a phagemid, a cosmid, a phage, a virus or an artificial chromosome.

Examples of suitable constructs include, but are not limited to, pcDNA3, pcDNA3.1 (+/-), pGL3, PzeoSV2 (+/-), pDisplay, pEF/myc/cyto, pCMV/myc/cyto each of which is commercially available from Invitrogen Co. (www.invitrogen.com). Examples of retroviral vector and packaging systems are those sold by Clontech, San Diego, Calif., including Retro-X vectors pLNCX and pLXSN, which permit cloning into multiple cloning sites and the transgene is transcribed from CMV promoter.

Vectors derived from Mo-MuLV are also included such as pBabe, where the transgene will be transcribed from the 5'LTR promoter.

It will be appreciated that the nucleic acid construct can be administered to the subject employing any suitable mode of administration, described hereinbelow (i.e., in-vivo gene therapy). Alternatively, the nucleic acid construct is introduced into a suitable cell via an appropriate gene delivery vehicle/method (transfection, transduction, homologous recombination, etc.) and an expression system as needed and then the modified cells are expanded in culture and returned to the individual (i.e., ex-vivo gene therapy).

Currently preferred in vivo nucleic acid transfer techniques include transfection with viral or non-viral constructs, such as adenovirus, lentivirus, Herpes simplex I virus, or adeno-associated virus (AAV) and lipid-based systems. Useful lipids for lipid-mediated transfer of the gene are, for example, DOTMA, DOPE, and DC-Chol [Tonkinson et al., *Cancer Investigation*, 14(1): 54-65 (1996)]. The most preferred constructs for use in gene therapy are viruses, most preferably adenoviruses, AAV, lentiviruses, or retroviruses. A viral construct such as a retroviral construct includes at least one transcriptional promoter/enhancer or locus-defining element(s), or other elements that control gene expression by other means such as alternate splicing, nuclear RNA export, or post-translational modification of messenger. Such vector constructs also include a packaging signal, long terminal repeats (LTRs) or portions thereof, and positive and negative strand primer binding sites appropriate to the virus used, unless it is already present in the viral construct. In addition, such a construct typically includes a signal sequence for secretion of the peptide from a host cell in which it is placed. Preferably the signal sequence for this purpose is a mammalian signal sequence or the signal sequence of the polypeptide variants of the present invention. Optionally, the construct may also include a signal that directs polyadenylation, as well as one or more restriction sites and a translation termination sequence. By way of example, such constructs will typically include a 5' LTR, a tRNA binding site, a packaging signal, an origin of second-strand DNA synthesis, and a 3' LTR or a portion thereof. Other vectors can be used that are non-viral, such as cationic lipids, polylysine, and dendrimers.

Agents for upregulating endogenous expression of specific splice variants of a given gene include antisense oligonucleotides, which are directed at splice sites of

interest, thereby altering the splicing pattern of the gene. This approach has been successfully used for shifting the balance of expression of the two isoforms of Bcl-x [Taylor (1999) Nat. Biotechnol. 17:1097-1100; and Mercatante (2001) J. Biol. Chem. 276:16411-16417]; IL-5R [Karras (2000) Mol. Pharmacol. 58:380-387]; and c-myc [Giles (1999) Antisense Acid Drug Dev. 9:213-220].

For example, interleukin 5 and its receptor play a critical role as regulators of hematopoiesis and as mediators in some inflammatory diseases such as allergy and asthma. Two alternatively spliced isoforms are generated from the IL-5R gene, which include (i.e., long form) or exclude (i.e., short form) exon 9. The long form encodes an intact membrane-bound receptor, while the shorter form encodes a secreted soluble non-functional receptor. Using 2'-O-MOE-oligonucleotides specific to regions of exon 9, Karras and co-workers (*supra*) were able to significantly decrease the expression of the wild type receptor and increase the expression of the shorter isoforms. Approaches which can be used to design and synthesize oligonucleotides according to the teachings of the present invention are described hereinbelow and by Sazani and Kole (2003) Progress in Molecular and Subcellular Biology 31:217-239.

Alternatively or additionally, upregulation may be effected by administering to the subject the polypeptide product *per se* or an active portion thereof, as described hereinabove. However, since the bioavailability of large polypeptides is relatively small due to high degradation rate and low penetration rate, administration of polypeptides is preferably confined to small peptide fragments (e.g., about 100 amino acids).

Polypeptide products can be biochemically synthesized such as by employing standard solid phase techniques. Such methods include exclusive solid phase synthesis, partial solid phase synthesis methods, fragment condensation, classical solution synthesis. These methods are preferably used when the peptide is relatively short (i.e., 10 kDa) and/or when it cannot be produced by recombinant techniques (i.e., not encoded by a nucleic acid sequence) and therefore involves different chemistry.

Solid phase polypeptide synthesis procedures are well known in the art and further described by John Morrow Stewart and Janis Dillaha Young, Solid Phase Peptide Syntheses (2nd Ed., Pierce Chemical Company, 1984).

Synthetic polypeptides can be purified by preparative high performance liquid chromatography [Creighton T. (1983) Proteins, structures and molecular principles.

WH Freeman and Co. N.Y.] and the composition of which can be confirmed via amino acid sequencing.

In cases where large amounts of a polypeptide are desired, it can be generated using recombinant techniques such as described by Bitter et al., (1987) Methods in Enzymol. 153:516-544, Studier et al. (1990) Methods in Enzymol. 185:60-89, Brisson et al. (1984) Nature 310:511-514, Takamatsu et al. (1987) EMBO J. 6:307-311, Coruzzi et al. (1984) EMBO J. 3:1671-1680 and Brogli et al., (1984) Science 224:838-843, Gurley et al. (1986) Mol. Cell. Biol. 6:559-565 and Weissbach & Weissbach, 1988, Methods for Plant Molecular Biology, Academic Press, NY, Section VIII, pp 421-463.

An agent capable of upregulating a biomolecular sequence of interest may also be any compound which is capable of increasing the transcription and/or translation of an endogenous DNA or mRNA encoding the desired protein product.

Downregulating

One example of an agent capable of downregulating the activity of a protein product is an antibody or antibody fragment capable of specifically binding to the specific protein product of the present invention and neutralizing its activity. Preferably, the antibody specifically binds at least one epitope of the protein product. As used herein, the term "epitope" refers to any antigenic determinant on an antigen to which the paratope of an antibody binds. For example, an antibody capable of specifically binding a truncated form of Follicular Stimulating Hormone Receptor (FSHR, SEQ ID NO: 46) may be used to downregulate this putative dysfunctional isoform of FSHR to thereby treat infertility problems associated therewith. Such an antibody is preferably directed at a bridging polypeptide (SEQ ID NO: 223) of SEQ ID NO: 46, to allow distinction of this isoform from the wild-type FSHR polypeptide.

Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or carbohydrate side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics.

The term "antibody" as used in this invention includes intact molecules as well as functional fragments thereof, such as Fab, F(ab')₂, and Fv that are capable of binding to macrophages. These functional antibody fragments are defined as follows:

- (1) Fab, the fragment which contains a monovalent antigen-binding fragment of an

antibody molecule, can be produced by digestion of whole antibody with the enzyme papain to yield an intact light chain and a portion of one heavy chain; (2) Fab', the fragment of an antibody molecule that can be obtained by treating whole antibody with pepsin, followed by reduction, to yield an intact light chain and a portion of the heavy chain; two Fab' fragments are obtained per antibody molecule; (3) (Fab')2, the fragment of the antibody that can be obtained by treating whole antibody with the enzyme pepsin without subsequent reduction; F(ab')2 is a dimer of two Fab' fragments held together by two disulfide bonds; (4) Fv, defined as a genetically engineered fragment containing the variable region of the light chain and the variable region of the heavy chain expressed as two chains; and (5) Single chain antibody ("SCA"), a genetically engineered molecule containing the variable region of the light chain and the variable region of the heavy chain, linked by a suitable polypeptide linker as a genetically fused single chain molecule.

Methods of producing polyclonal and monoclonal antibodies as well as fragments thereof are well known in the art (See for example, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York, 1988, incorporated herein by reference).

Antibody fragments according to the present invention can be prepared by proteolytic hydrolysis of the antibody or by expression in *E. coli* or mammalian cells (e.g. Chinese hamster ovary cell culture or other protein expression systems) of DNA encoding the fragment. Antibody fragments can be obtained by pepsin or papain digestion of whole antibodies by conventional methods. For example, antibody fragments can be produced by enzymatic cleavage of antibodies with pepsin to provide a 5S fragment denoted F(ab')2. This fragment can be further cleaved using a thiol reducing agent, and optionally a blocking group for the sulphydryl groups resulting from cleavage of disulfide linkages, to produce 3.5S Fab' monovalent fragments. Alternatively, an enzymatic cleavage using pepsin produces two monovalent Fab' fragments and an Fc fragment directly. These methods are described, for example, by Goldenberg, U.S. Pat. Nos. 4,036,945 and 4,331,647, and references contained therein, which patents are hereby incorporated by reference in their entirety. See also Porter, R. R. [Biochem. J. 73: 119-126 (1959)]. Other methods of cleaving antibodies, such as separation of heavy chains to form monovalent light-heavy chain fragments, further cleavage of fragments, or other enzymatic, chemical, or genetic

techniques may also be used, so long as the fragments bind to the antigen that is recognized by the intact antibody.

Fv fragments comprise an association of VH and VL chains. This association may be noncovalent, as described in Inbar et al. [Proc. Nat'l Acad. Sci. USA 69:2659-62 (1972)]. Alternatively, the variable chains can be linked by an intermolecular disulfide bond or cross-linked by chemicals such as glutaraldehyde. Preferably, the Fv fragments comprise VH and VL chains connected by a peptide linker. These single-chain antigen binding proteins (sFv) are prepared by constructing a structural gene comprising DNA sequences encoding the VH and VL domains connected by an oligonucleotide. The structural gene is inserted into an expression vector, which is subsequently introduced into a host cell such as *E. coli*. The recombinant host cells synthesize a single polypeptide chain with a linker peptide bridging the two V domains. Methods for producing sFvs are described, for example, by [Whitlow and Filpula, Methods 2: 97-105 (1991); Bird et al., Science 242:423-426 (1988); Pack et al., Bio/Technology 11:1271-77 (1993); and U.S. Pat. No. 4,946,778, which is hereby incorporated by reference in its entirety.

Another form of an antibody fragment is a peptide coding for a single complementarity-determining region (CDR). CDR peptides ("minimal recognition units") can be obtained by constructing genes encoding the CDR of an antibody of interest. Such genes are prepared, for example, by using the polymerase chain reaction to synthesize the variable region from RNA of antibody-producing cells. See, for example, Larrick and Fry [Methods, 2: 106-10 (1991)].

Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab').sub.2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or

framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature* 332:323-327 (1988); Verhoeyen et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introduction of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described,

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for example, in U.S. Pat. Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology 10: 779-783 (1992); Lonberg et al., Nature 368: 856-859 (1994); Morrison, Nature 368 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14: 826 (1996); and Lonberg and Huszar, Intern. Rev. Immunol. 13, 65-93 (1995).

Another agent capable of downregulating a biomolecular sequence of the present invention is a small interfering RNA (siRNA) molecule. RNA interference is a two-step process. The first step, which is termed as the initiation step, input dsRNA is digested into 21-23 nucleotide (nt) small interfering RNAs (siRNA), probably by the action of Dicer, a member of the RNase III family of dsRNA-specific ribonucleases, which processes (cleaves) dsRNA (introduced directly or via a transgene or a virus) in an ATP-dependent manner. Successive cleavage events degrade the RNA to 19-21 bp duplexes (siRNA), each with 2-nucleotide 3' overhangs [Hutvagner and Zamore Curr. Opin. Genetics and Development 12:225-232 (2002); and Bernstein Nature 409:363-366 (2001)].

In the effector step, the siRNA duplexes bind to a nuclease complex to form the RNA-induced silencing complex (RISC). An ATP-dependent unwinding of the siRNA duplex is required for activation of the RISC. The active RISC then targets the homologous transcript by base pairing interactions and cleaves the mRNA into 12 nucleotide fragments from the 3' terminus of the siRNA [Hutvagner and Zamore Curr. Opin. Genetics and Development 12:225-232 (2002); Hammond et al. (2001) Nat. Rev. Gen. 2:110-119 (2001); and Sharp Genes. Dev. 15:485-90 (2001)]. Although the mechanism of cleavage is still to be elucidated, research indicates that each RISC contains a single siRNA and an RNase [Hutvagner and Zamore Curr. Opin. Genetics and Development 12:225-232 (2002)].

Because of the remarkable potency of RNAi, an amplification step within the RNAi pathway has been suggested. Amplification could occur by copying of the input dsRNAs which would generate more siRNAs, or by replication of the siRNAs formed. Alternatively or additionally, amplification could be effected by multiple turnover events of the RISC [Hammond et al. Nat. Rev. Gen. 2:110-119 (2001), Sharp Genes. Dev. 15:485-90 (2001); Hutvagner and Zamore Curr. Opin. Genetics and Development 12:225-232 (2002)]. For more information on RNAi see the following

reviews Tuschl ChemBiochem. 2:239-245 (2001); Cullen Nat. Immunol. 3:597-599 (2002); and Brantl Biochem. Biophys. Act. 1575:15-25 (2002).

Synthesis of RNAi molecules suitable for use with the present invention can be effected as follows. First, the mRNA sequence is scanned downstream of the AUG start codon for AA dinucleotide sequences. Occurrence of each AA and the 3' adjacent 19 nucleotides is recorded as potential siRNA target sites. Preferably, siRNA target sites are selected from the open reading frame, as untranslated regions (UTRs) are richer in regulatory protein binding sites. UTR-binding proteins and/or translation initiation complexes may interfere with binding of the siRNA endonuclease complex [Tuschl ChemBiochem. 2:239-245]. It will be appreciated though, that siRNAs directed at untranslated regions may also be effective, as demonstrated for GAPDH wherein siRNA directed at the 5' UTR mediated about 90 % decrease in cellular GAPDH mRNA and completely abolished protein level (www.ambion.com/techlib/mn/91/912.html).

Second, potential target sites are compared to an appropriate genomic database (e.g., human, mouse, rat etc.) using any sequence alignment software, such as the BLAST software available from the NCBI server (www.ncbi.nlm.nih.gov/BLAST/). Putative target sites which exhibit significant homology to other coding sequences are filtered out.

Qualifying target sequences are selected as template for siRNA synthesis. Preferred sequences are those including low G/C content as these have proven to be more effective in mediating gene silencing as compared to those with G/C content higher than 55 %. Several target sites are preferably selected along the length of the target gene for evaluation. For better evaluation of the selected siRNAs, a negative control is preferably used in conjunction. Negative control siRNA preferably include the same nucleotide composition as the siRNAs but lack significant homology to the genome. Thus, a scrambled nucleotide sequence of the siRNA is preferably used, provided it does not display any significant homology to any other gene.

Another agent capable of downregulating a biomolecular sequence of the present invention is a DNAzyme molecule capable of specifically cleaving an mRNA transcript or DNA sequence of the biomolecular sequence. DNAzymes are single-stranded polynucleotides which are capable of cleaving both single and double stranded target sequences (Breaker, R.R. and Joyce, G. Chemistry and Biology

1995;2:655; Santoro, S.W. & Joyce, G.F. Proc. Natl. Acad. Sci. USA 1997;94:4262) A general model (the "10-23" model) for the DNAzyme has been proposed. "10-23" DNAzymes have a catalytic domain of 15 deoxyribonucleotides, flanked by two substrate-recognition domains of seven to nine deoxyribonucleotides each. This type of DNAzyme can effectively cleave its substrate RNA at purine:pyrimidine junctions (Santoro, S.W. & Joyce, G.F. Proc. Natl. Acad. Sci. USA 199; for rev of DNAzymes see Khachigian, LM [Curr Opin Mol Ther 4:119-21 (2002)].

Examples of construction and amplification of synthetic, engineered DNAzymes recognizing single and double-stranded target cleavage sites have been disclosed in U.S. Pat. No. 6,326,174 to Joyce et al. DNAzymes of similar design directed against the human Urokinase receptor were recently observed to inhibit Urokinase receptor expression, and successfully inhibit colon cancer cell metastasis in vivo (Itoh et al; 20002, Abstract 409, Ann Meeting Am Soc Gen Ther www.asgt.org). In another application, DNAzymes complementary to bcr-abl oncogenes were successful in inhibiting the oncogenes expression in leukemia cells, and lessening relapse rates in autologous bone marrow transplant in cases of CML and ALL.

Downregulation of a biomolecular sequence can also be effected by using an antisense oligonucleotide capable of specifically hybridizing with an mRNA transcript of interest.

Design of antisense molecules must be effected while considering two aspects important to the antisense approach. The first aspect is delivery of the oligonucleotide into the cytoplasm of the appropriate cells, while the second aspect is design of an oligonucleotide which specifically binds the designated mRNA within cells in a way which inhibits translation thereof.

The prior art teaches of a number of delivery strategies which can be used to efficiently deliver oligonucleotides into a wide variety of cell types [see, for example, Luft J Mol Med 76: 75-6 (1998); Kronenwett et al. Blood 91: 852-62 (1998); Rajur et al. Bioconjug Chem 8: 935-40 (1997); Lavigne et al. Biochem Biophys Res Commun 237: 566-71 (1997) and Aoki et al. (1997) Biochem Biophys Res Commun 231: 540-5 (1997)].

In addition, algorithms for identifying those sequences with the highest predicted binding affinity for their target mRNA based on a thermodynamic cycle that

accounts for the energetics of structural alterations in both the target mRNA and the oligonucleotide are also available [see, for example, Walton et al. Biotechnol Bioeng 65: 1-9 (1999)].

Such algorithms have been successfully used to implement an antisense approach in cells. For example, the algorithm developed by Walton et al. enabled scientists to successfully design antisense oligonucleotides for rabbit beta-globin (RBG) and mouse tumor necrosis factor-alpha (TNF alpha) transcripts. The same research group has more recently reported that the antisense activity of rationally selected oligonucleotides against three model target mRNAs (human lactate dehydrogenase A and B and rat gp130) in cell culture as evaluated by a kinetic PCR technique proved effective in almost all cases, including tests against three different targets in two cell types with phosphodiester and phosphorothioate oligonucleotide chemistries.

In addition, several approaches for designing and predicting efficiency of specific oligonucleotides using an in vitro system were also published (Matveeva et al., Nature Biotechnology 16: 1374 - 1375 (1998)).

Several clinical trials have demonstrated safety, feasibility and activity of antisense oligonucleotides. For example, antisense oligonucleotides suitable for the treatment of cancer have been successfully used [Holmund et al., Curr Opin Mol Ther 1:372-85 (1999)], while treatment of hematological malignancies via antisense oligonucleotides targeting c-myb gene, p53 and Bcl-2 had entered clinical trials and had been shown to be tolerated by patients [Gerwitz Curr Opin Mol Ther 1:297-306 (1999)].

More recently, antisense-mediated suppression of human heparanase gene expression has been reported to inhibit pleural dissemination of human cancer cells in a mouse model [Uno et al., Cancer Res 61:7855-60 (2001)].

Thus, the current consensus is that recent developments in the field of antisense technology which, as described above, have led to the generation of highly accurate antisense design algorithms and a wide variety of oligonucleotide delivery systems, enable an ordinarily skilled artisan to design and implement antisense approaches suitable for downregulating expression of known sequences without having to resort to undue trial and error experimentation.

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Another agent capable of downregulating a biomolecular sequence of interest is a ribozyme molecule capable of specifically cleaving an mRNA transcript encoding a specific protein product. Ribozymes are being increasingly used for the sequence-specific inhibition of gene expression by the cleavage of mRNAs encoding proteins of interest [Welch et al., *Curr Opin Biotechnol.* 9:486-96 (1998)]. The possibility of designing ribozymes to cleave any specific target RNA has rendered them valuable tools in both basic research and therapeutic applications. In the therapeutics area, ribozymes have been exploited to target viral RNAs in infectious diseases, dominant oncogenes in cancers and specific somatic mutations in genetic disorders [Welch et al., *Clin Diagn Virol.* 10:163-71 (1998)]. Most notably, several ribozyme gene therapy protocols for HIV patients are already in Phase 1 trials. More recently, ribozymes have been used for transgenic animal research, gene target validation and pathway elucidation. Several ribozymes are in various stages of clinical trials. ANGIOZYME was the first chemically synthesized ribozyme to be studied in human clinical trials. ANGIOZYME specifically inhibits formation of the VEGF-r (Vascular Endothelial Growth Factor receptor), a key component in the angiogenesis pathway. Ribozyne Pharmaceuticals, Inc., as well as other firms have demonstrated the importance of anti-angiogenesis therapeutics in animal models. HEPTAZYME, a ribozyme designed to selectively destroy Hepatitis C Virus (HCV) RNA, was found effective in decreasing Hepatitis C viral RNA in cell culture assays (Ribozyne Pharmaceuticals, Incorporated - WEB home page).

An additional method of regulating the expression of a biomolecular sequence in cells is via triplex forming oligonucleotides (TFOs). Recent studies have shown that TFOs can be designed which can recognize and bind to polypurine/polypyrimidine regions in double-stranded helical DNA in a sequence-specific manner. These recognition rules are outlined by Maher III, L. J., et al., *Science*, 1989;245:725-730; Moser, H. E., et al., *Science*, 1987;238:645-630; Beal, P. A., et al., *Science*, 1992;251:1360-1363; Cooney, M., et al., *Science*, 1988;241:456-459; and Hogan, M. E., et al., EP Publication 375408. Modification of the oligonucleotides, such as the introduction of intercalators and backbone substitutions, and optimization of binding conditions (pH and cation concentration) have aided in overcoming inherent obstacles to TFO activity such as charge repulsion and instability, and it was

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recently shown that synthetic oligonucleotides can be targeted to specific sequences (for a recent review see Seidman and Glazer, J Clin Invest 2003;112:487-94).

In general, the triplex-forming oligonucleotide has the sequence correspondence:

oligo	3'-A	G	G	T
duplex	5'-A	G	C	T
duplex	3'-T	C	G	A

However, it has been shown that the A-AT and G-GC triplets have the greatest triple helical stability (Reither and Jeltsch, BMC Biochem, 2002, Sept12, Epub). The same authors have demonstrated that TFOs designed according to the A-AT and G-GC rule do not form non-specific triplexes, indicating that the triplex formation is indeed sequence specific.

Triplex-forming oligonucleotides preferably are at least about 15, more preferably about 25, still more preferably about 30 or more nucleotides in length, up to about 50 or about 100 bp.

Transfection of cells (for example, via cationic liposomes) with TFOs, and formation of the triple helical structure with the target DNA induces steric and functional changes, blocking transcription initiation and elongation, allowing the introduction of desired sequence changes in the endogenous DNA and resulting in the specific downregulation of gene expression. Examples of such suppression of gene expression in cells treated with TFOs include knockout of episomal supFG1 and endogenous HPRT genes in mammalian cells (Vasquez et al., Nucl Acids Res. 1999;27:1176-81, and Puri, et al, J Biol Chem, 2001;276:28991-98), and the sequence- and target specific downregulation of expression of the Ets2 transcription factor, important in prostate cancer etiology (Carbone, et al, Nucl Acid Res. 2003;31:833-43), and the pro-inflammatory ICAM-1 gene (Besch et al, J Biol Chem, 2002;277:32473-79). In addition, Vuyisich and Beal have recently shown that sequence specific TFOs can bind to dsRNA, inhibiting activity of dsRNA-dependent enzymes such as RNA-dependent kinases (Vuyisich and Beal, Nuc. Acids Res 2000;28:2369-74).

Additionally, TFOs designed according to the abovementioned principles can induce directed mutagenesis capable of effecting DNA repair, thus providing both downregulation and upregulation of expression of endogenous genes (Seidman and

Glazer, J Clin Invest 2003;112:487-94). Detailed description of the design, synthesis and administration of effective TFOs can be found in U.S. Patent Application Nos. 2003 017068 and 2003 0096980 to Froehler et al, and 2002 0128218 and 2002 0123476 to Emanuele et al, and U.S. Pat. No. 5,721,138 to Lawn.

Oligonucleotides designed for carrying out the methods of the present invention for any of the sequences provided herein (designed as described above) can be generated according to any oligonucleotide synthesis method known in the art such as enzymatic synthesis or solid phase synthesis. Equipment and reagents for executing solid-phase synthesis are commercially available from, for example, Applied Biosystems. Any other means for such synthesis may also be employed; the actual synthesis of the oligonucleotides is well within the capabilities of one skilled in the art.

Oligonucleotides used according to this aspect of the present invention are those having a length selected from a range of about 10 to about 200 bases preferably about 15 to about 150 bases, more preferably about 20 to about 100 bases, most preferably about 20 to about 50 bases.

The oligonucleotides of the present invention may comprise heterocyclic nucleosides consisting of purines and the pyrimidines bases, bonded in a 3' to 5' phosphodiester linkage.

Preferably used oligonucleotides are those modified in either backbone, internucleoside linkages or bases, as is broadly described hereinunder. Such modifications can oftentimes facilitate oligonucleotide uptake and resistivity to intracellular conditions.

Specific examples of preferred oligonucleotides useful according to this aspect of the present invention include oligonucleotides containing modified backbones or non-natural internucleoside linkages. Oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone, as disclosed in U.S. Pat. Nos: ,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466, 677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; and 5,625,050.

Preferred modified oligonucleotide backbones include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters,

aminoalkyl phosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms can also be used.

Alternatively, modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH₂ component parts, as disclosed in U.S. Pat. Nos. 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623, 070; 5,663,312; 5,633,360; 5,677,437; and 5,677,439.

Other oligonucleotides which can be used according to the present invention, are those modified in both sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for complementation with the appropriate polynucleotide target. An example for such an oligonucleotide mimetic, includes peptide nucleic acid (PNA). A PNA oligonucleotide refers to an oligonucleotide where the sugar-backbone is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The bases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. United States patents that teach the preparation of PNA compounds include, but are not limited to, U.S. Pat. Nos. 5,539,082; 5,714,331;

and 5,719,262, each of which is herein incorporated by reference. Other backbone modifications, which can be used in the present invention are disclosed in U.S. Pat. No: 6,303,374.

Oligonucleotides of the present invention may also include base modifications or substitutions. As used herein, "unmodified" or "natural" bases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified bases include but are not limited to other synthetic and natural bases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further bases include those disclosed in U.S. Pat. No: 3,687,808, those disclosed in The Concise Encyclopedia Of Polymer Science and Engineering, pages 858-859, Kroschwitz, J. I., ed. John Wiley & Sons, 1990, those disclosed by Englisch et al., Angewandte Chemie, International Edition, 1991, 30, 613, and those disclosed by Sanghvi, Y. S., Chapter 15, Antisense Research and Applications, pages 289-302, Crooke, S. T. and Lebleu, B. , ed., CRC Press, 1993. Such bases are particularly useful for increasing the binding affinity of the oligomeric compounds of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2°C. [Sanghvi YS et al. (1993) Antisense Research and Applications, CRC Press, Boca Raton 276-278] and are presently preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

Another modification of the oligonucleotides of the invention involves chemically linking to the oligonucleotide one or more moieties or conjugates, which enhance the activity, cellular distribution or cellular uptake of the oligonucleotide.

Such moieties include but are not limited to lipid moieties such as a cholesterol moiety, cholic acid, a thioether, e.g., hexyl-S-tritylthiol, a thiocholesterol, an aliphatic chain, e.g., dodecandiol or undecyl residues, a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate, a polyamine or a polyethylene glycol chain, or adamantane acetic acid, a palmitoyl moiety, or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety, as disclosed in U.S. Pat. No. 6,303,374.

It is not necessary for all positions in a given oligonucleotide molecule to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an oligonucleotide.

The above-described agents can be provided to the subject *per se*, or as part of a pharmaceutical composition where they are mixed with a pharmaceutically acceptable carrier.

As used herein a "pharmaceutical composition" refers to a preparation of one or more of the active ingredients described herein with other chemical components such as physiologically suitable carriers and excipients. The purpose of a pharmaceutical composition is to facilitate administration of a compound to an organism.

Herein the term "active ingredient" refers to the preparation accountable for the biological effect.

Hereinafter, the phrases "physiologically acceptable carrier" and "pharmaceutically acceptable carrier" which may be interchangeably used refer to a carrier or a diluent that does not cause significant irritation to an organism and does not abrogate the biological activity and properties of the administered compound. An adjuvant is included under these phrases. One of the ingredients included in the pharmaceutically acceptable carrier can be for example polyethylene glycol (PEG), a biocompatible polymer with a wide range of solubility in both organic and aqueous media (Mutter et al. (1979)).

Herein the term "excipient" refers to an inert substance added to a pharmaceutical composition to further facilitate administration of an active ingredient. Examples, without limitation, of excipients include calcium carbonate, calcium

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phosphate, various sugars and types of starch, cellulose derivatives, gelatin, vegetable oils and polyethylene glycols.

Techniques for formulation and administration of drugs may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition, which is incorporated herein by reference.

Suitable routes of administration may, for example, include oral, rectal, transmucosal, especially transnasal, intestinal or parenteral delivery, including intramuscular, subcutaneous and intramedullary injections as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Alternately, one may administer a preparation in a local rather than systemic manner, for example, via injection of the preparation directly into a specific region of a patient's body.

Pharmaceutical compositions of the present invention may be manufactured by processes well known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries, which facilitate processing of the active ingredients into preparations which, can be used pharmaceutically. Proper formulation is dependent upon the route of administration chosen.

For injection, the active ingredients of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hank's solution, Ringer's solution, or physiological salt buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for oral ingestion by a patient. Pharmacological preparations for oral use can be made using a solid excipient, optionally grinding the resulting mixture, and processing the mixture of granules, after adding suitable

auxiliaries if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethylcellulose, sodium carbomethylcellulose; and/or physiologically acceptable polymers such as polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, titanium dioxide, lacquer solutions and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical compositions, which can be used orally, include push-fit capsules made of gelatin as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules may contain the active ingredients in admixture with filler such as lactose, binders such as starches, lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active ingredients may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for the chosen route of administration.

For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by nasal inhalation, the active ingredients for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from a pressurized pack or a nebulizer with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane or carbon dioxide. In the case of a pressurized aerosol, the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in a dispenser may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

The preparations described herein may be formulated for parenteral administration, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multidose containers with optionally, an added preservative. The compositions may be suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical compositions for parenteral administration include aqueous solutions of the active preparation in water-soluble form. Additionally, suspensions of the active ingredients may be prepared as appropriate oily or water based injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acids esters such as ethyl oleate, triglycerides or liposomes. Aqueous injection suspensions may contain substances, which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the active ingredients to allow for the preparation of highly concentrated solutions.

Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile, pyrogen-free water based solution, before use.

The preparation of the present invention may also be formulated in rectal compositions such as suppositories or retention enemas, using, e.g., conventional suppository bases such as cocoa butter or other glycerides.

Pharmaceutical compositions suitable for use in context of the present invention include compositions wherein the active ingredients are contained in an amount effective to achieve the intended purpose. More specifically, a therapeutically effective amount means an amount of active ingredients effective to prevent, alleviate or ameliorate symptoms of disease or prolong the survival of the subject being treated.

Determination of a therapeutically effective amount is well within the capability of those skilled in the art.

For any preparation used in the methods of the invention, the therapeutically effective amount or dose can be estimated initially from in vitro assays. For example, a dose can be formulated in animal models and such information can be used to more accurately determine useful doses in humans.

Toxicity and therapeutic efficacy of the active ingredients described herein can be determined by standard pharmaceutical procedures *in vitro*, in cell cultures or experimental animals. The data obtained from these *in vitro* and cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage may vary depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g., Fingl, et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1).

Depending on the severity and responsiveness of the condition to be treated, dosing can be of a single or a plurality of administrations, with course of treatment lasting from several days to several weeks or until cure is effected or diminution of the disease state is achieved.

The amount of a composition to be administered will, of course, be dependent on the subject being treated, the severity of the affliction, the manner of administration, the judgment of the prescribing physician, etc.

Compositions including the preparation of the present invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

Pharmaceutical compositions of the present invention may, if desired, be presented in a pack or dispenser device, such as an FDA approved kit, which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. The pack or dispenser may also be accommodated by a notice associated with the container in a form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals, which notice is reflective of approval by the agency of the form of the compositions or human or veterinary administration. Such notice, for example, may be of labeling approved by the U.S. Food and Drug Administration for prescription drugs or of an approved product insert.

It will be appreciated that treatment of a disease according to the present invention may be combined with other prior art treatment methods, also known as combination therapy.

As mentioned hereinabove, the splice variants of the present invention may also have diagnostic value. For example, the present inventors uncovered soluble extracellular isoforms of follicular stimulating hormone receptor (FSHR, GenBank Accession: FSHR_human) and luteinizing hormone receptor [LSHR_human, see Table 3 below), each of which can serve as a diagnostic marker for fertility and menopausal disorders.

Thus, the present invention envisages diagnosing in a subject predisposition to, or presence of a disease, which depends on expression and/or activity of a biomolecular sequence of the present invention for its onset or progression or is associated with abnormal activity or expression of a biomolecular sequence of the present invention.

As used herein the term "diagnosing" refers to classifying a disease or a symptom, determining a severity of the disease, monitoring disease progression, forecasting an outcome of a disease and/or prospects of recovery.

Diagnosis of a disease according to the present invention can be effected by determining a level of a polynucleotide or a polypeptide of the present invention in a biological sample obtained from the subject, wherein the level determined can be correlated with predisposition to, or presence or absence of the disease.

As used herein, the term "level" refers to expression levels of RNA and/or protein or to DNA copy number of a splice variant of the present invention.

Typically the level of the splice variant in a biological sample obtained from the subject is different (i.e., increased or decreased) from the level of the same variant in a similar sample obtained from a healthy individual.

As used herein "a biological sample" refers to a sample of tissue or fluid isolated from a subject, including but not limited to, for example, plasma, serum, spinal fluid, lymph fluid, the external sections of the skin, respiratory, intestinal, and genitourinary tracts, tears, saliva, milk, blood cells, tumors, neuronal tissue, organs, and also samples of *in vivo* cell culture constituents.

Numerous well known tissue or fluid collection methods can be utilized to collect the biological sample from the subject in order to determine the level of DNA, RNA and/or polypeptide of the variant of interest in the subject.

Examples include, but are not limited to, fine needle biopsy, needle biopsy, core needle biopsy and surgical biopsy (e.g., brain biopsy).

Regardless of the procedure employed, once a biopsy is obtained the level of the variant can be determined and a diagnosis can thus be made.

Determining the level of the same variant in normal tissues of the same origin is preferably effected along-side to detect an elevated expression and/or amplification.

Typically, detection of a nucleic acid of interest in a biological sample is effected by hybridization-based assays using an oligonucleotide probe.

Hybridization based assays which allow the detection of a variant of interest (i.e., DNA or RNA) in a biological sample rely on the use of oligonucleotide which can be 10, 15, 20, or 30 to 100 nucleotides long preferably from 10 to 50, more preferably from 40 to 50 nucleotides.

Hybridization of short nucleic acids (below 200 bp in length, e.g. 17-40 bp in length) can be effected using the following exemplary hybridization protocols which can be modified according to the desired stringency; (i) hybridization solution of 6 x SSC and 1 % SDS or 3 M TMACl, 0.01 M sodium phosphate (pH 6.8), 1 mM EDTA (pH 7.6), 0.5 % SDS, 100 µg/ml denatured salmon sperm DNA and 0.1 % nonfat dried milk, hybridization temperature of 1 - 1.5 °C below the T_m, final wash solution of 3 M TMACl, 0.01 M sodium phosphate (pH 6.8), 1 mM EDTA (pH 7.6), 0.5 % SDS at 1 - 1.5 °C below the T_m; (ii) hybridization solution of 6 x SSC and 0.1 % SDS or 3 M TMACl, 0.01 M sodium phosphate (pH 6.8), 1 mM EDTA (pH 7.6), 0.5 % SDS, 100 µg/ml denatured salmon sperm DNA and 0.1 % nonfat dried milk, hybridization temperature of 2 - 2.5 °C below the T_m, final wash solution of 3 M TMACl, 0.01 M sodium phosphate (pH 6.8), 1 mM EDTA (pH 7.6), 0.5 % SDS at 1 - 1.5 °C below the T_m, final wash solution of 6 x SSC, and final wash at 22 °C; (iii) hybridization solution of 6 x SSC and 1 % SDS or 3 M TMACl, 0.01 M sodium phosphate (pH 6.8), 1 mM EDTA (pH 7.6), 0.5 % SDS, 100 µg/ml denatured salmon sperm DNA and 0.1 % nonfat dried milk, hybridization temperature.

The detection of hybrid duplexes can be carried out by a number of methods. Typically, hybridization duplexes are separated from unhybridized nucleic acids and the labels bound to the duplexes are then detected. Such labels refer to radioactive, fluorescent, biological or enzymatic tags or labels of standard use in the art. A label can be conjugated to either the oligonucleotide probes or the nucleic acids derived from the biological sample.

For example, oligonucleotides of the present invention can be labeled subsequent to synthesis, by incorporating biotinylated dNTPs or rNTP, or some similar means (e.g., photo-cross-linking a psoralen derivative of biotin to RNAs), followed by addition of labeled streptavidin (e.g., phycoerythrin-conjugated streptavidin) or the equivalent. Alternatively, when fluorescently-labeled oligonucleotide probes are used, fluorescein, lissamine, phycoerythrin, rhodamine (Perkin Elmer Cetus), Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7, FluorX (Amersham) and others [e.g., Kricka et al. (1992), Academic Press San Diego, Calif] can be attached to the oligonucleotides.

Traditional hybridization assays include PCR, RT-PCR, Real-time PCR, RNase protection, in-situ hybridization, primer extension, Southern blot, Northern Blot and dot blot analysis.

Those skilled in the art will appreciate that wash steps may be employed to wash away excess target DNA or probe as well as unbound conjugate. Further, standard heterogeneous assay formats are suitable for detecting the hybrids using the labels present on the oligonucleotide primers and probes.

It will be appreciated that a variety of controls may be usefully employed to improve accuracy of hybridization assays. For instance, samples may be hybridized to an irrelevant probe and treated with RNase A prior to hybridization, to assess false hybridization.

It will be appreciated that antisense oligonucleotides may be employed to quantify expression of a splice isoform of interest. Such detection is effected at the pre-mRNA level. Essentially the ability to quantitate transcription from a splice site of interest can be effected based on splice site accessibility. Oligonucleotides may compete with splicing factors for the splice site sequences. Thus, low activity of the antisense oligonucleotide is indicative of splicing activity [see Sazani and Kole (2003), *supra*].

Polymerase chain reaction (PCR)-based methods may be used to identify the presence of an mRNA of interest. For PCR-based methods a pair of oligonucleotides is used, which is specifically hybridizable with the polynucleotide sequences described hereinabove in an opposite orientation so as to direct exponential amplification of a portion thereof (including the hereinabove described sequence alteration) in a nucleic

acid amplification reaction. Examples, of oligonucleotide pair of primers which can be used to detect variants of the present invention are listed in Table 2, below.

The polymerase chain reaction and other nucleic acid amplification reactions are well known in the art and require no further description herein. The pair of oligonucleotides according to this aspect of the present invention are preferably selected to have compatible melting temperatures (T_m), e.g., melting temperatures which differ by less than that 7 °C, preferably less than 5 °C, more preferably less than 4 °C, most preferably less than 3 °C, ideally between 3 °C and 0 °C.

Hybridization to oligonucleotide arrays may be also used to determine expression of variants of the present invention. Such screening has been undertaken in the BRCA1 gene and in the protease gene of HIV-1 virus [see Hacia et al., (1996) Nat Genet 1996;14(4):441-447; Shoemaker et al., (1996) Nat Genet 1996;14(4):450-456; Kozal et al., (1996) Nat Med 1996;2(7):753-759].

The nucleic acid sample which includes the candidate region to be analyzed is isolated, amplified and labeled with a reporter group. This reporter group can be a fluorescent group such as phycoerythrin. The labeled nucleic acid is then incubated with the probes immobilized on the chip using a fluidics station. For example, Manz et al. (1993) Adv. in Chromatogr 1993; 33:1-66 describe the fabrication of fluidics devices and particularly microcapillary devices, in silicon and glass substrates.

Once the reaction is completed, the chip is inserted into a scanner and patterns of hybridization are detected. The hybridization data is collected, as a signal emitted from the reporter groups already incorporated into the nucleic acid, which is now bound to the probes attached to the chip. Since the sequence and position of each probe immobilized on the chip is known, the identity of the nucleic acid hybridized to a given probe can be determined.

It will be appreciated that when utilized along with automated equipment, the above described detection methods can be used to screen multiple samples for diseases both rapidly and easily.

The presence of the variant of interest may also be detected at the protein level. Numerous protein detection assays are known in the art, examples include, but are not limited to, chromatography, electrophoresis, immunodetection assays such as ELISA and western blot analysis, immunohistochemistry and the like, which may be effected using antibodies specific to the variants of the present invention.

Preferably used are antibodies, which specifically interact with the polypeptide variants of the present invention and not with wild type.

The diagnostic reagents described hereinabove can be included in diagnostic kits. For example a kit for diagnosing a fertility disorder in a subject can include the set of oligonucleotide primers set forth in SEQ ID NOs: 9 and 10 in a container and a second container with appropriate buffers and preservatives for executing a PCR reaction.

Diagnostics using the above-described methodology can be validated using other diagnostic methods which are well known in the art such as by imaging, molecular detection of known markers and the like.

Apart of clinical applications, the biomolecular sequences of the present invention can find other commercial uses such as in the food, agricultural, electro-mechanical, optical and cosmetic industries [<http://www.physics.unc.edu/~rsuper/XYZweb/> XYZchipbiomotors.rs1.doc; <http://www.bio.org/er/industrial.asp>]. For example, newly uncovered gene products, which can disintegrate connective tissues, can be used as potent anti scarring agents for cosmetic purposes. For example, newly uncovered gene products, which can disintegrate connective tissues, can be used as potent anti scarring agents for cosmetic purposes. Non-limiting examples of such gene products include the matrix metalloproteinase family of proteins (MMP), which are a group of proteases having varying specificities for ECM components as substrates, non-limiting examples of which have the gene symbols "CLG" and "CGL4B" in the attached files. These proteins are involved in ECM break-down as part of the wound healing process, for example for cell migration. The activity of these proteins is also modulated by specific tissue inhibitors of MMPs (TIMP) and other factors in the microenvironment in and around the wound area. Therefore, one possible optional application for the present invention would be the selection of appropriate antisense oligonucleotides for either one or more MMPs and /or for factors related to TIMPs, in order to modulate wound healing activities (and/or as previously noted, for treatment of arthritis).

As another optional treatment, production of collagen may be optionally modulated through the use of appropriate antisense oligonucleotides. Collagen is an important connective tissue element, but is also involved in pathological conditions such as fibrosis and the formation of adhesions between tissues of different organs, a

condition which may occur for example after surgery. Therefore, modulation of collagen production, for example to reduce collagen production, may optionally be performed according to the present invention.

Other applications include, but are not limited to, the making of gels, emulsions, foams and various specific products, including photographic films, tissue replacers and adhesives, food and animal feed, detergents, textiles, paper and pulp, and chemicals manufacturing (commodity and fine, e.g., bioplastics).

Research applications include, for example, differential cloning, detection of rearrangements in DNA sequences as disclosed in U.S. Pat. No: 5,994,320, drug discovery and the like.

As used herein the term "about" refers to $\pm 10\%$.

Additional objects, advantages, and novel features of the present invention will become apparent to one ordinarily skilled in the art upon examination of the following examples, which are not intended to be limiting. Additionally, each of the various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below finds experimental support in the following examples:

EXAMPLES

Reference is now made to the following examples, which together with the above descriptions, illustrate the invention in a non limiting fashion.

Generally, the nomenclature used herein and the laboratory procedures utilized in the present invention include molecular, biochemical, microbiological and recombinant DNA techniques. Such techniques are thoroughly explained in the literature. See, for example, "Molecular Cloning: A laboratory Manual" Sambrook et al., (1989); "Current Protocols in Molecular Biology" Volumes I-III Ausubel, R. M., ed. (1994); Ausubel et al., "Current Protocols in Molecular Biology", John Wiley and Sons, Baltimore, Maryland (1989); Perbal, "A Practical Guide to Molecular Cloning", John Wiley & Sons, New York (1988); Watson et al., "Recombinant DNA", Scientific American Books, New York; Birren et al. (eds) "Genome Analysis: A Laboratory Manual Series", Vols. 1-4, Cold Spring Harbor Laboratory Press, New York (1998); methodologies as set forth in U.S. Pat. Nos. 4,666,828; 4,683,202;

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4,801,531; 5,192,659 and 5,272,057; "Cell Biology: A Laboratory Handbook", Volumes I-III Cellis, J. E., ed. (1994); "Current Protocols in Immunology" Volumes I-III Coligan J. E., ed. (1994); Stites et al. (eds), "Basic and Clinical Immunology" (8th Edition), Appleton & Lange, Norwalk, CT (1994); Mishell and Shiigi (eds), "Selected Methods in Cellular Immunology", W. H. Freeman and Co., New York (1980); available immunoassays are extensively described in the patent and scientific literature, see, for example, U.S. Pat. Nos. 3,791,932; 3,839,153; 3,850,752; 3,850,578; 3,853,987; 3,867,517; 3,879,262; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; 4,098,876; 4,879,219; 5,011,771 and 5,281,521; "Oligonucleotide Synthesis" Gait, M. J., ed. (1984); "Nucleic Acid Hybridization" Hames, B. D., and Higgins S. J., eds. (1985); "Transcription and Translation" Hames, B. D., and Higgins S. J., Eds. (1984); "Animal Cell Culture" Freshney, R. I., ed. (1986); "Immobilized Cells and Enzymes" IRL Press, (1986); "A Practical Guide to Molecular Cloning" Perbal, B., (1984) and "Methods in Enzymology" Vol. 1-317, Academic Press; "PCR Protocols: A Guide To Methods and Applications", Academic Press, San Diego, CA (1990); Marshak et al., "Strategies for Protein Purification and Characterization - A Laboratory Course Manual" CSHL Press (1996); all of which are incorporated by reference as if fully set forth herein. Other general references are provided throughout this document. The procedures therein are believed to be well known in the art and are provided for the convenience of the reader. All the information contained therein is incorporated herein by reference.

EXAMPLE 1*Computational identification of alternative splicing without usage of expressed sequence data and "alternativeness score"***Background**

Alternative splicing is a mechanism by which multiple gene products are generated from a single gene. Currently, the only way for large-scale computational detection of alternative splicing is by Expressed Sequence Tags (ESTs) analysis, and microarray technology.

While reducing the present invention to practice, the present inventors designed a new approach for computational identification of splice variants without needing expressed sequence data. The present inventors have first uncovered that alternatively spliced exons have unique characteristics differentiating them from constitutively spliced ones. Using machine-learning techniques, a combination of these characteristics was found to identify alternatively spliced exons with very high probability.

Experimental Procedures

Compiling the training sets of conserved alternative and constitutive exons - Human and ESTs and cDNAs were obtained from NCBI GenBank version 131 (August 2002) (www.ncbi.nlm.nih.gov/dbEST) and aligned to the human genome build 30 (August 2002). (www.ncbi.nlm.nih.gov/genome/guide/human) using the LEADS clustering and assembly system as described in Sorek et al. (2002) Genome Res. 12:1060-1067. Briefly, the software cleans expressed sequences from repeats, vector contaminations and immunoglobulins. It then aligns expressed sequences to the genome taking alternative splicing into account, and clusters overlapping expressed sequences into "clusters" that represent genes or partial genes.

Alternatively spliced internal exons and constitutively spliced internal exons were identified using the same methods described in Sorek et al. (2002). In brief, these methods screen for reliable exons requiring canonical splice sites and discarding possible genomic contamination events. A constitutively spliced internal exon was defined as an internal exon supported by at least 4 sequences, for which no alternative splicing was observed. An alternatively spliced internal exon was defined as such if there was at least one sequence that contained both the internal exon and the 2

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flanking exons (exon inclusion), and one sequence that contained the two flanking exons but skipped the middle one (exon skipping).

Mouse ESTs and cDNAs from GenBank version 131 were aligned to the human genome build 30 as follows. Mouse ESTs and cDNAs were cleaned from terminal vector sequences, and low complexity stretches and repeats in the expressed sequences were masked. Sequences with internal vector contamination were discarded. Sequences identified as immunoglobulins or T-cell receptors were discarded. In the next stage, expressed sequences were heuristically compared to the genome to find likely high-quality hits. They were then aligned to the genome using a spliced alignment model that allows long gaps. Single hits of mouse expressed sequences to the human genome shorter than 20 bases, or having less than 75 % identity to the human genome, were discarded. Using these parameters, 1,341,274 mouse ESTs were mapped to the human genome, 511,381 of them having all their introns obeying the GT/AG or GC/AG rules.

To determine if the borders of a human intron (which define the borders of the flanking exons) were conserved in mouse, a mouse EST spanning the same intron-borders while aligned to the human genome was required (with alignment of at least 25 bp on each side of the exon-exon junction). In addition, this mouse EST was required to span an intron (i.e., open a long gap) at the same position along the EST while aligned to the mouse genome.

Alignment of intronic regions was done using sim4 [Florea (1998) *Nat. Rev. Genet.* 3:285-298]. An alignment was considered significant according to sim4 default parameters, i.e., at least one word of 10 consecutive identical nucleotides. Lengths of alignments and identity levels were parsed from sim4 standard output. For per-position conservation calculation, the GCG GAP program was run of the 100 intronic nucleotides from each side of the exon, and the alignments were achieved.

Compilation of dataset of 110,932 human exons with mouse orthologues -
Human and ESTs and cDNAs were obtained from NCBI GenBank version 136 (2003) (www.ncbi.nlm.nih.gov/dbEST) and were mapped to the human genome April 2003 assembly (www.ncbi.nlm.nih.gov/genome/guide/human) using the spliced alignment module of LEADS. For each expressed sequence, all mappings of internal exons on the human genome were retrieved. Only exons flanked by AG/GT or

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AG/GC splice sites were allowed. 185,799 human exons mapped to the human genome were thus retrieved.

To find the mouse orthologue for each human exon, mouse expressed sequences from GenBank version 136 were first aligned to the human genome, as described above. Mouse sequences exactly spanning human exons were aligned to the mouse genome as well, and the corresponding sequence on the mouse genome was declared as the orthologous mouse exon, if AG/GT or AG/GC legal splice sites flanked it.

Human exons for which no spanning mouse expressed sequence was detected were aligned directly to the mouse genome using the LEADS "cluster" module. Hits spanning the full length of the exon, that were flanked by AG/GT or AG/GC legal splice sites, were declared as the orthologous mouse exons.

Altogether, these searches retrieved 110,932 pairs of exons in the human and mouse genomes. For each such exon, all classifying parameters were calculated as follows. Conservation between exons was calculated from aligning the human exon to the mouse exon using the sim4 alignment program. Conservation in the flanking intronic sequences was calculated as described above (in the "Compiling the training sets..." section of the methods). Exon size and divisibility by 3 were retrieved from the exon sequence itself. Score was calculated for each exon as described in the results section.

Results

The present inventors have previously compiled sets of alternatively spliced (cassette) and constitutively spliced exons that are conserved between human and mouse. [Sorek (2003) *Genome Res.* 13:1631-1637]. Interestingly, alternatively spliced exons were found to be frequently flanked by intronic sequences conserved between human and mouse, but constitutively spliced exons were not [Sorek (2003) *supra* and Figures 1a-b, as described below and in Table 1]. Such conserved intronic sequences are probably involved in the regulation of alternative splicing.

The training sets of exons used herein initially contained 243 alternative exons and 1966 constitutive exons. These sets were based on EST analyses of GenBank 131, where the constitutive exons were defined as such if there were at least 4 expressed sequences supporting them, and no EST skipping them, both in human and in mouse. For the present analysis constitutive exons for which an evidence for

alternative splicing appeared in the newer version of GenBank, 136 were eliminated to provide a training set of 1753 constitutive exons.

Further features that distinct alternatively spliced exons from constitutively spliced exons were then sought. Figures 1a-e show structural differences between alternatively spliced exons and constitutively spliced exons. Figure 1a shows high level of sequence conservation in the last 100 nucleotides of introns flanking alternative exons but not constitutive exons. A conserved sequence region refers to length of alignment between human and mouse DNA in that region. Similar conservation was seen in the first 100 nucleotides of downstream introns flanking alternative exons (Figure 1b). Furthermore, alternatively spliced exons exhibited much higher level of human-mouse sequence conservation (i.e., 50 % of exons showed more than 95 % identity) than constitutively spliced exons (i.e., 50 % of constitutively spliced exons showed 90 % identity, see Figure 1c). The size of alternative splices exons was found to be shorter than that of constitutive exons (Figure 1d). Essentially, the average length of alternative exon (i.e., 50 % of the exon data set) was about 75, while the average length of constitutive exons was almost twice as much. Finally, highly conserved exons which are divisible by 3 were much more frequent in the alternative exon dataset than in the constitutive exon dataset (Figure 1e). Table 1 below, summarizes the major classifying features which were found.

Table 1: Features differentiating between alternatively spliced exons and constitutively spliced exons

	Alternatively spliced exons	Constitutively spliced exons	P value ^a
Average size	87	128	$p < 10^{-16}$
Percent exons that are a multiple of 3	73% (177/243)	37% (642/1753)	$p < 10^{-9}$
Average human-mouse exon conservation	94%	89%	$p < 10^{-36}$
Percent exons with upstream intronic elements conserved in mouse ^b	92% (223/243)	45% (788/1753)	$p < 10^{-11}$
Percent exons with downstream intronic elements conserved in mouse ^b	82% (199/243)	35% (611/1753)	$p < 10^{-14}$
Percent exons with both upstream and downstream intronic elements conserved in mouse ^b	77% (188/243)	17% (292/1753)	$p < 10^{-37}$

^a P value was calculated using Fisher's exact test, except for the "average size" and "average human-mouse exon conservation", for which p value was calculated using student's T test.

^b Conservation was detected in the 100 intronic nucleotides immediately upstream or downstream the exon using local alignment with the mouse 100 counterpart intronic nucleotides. A minimum hit was 12 consecutive perfectly matching nucleotides.

In short, conserved alternatively spliced exons are much shorter than constitutively spliced ones, their size tends to be a multiple of 3, and they share higher identity level with their mouse counterpart exon (Figures 1c-e). These differences probably stem from the unique function of the alternative exons: Since these exons are cassette exons that are sometimes inserted and sometimes skipped, they should be dividable by 3 such that the reading frame is kept when skipped. This constraint does not apply to constitutively spliced exons. The higher identity level between human and mouse could be explained by the fact that alternatively spliced exons frequently contain sequences that regulate their splicing [exonic splicing enhancers and silencers, reviewed by Cartegni (2002) *Nat. Rev. Genet.* 3:285-298]. These regulatory sequences add another level of conservation constraint on the exon sequence. The fact that alternatively spliced exons are smaller than constitutively spliced ones was previously reported [Thanaraj (2003) *Prog. Mol. Subcell. Biol.* 31:1-31] and may be attributed to the fact that the spliceosome sub-optimally recognizes smaller exons [Berget (1995) *J. Biol. Chem.* 270(6):2411-4].

The above-described sequence features can be used to identify alternatively spliced exons in the human and the mouse genomes. However, each feature by itself is not strong enough to classify an exon. Therefore a combination of features that would exclusively "define" alternative exons was determined by complete iteration on the above-described training sets of alternative and constitutive exons. The classifying parameters that were iterated over were the following: Exon length, dividable/not dividable by 3, percent identity when aligned to the mouse counterpart, length of conserved intronic sequence in the 100 bases immediately upstream the exon, identity level in the conserved upstream intronic sequence stretch, length of conserved intronic sequence in the 100 bases immediately downstream the exon, and identity level in the downstream conserved intronic sequence stretch. The output was a set of rules, from which a specific combination that would supply maximum specificity for identifying alternatively spliced exons was searched.

The best combination from this iteration was the following: At least 95 % identity with the mouse exon counterpart; exon size is a multiple of 3; at least 15 conserved intronic nucleotides out of the first 100 nucleotides downstream the exon; and at least 12 conserved intronic nucleotides upstream the exon with at least 85 % identity. 76 exons, or 31 % of the training set of 243 alternatively spliced exons,

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exhibited this combination of features. However, none of the exons from the set of 1753 constitutively spliced exons matched these features.

The above combination of parameters can therefore be used to identify alternatively spliced exons with very high specificity and ~30 % sensitivity.

To test this 110,932 human exons were collected, for which a mouse counterpart could be identified (see methods). For each of these exons, all classifying parameters were calculated.

Out of the 110,932 human exons, 1,030, or ~ 1%, were found to comply with the above-mentioned combination of parameters. To check if these exons are indeed alternatively spliced, human expressed sequences (ESTs or cDNAs) that skip the exons but contain the two exons flanking it were searched. For 518 (50 %) of the candidate alternative exons there was such skipping evidence. For comparison, only 7 % out of the entire set of 110,932 human exons had similar skipping EST evidence. This means that the combination of parameters, which were chosen indeed caused alternatively spliced exons to be retrieved.

The remaining 512 candidate alternative exons were manually examined using the UCSC genome browser (April 2003), and found that for 195 additional exons there was a human expressed sequence showing patterns of alternative splicing other than exon skipping (e.g., intron retention, alternative donor/acceptor, mutually exclusive exons). Thus, 707 (69 %) of the candidate alternative exons identified by the above-described methodology were supported by independent evidence for alternative splicing deriving from dbEST and RefSeq.

But what about the remaining 317 (31 %) of the candidate exons? These can still be alternatively spliced exons for which not enough ESTs exist, so that a skipping variant has not appeared in dbEST yet. Indeed, while on average there were 32 supporting expressed sequences per exon in the general set of 110,932 exons (median 10), the support for the 317 candidate alternatives was much smaller, averaging in 14 sequences (median 7).

The method of identifying cassette exons without using ESTs, as described herein, allows estimation of the absolute number of alternatively spliced exons in the human genome. The above-described results show that the combination of characteristics presented herein identifies 31 % of the cassette exons in the training set. This combination retrieved 1,030 (1 %) out of the 110,932 exons tested. It can

thus be concluded that 1 % / 0.31, or ~ 3 % of all human exons, are alternatively spliced in an exon skipping manner. Moreover, the exons in the initial training set of 243 cassette exons were all alternatively spliced in a pattern of exon skipping, so that the present method would retrieve mainly skipped exons. Exon skipping is known to comprise only about 50 % of all types of alternative splicing, with other types, such as alternative donor/acceptor, mutually exclusive exons, and intron retention comprise the remaining 50 %. Therefore, it is estimated that up to 2 · 3 % (i.e., 6 %) of all human exons, are alternatively spliced. As the human genome contains ~210,000 exons [Lander (2001) Nature 409:860-921], 6% or ~12,000 exons, are alternatively spliced.

Understanding this it is now possible to devise an "alternativeness score" that reports on the probability that a given exon is alternatively spliced. The characterizing features are characterized for a given exon (length of conserved introns upstream and downstream, exon length, conservation with mouse counterpart exon, and divisibility by 3). Then, the fraction of alternative exons from the training set of 243 alternative exons (let X be this number) that answers to this combination of parameters is calculated (have intronic conservation greater or equal to its intronic conservation; have length lesser or equal to its length; has exon conservation greater or equal to its exon conservation; and divides/not divides by 3 as the tested exon). Similarly, the fraction of constitutive exons is calculated from the set of 1753 that answers to this combination of parameters (let Y be this number). Then the fraction of alternative exons is multiplied by 12,000 (the actual number of alternatives in the human genome), and the fraction of constitutive exons by 200,000 (the actual number of constitutive exons in the human genome). The sum of the resulting numbers is the actual number of exons that have this combination of parameters that are expected to be found in the human genome. The "alternativeness score" is the number of predicted alternative exons divided by the above-described sum.

Presenting this mathematically, the "alternativeness score" (denoted as "A") is:

$$A = (X * 12,000) / (X * 12,000 + Y * 200,000)$$

As an example the following parameters are used:

- Size 123 bp
- Divides by 3

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- Length of upstream conserved region: 73 bp
- Length of downstream conserved region: 100 bp
- Human-Mouse exon conservation: 96 %

13 out of 243 ($X = 5.3\%$) alternative exons have these features, while 1/1753 (0.05%) constitutive exons have these features. $5.3\% \times 12,000 = 636$ and $0.05\% \times 200,000 = 100$.

Therefore, the alternativeness score A is : $A = 636 / (636 + 100) = 86\%$.

Using this alternativeness scoring, 4042 exons in the human genome exhibited a score of 100 %, 749 additional exons exhibited a score between 90 % to 100 % and 2032 exons exhibited a score between 80 % to 90 %.

The classification rule that was chosen for the experimental verification retrieves alternatively spliced exons with a very high specificity (less than 0.3% false positive rate) but at the price of a relatively low sensitivity (32%). Other rules can be chosen in which sensitivity is higher, but naturally this would increase the false positive rate of the prediction. Figure 6 presents a sensitivity versus false positive rate plot (ROC curve) for different rules selecting for increasing number of alternative exons from our test set of 243 exons. As shown in the figure, it is possible to employ a rule that would identify up to 73% of the alternative exons, but this rule would also retrieve 36% of the constitutively spliced exons (the upper limit of 73% is due to the Boolean nature of the "divisibility by 3" feature). Note, that since most of the exons in the human genome are constitutive, such a rule would have low predictability for exon skipping: Assuming, for example, that ~10%, or 20,000 out of the ~200,000 predicted exons in the human genome, are alternative, the probability that an exon identified by the 73%:36% rule would really be alternative is only 18% ($0.73 * 20,000 / [0.73 * 20,000 + 0.36 * 180,000]$). Therefore, preferably a rule is selected with close to zero false positives. The curve in Figure 6 presents a variety of alternatives, and allows the selection of a rule for a desired target specificity or sensitivity. For example, 50% sensitivity is achievable at about 1.8% false positive rate.

EXAMPLE 2

Experimental evidence for putative alternative exons uncovered using the methodology of the present invention

Biological relevance of computationally identified alternative exons in the absence of EST data support was determined according to RT-PCR results.

Experimental Procedures

RT-PCR - RT was done on total RNA samples. RT-PCR reactions were effected using random hexamer primer mix (Invitrogen) and Superscript II Reverse transcriptase (Invitrogen). Conditions used were as follows: denaturation at 70 °C (5 min), annealing on ice, RT at 37 °C (1 hour). "Hot-Star" Taq polymerase (Qiagen) was used in all reaction samples. Some reactions required addition of Q solution (Qiagen) to enhance the reaction. Reaction composition included: total volume of 25 µl, Taq Buffer x10 – 2.5 µl, DNTPs (mix of 4) x12.5 – 2µl, Primers – 0.5 µl of each (total 1 µl), cDNA - 1 µl (1-2 ng/µl), Taq Enzyme – 0.5 µl, Q solution (when needed) x5 - 5 µl, H₂O was added to complete a final volume of 25 µl.

Primers are listed in Table 2, below.

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Table 2

<i>Gene</i>	<i>Forward primer/SEQ ID NO:</i>	<i>Reverse Primer / SEQ ID NO:</i>	<i>Predicted product size (bp)</i>	<i>Predicted product size of novel variant</i>
EFNA	ACCGGCCTCACTCTCCAAA TGG/1	TGGCTCGGCTGACTC ATGTACGG/2	287	206
EPHB1	AAGCTCCAGCATTACAGC ACAGGCC/3	ACCCTCCAGGCAGAAT GATGTTAGG/4	324	201
FGF11	CCAAGGTGCGACTGTGCG G/5	GGTAGAGAGCAGAG GCGTACAGGACG/6	344	233
VLDLR	TGAGCCCCCTGAAAGAGTG TCATATAAACG/7	TCTAAGCCAATCTTC CTGATGTCTCTCG/8	324	198
FSHR	CCTGCTCTACATCAACCC GAGGCC/9	CCATAGCTAGGCAGG GAATGGATCC/10	394	skipping 7: 325; skipping 8: 319; skipping 7&8: 250; intron 7 retention : 505
NOTCH2	GAACACGGATGGGCCCT CC/ 11	GGGGCAAAGTGTATC GATCACCCG/12	352	238
NTRK2	GGTCGGGAACATCTCTCGG TCATGC/13	GCTCCCTTTCAAGAA CAATGTTATGTCGC/1 4	400	211
PTPRZ1	AAAAGATGCTGATGGGAT CCTGGC/15	TGCAGTCTGGAAGCA TTTCCTGCC/16	138	138
VEGFC	CAGCACGAGCTACCTCAG CAAGACG/17	CACTGACAGGTCTCT TCATCCAGCTCC/18	351	199
HPSE2	TCACCTCGTGGACCAGAAT TTTAACCC/19	ACTAAGGGCTGGCCA TTCAGTTGC/20	357	205
HGF	GGATCATCAGACACCACA CCGGC/21	CGTGAGGATACTGAG AATCCCAACGC/22	302	183

Reaction conditions were as follows: Activation of HotStar Taq – 95 °C for 5 min; [denaturation – 94 °C for 45 sec; annealing - Tm (specific for each set of primers) – 4-5 °C for 45 sec; extension – 72 °C for 1 min] x 34 cycles]; Gap filling – 72 °C for 10 min; storage – 10 °C Forever.

Reaction products were separated on a 2 % agarose gel in TBEx5 at ~150V. DNA was extracted from gel using a Qiaquick (Qiagen) kit, and DNA was sent out for direct sequencing using same primers.

Tissues and cell-lines – All samples were cDNA pools generated by RT-PCR. Sample 1: Cervix pool – included a pool of 3 cervix derived RNA samples. Samples were of mixed origin (tumor and normal). The cervix pool also included mRNA from

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HeLa cell-line (cervical cancer). Sample 2: Uterus pool – included a pool of 3 uterus derived RNA samples. Samples were of mixed origin (tumor and normal). Sample 3: Ovary pool - included a pool of 5 normal ovary derived RNA samples (Biochain www.biochain.com). The ovary pool was supplemented with two ovary samples of Mix origin (Tumor and Normal). Sample 4: Placenta – included one sample of Placenta derived RNA of a normal origin (Biochain). Sample 5: Breast Pool – included a pool of 3 breast derived RNA samples of mixed origin (i.e., 2 samples from a tumorous origin and one from a normal origin). Sample 6: Colon and intestine – included a pool of 5 colon derived RNA of mixed origin (tumor and normal). The pool was supplemented with one intestine (Normal) derived RNA sample. Sample 7: Pancreas – included one sample of normal pancreas derived RNA (Biochain). Sample 8: Liver and Spleen pool– included one sample of normal liver derived RNA (Biochain), one sample of normal spleen derived RNA (Biochain) and one sample of HepG2 cell line (liver tumor) derived RNA. Sample 9: Brain pool – included a pool of normal brain derived RNA samples (Biochain). Sample 10: Prostate pool – included a pool of normal prostate derived RNA samples (Biochain). Sample 11: Testis pool – included a pool of normal testis derived RNA samples (Biochain). Sample 12: Kidney pool – included a pool of normal kidney derived RNA samples (Biochain). Sample 13: Thyroid pool – included a pool of normnal thyroid derived RNA samples (Biochain – Normal). Sample 14: Assorted cell-line pool – included a pool of RNA samples from the following cell-lines: DLD, MiaPaCa, HT29, THP1, MCF7 (Obtained from the ATCC, USA).

Results

To show that candidate alternative exons for which no EST data exists are indeed alternative, 11 of them were randomly selected for experimental verification. For each of these exons, primers were designed from two flanking exons. RT-PCR reactions were carried out with RNA extractions of 14 different tissue types (Figures 2a-i). For 9 of these exons, a skipping splice variant was detected in at least one of the 14 tissues tested. In the tenth gene (VLDLR), it was predicted that exon 9 would be skipped; instead, the RT-PCR showed another type of alternative splicing - retention of intron 8. Only in one out of the 11 genes tested, the predicted skipping was not detected (skipping on exon 7 in FSHR).

In short, RT-PCR detected alternative splicing in 10 out of 11 predicted cases, in 9 of which this alternative splicing was an exon skipping event as predicted. This reflects a rate of success of at least 80 %-90 %. Moreover, the fact that the two predicted exon skipping events were not detected does not mean they do not exist, as they could still exist in a tissue other than the 14 that were tested, or in a particular embryonic developmental stage for example.

A similar protocol was followed for the experimental results in Figure 2j, except that a different set of primers was used (see Table 8 below).

Table 8: Primers used for validation of alternative exons.

Gene and direction	Primer sequences	TM
FGF11 Forward	5' – CCAAGGTGCGACTGTGCGG – 3'	68°C
FGF11 Reverse	5' – GGTAGAGAGCAGAGCGTACAGGACG – 3'	66°C
EFNA5 Forward	5' – ACCGGCCTCACTCTCCAAATGG – 3'	65°C
EFNA5 Reverse	5' – TGGCTCGGCTGACTCATGTACGG – 3'	67°C
NCOA1 Forward	5' – AGGCAACACGACGAAATAGCCATACC – 3'	66°C
NCOA1 Reverse	5' – TCTGGCATAAGATGGTTCTGCC – 3'	65°C
PAM Forward	5' – TGTCCCAGTGCCCCGGG – 3'	61°C
PAM Reverse	5' – GGTGAAATCCACAGCTGACTTGG – 3'	62°C
GOLGA4Forward	5' – TCAAGAGAACCTACTTAAGCGTTGTAAGG – 3'	61°C
GOLGA4Reverse	5' – TGAGCAATTCTTCTTCTTCATTCC – 3'	61°C
NPR2 Forward	5' – CATGTTGGTGTTCAGCTTCC – 3'	62°C
NPR2 Reverse	5' – CGGGTCAGCTCAATGCGC – 3'	62°C
VLDLR Forward	5' – TGAGCCCCCTGAAAGAGTGTCAATAAACG – 3'	66°C
VLDLR Reverse	5' – TCTAAGCCAATCTTCTGATGTCTCTCG – 3'	66°C
BAZ1A Forward	5' – TGCTCTGATGGTTGGAGTTCC – 3'	61°C
BAZ1A Reverse	5' – CGTTTTGATATCTATACTTGCATTGC – 3'	60°C
SMARCD1Forward	5' – CAGCCTTGTCCAAATATGATGCC – 3'	61°C
SMARCD1Reverse	5' – AAACCTCCGCTCGTGAGGG – 3'	61°C

DICER1 Forward	5' – AACTCATTCAAGGTTGGG – 3'	61°C
DICER1 Reverse	5' – CCAGGTCAGTGCAGTTTCAGC – 3'	61°C
HATB Forward	5' – AGGCTTCAGACCTTTGATGTGG – 3'	62°C
HATB Reverse	5' – CTTCCGCTGTAATATCAAGAACTGTAGG – 3'	61°C
PRKCM Forward	5' – AAGTACTGGGTTCTGGACAGTTGG – 3'	61°C
PRKCM Reverse	5' – CTGGTTGAGGTACAGTGAACG – 3'	61°C
RNASE3L Forward	5' – CGGAGAATTTTGTGTGAAAGGG – 3'	61°C
RNASE3L Reverse	5' – CCAGCTCCTCCACTGAAGC – 3'	61°C
TIAM2 Forward	5' – AACGACAGTCAGGCCAACGG – 3'	62°C
TIAM2 Reverse	5' – CCAGAAACACCTTCTGAAACTCAAGC – 3'	62°C
MDA5 Forward	5' – AAATCTGGAGAAGGAGGTCTGGG – 3'	61°C
MDA5 Reverse	5' – CCACTCTGGTTTCCACTCCC – 3'	61°C

Table 9 shows a description of the results obtained in the experiment (shown in Figure 2j).

Table 9: Experimental validation of predicted alternatively spliced exons

Gene	Alt Exon ^a	PCR confirmed ^b	Type of alternative confirmed ^c	Gene Description
FGF11	2	Yes	Skip	fibroblast growth factor 11
EFNA5	4	Yes	Skip	ephrin-A5
NCOA1	8	Yes	Skip	steroid nuclear receptor coactivator
PAM	22	Yes	Skip	protein associated with Myc mRNA
GOLGA4	9	Yes	Skip	golgi autoantigen, golgin

				subfamily a, 4
NPR2	9	Yes	Skip	natriuretic peptide receptor B/guanylate cyclase B
VLDLR	9	Yes	Int Ret ^d	very low density lipoprotein receptor
BAZ1A	12	Yes	Alt 3'ss ^e	bromodomain adjacent to zinc finger domain protein 1A
SMARCD1	7	Yes	Alt 3'ss ^f	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1
PRKCM	15	No		protein kinase C, mu
TIAM2	12	No		T-cell lymphoma invasion and metastasis 2
MDA5	4	No		melanoma differentiation associated protein-5
RNASE3L	15	No		nuclear RNase III
HAT1	7	No		histone acetyltransferase 1
DICER1	6	No		Dicer1, Dcr-1 homolog (Drosophila)

^a Serial number of exon (out of gene's exons) identified as alternative

^b For each predicted exons, primers were designed from its flanking exons and

RT PCR was conducted using total RNA from 14 different tissue types: cervix,

uterus, ovary, placenta, breast, colon, pancreas, liver + spleen, brain, prostate, testis,

kidney, thyroid, and assorted cell-lines. Products were sequenced, and alternative splicing was searched.

^c Type of alternative splicing: Skip, exon-skipping; Alt 3'ss, alternative 3' splice site (acceptor); Int Ret., intron retention.

^d Retention of intron 8 (size 103 nucleotides) was detected in VLDLR.

^e Deletion of 86 nucleotides was detected on the 3' end of exon 12 7 of BAZ1A.

^f Extension of 44 nucleotides was detected on the 3' end of exon 12 of SMARCD1.

EXAMPLE 3

Examples of annotations for selected variants uncovered using the teachings of the present invention

500 clinically relevant genes were scanned and manually annotated. These annotations are listed in Table 3, below. Protein structure of the below listed genes and corresponding splice variants are shown in Figures 3a-z and 4a-m.

Table 3

#	Gene name and Swiss-prot	Examples for indications	Mechanism of splicing	CDs features (incl. Unique sequence)	#pep_num	Protein Product - SEQ ID NOS:
1	VLDLR Very low density Lipoprotein Receptor LDVR_HUMAN	Some variants could be used as soluble traps for LDL and as such to reduce risk of heart diseases, Vascular diseases and hypertension. It could also be used as : Anti hyperlipidemia Anti cholesterol Anti gallstones	Skipping exons : 8 9 12 14 15 Retention of intron 8 – see fig. 2i	Deletion of EGF Deletion of EGF Truncation – Soluble receptor Truncation – soluble receptor Deletion of EGF Truncation – Soluble receptor Confirmed by sequencing	1 2 3 4 5 6	23, 273 24, 274 25, 275 26, 276 27, 277 28, 278
2	VEGFC Vascular Endothelial Growth Factor VEGC_HUMAN	Might be used as agonist for cardiovascular diseases and diabetes (agonist of VEGFR2); Might be an antagonist to VEGF receptors and as such be used for treatment of cancer, diabetes and Asthma. Might also be used for Psoriasis.	Skipping exon 4 – see fig. 2b	Truncates the protein within VEGF peptide. Probable Elevation of VEGF2 specificity Confirmed by sequencing	7	29, 279
3	FLT1 Vascular	Might be an antagonist to VEGF receptors	Skipping exon	Deletion reduces Protein kinase domain	8	30, 280

	endothelial growth factor receptor 1 precursor VGR1_HUMAN	and as such be used for treatment of cancer, diabetes and Asthma. Might also be used for Psoriasis.	19			
4	KDR Vascular endothelial growth factor receptor 2 precursor VGR2_HUMAN	Mostly the two first variants (which might serve as a soluble/anchored decoy receptors for VEGF) might serve an antagonist to VEGF receptors and as such be used for treatment of cancer, diabetes and Asthma. Might also be used for Psoriasis.	Skipping exon 16(TM)	Truncates the protein right before TM (Soluble receptor)	9	31, 281
			17	Truncation deletes all of the ICD	10	32, 282
			27	Truncation doesn't affect domain	11	33, 283
			28	Truncation doesn't affect domain	12	34, 284
			29	Truncation doesn't affect domain	13	35, 285
5	ITAV Integrin alpha-V precursor ITAV_Human	Might be used as Integrin antagonist: Would be used as anti-inflammatory (especially for GI), immunosuppressant, anti Asthma and anti cancer.	Skipping exon 11	Truncation – Soluble Receptor.	14	36, 286
			20	Truncation – Soluble Receptor.	15	37, 287
			21	Deletion in heavy chain	16	38, 288
			25	Deletion in heavy chain	17	39, 289
6	MET (HGF receptor) MET_Human	Soluble receptor might serve as MET antagonist. The variant might be involved in prevention of proliferation and prevention of metastases and cell motility. It might be used for diabetes, skin conditions and for urological disorders.	Skipping exon 12	Skipping TM – Soluble receptor (evidence for extension)	18	40, 290
			14	Deletion after TM – may affect TM	19	41, 291
			18	Truncates most of the PK domain	20	42, 292
8	FSHR Follicular stimulating hormone Receptor FSHR_Human	Soluble chain might serve as a diagnostic marker for fertility and menopausal disorders. Both truncated forms could also be used as contraceptives. Could also be used for mail fertility diagnostic and treatment.	Skipping exon 7	Deletion of LRR	26	43, 293
			8	Deletion of LRR	27	44, 294
			intron 7 retention	Truncation – Soluble extracellular Chain	28	45, 295
			Novel exon 8A (102bp)	Truncation – Soluble extracellular Chain – A unique tail ; Validated by sequencing	29	46, 296
9	LSHR Luteinizing hormone receptor LSHR_Human	Soluble chain might serve as a diagnostic marker for fertility and menopausal disorders. Both truncated forms could also be used as contraceptives. Could also be used for mail fertility diagnostic and treatment.	Skipping exon 2	Deletion LRR	30	47, 297
			3	Deletion LRR	31	48, 298
			5	Deletion LRR	32	49, 299
			6	Deletion LRR	33	50, 300
			7	Deletion LRR	34	51, 301
			10	Deletion LSHR	35	52, 302
			Intron 5 retention	Truncation – Soluble extracellular Chain	36	53, 303
10	FGF11 Fibroblast growth Factor FGFB_HUMAN	The soluble form might be used as FGFR agonist/antagonist. Might be used for treatment of Cancer, cardiovascular diseases and as a growth	Skipping exon 2 – see fig. 2d	In-frame Deletion of 37 AA Validated by sequencing	37	54, 304

		factor. Deletion might cause Antagonist effect, and thus be used for treatment of cancer as well as diabetes and respiratory conditions.				
1 1	FGF12 Fibroblast growth Factor FGFC_HUMAN	The soluble form might be used as FGFR agonist/antagonist. Might be used for treatment of Cancer, cardiovascular diseases and as a growth factor. Deletion might cause Antagonist effect, and thus be used for treatment of cancer as well as diabetes and respiratory conditions.	Skipping exon 2 long isoform Skipping exon 2 short isoform	In-frame Deletion of 37 AA Soluble secreted form In-frame Deletion of 37 AA Soluble secreted form	38 39	55, 305 56, 306
1 2	FGF13 Fibroblast growth Factor FGFD_HUMAN	The soluble form might be used as FGFR agonist/antagonist. Might be used for treatment of Cancer, cardiovascular diseases and as a growth factor. Deletion might cause Antagonist effect, and thus be used for treatment of cancer as well as diabetes and respiratory conditions.	Skipping exon 2 long isoform Skipping exon 2 short isoform Skipping exon 3 long isoform Skipping exon 3 short isoform	In-frame Deletion of 37 AA Soluble secreted form In-frame Deletion of 37 AA Soluble secreted form Truncation of protein. Truncation of protein.	40 40a 41 41a	57, 307 58, 308 59, 309 60, 310
1 3	EFNA1 Ephrin A EFA1_human	Ephrin ligands and receptors have a variety of roles in development and cancer. Variant's indication would be either cause or prevent proliferation of certain tissues – treatment of cancer as well as wound healing and anti-inflammatory.	Skipping exon 3	In-frame deletion - Reduction of Ephrin domain.	42	61, 311
1 4	EFNA3 Ephrin A EFA3_human	Ephrin ligands and receptors have a variety of roles in development and cancer. Variant's indication would be either cause or prevent proliferation of certain tissues – treatment of cancer as well as wound healing and anti-inflammatory.	Skipping exon 3 4	In-frame deletion - Reduction of Ephrin domain. In-frame deletion - Reduction of Ephrin domain. (supported by 1 EST)	43 44	62, 312 63, 313
1 5	EFNA5 Ephrin A EFA5_human	Ephrin ligands and receptors have a variety of roles in development and cancer. Variant's indication would be either cause or prevent proliferation of certain tissues – treatment of cancer as well as wound healing and anti-inflammatory.	Skipping exon 3 – see Fig. 2c 4	In-frame deletion - Reduction of Ephrin domain. In-frame deletion - Reduction of Ephrin domain. Validated by sequencing	45 46	64, 314 65, 315
1 6	EFNB2 Ephrin B EFB2_Human	Ephrin ligands and receptors have a variety of roles in development and cancer. Variant's indication would be either cause or prevent proliferation of certain	Skipping exon 2 3	Truncation of most Ephrin domain. Reduction of Ephrin	47 48	66, 316 67, 317

		tissues – treatment of cancer as well as wound healing and anti-inflammatory.	4	domain. Reduction of distance between Ephrin domain and TM	49	68, 318
1 7	EPHA4 Ephrin A receptor (Tyrosine Kinase) EPA4_Human	Ephrin ligands and receptors have a variety of roles in development and cancer. Variant's indication would be either cause or prevent proliferation of certain tissues – treatment of cancer as well as wound healing and anti-inflammatory.	<i>Skipping exon 2</i> 12	Truncation most of the protein	50	69, 319
				Truncation leaving LBD reduced and a long unique sequence	51	70, 320
				Reducing distance LBD-FN III	52	71, 321
				Truncation of SAM and most TK	53	72, 322
1 8	EPHA5 Ephrin A receptor (Tyrosine Kinase) EPA5_Human	Ephrin ligands and receptors have a variety of roles in development and cancer. Variant's indication would be either cause or prevent proliferation of certain tissues – treatment of cancer as well as wound healing and anti-inflammatory.	<i>Skipping exon</i> 17	Reducing distance LBD-FN III	54	73, 323
				Abolishes the 1st FN III	55	74, 324
				Soluble ECD (Soluble receptor) and a long unique sequence	56	75, 325
				Truncation of ICD (SAM and TK)	57	76, 326
				Reducing Protein kinase domain	58	77, 327
				Truncation of SAM and most Protein kinase	59	78, 328
				Reduces SAM domain	60	79, 329
1 9	EPHA7 Ephrin A receptor (Tyrosine Kinase) EPA7_Human	Ephrin ligands and receptors have a variety of roles in development and cancer. Variant's indication would be either cause or prevent proliferation of certain tissues – treatment of cancer as well as wound healing and anti-inflammatory.	<i>Skipping exon 10</i> 15	Deletion truncates most of ICD	61	80, 330
				Truncation of SAM and most of the Protein kinase.	62	81, 331
2 0	EPHB1 Ephrin B receptor (Tyrosine Kinase) EPB1_Human	Ephrin ligands and receptors have a variety of roles in development and cancer. Variant's indication would be either cause or prevent proliferation of certain tissues – treatment of cancer as well as wound healing and anti-inflammatory.	<i>Skipping exon 6</i> 8 (TM) 10- see fig. 2a	Truncated Soluble Receptor	63	82, 332
				Truncation of ECD - Soluble Receptor ; long Unique sequence.	64	83, 333
				In-frame deletion Reduces Protein kinase – Validated by Sequencing	65	84, 334
2 1	PTPRZ1 Protein-tyrosine phosphatase zeta PTPZ_Human	Protein tyrosine phosphatase receptors have a variety of roles in development, metabolism and cancer. Variant's indication would be either cause or prevent proliferation of certain tissues – treatment of cancer as well as cardiovascular disorders and diabetes	<i>Skipping exon 7</i> 11 13 (TM) see Fig. 15 16 22	Truncation of most protein domains	66	85, 335
				Truncation after 2 nd fibronectin	67	86, 336
				A soluble receptor – validated	68	87, 337
				abolishing most of ICD Long Unique sequence	69	88, 338
				doesn't effect any domain	70	89, 339
				abolishes 2nd PTP – Long Unique	71	90, 340

2	PTPRB Protein-tyrosine phosphatase Beta PTPB_Human	Protein tyrosine phosphatase receptors have a variety of roles in development, metabolism and cancer. Variant's indication would be either cause or prevent proliferation of certain tissues - treatment of cancer as well as cardiovascular disorders and diabetes	Skipping exon 26	Truncation abolishes all ICD with a short unique sequence.	72	91, 341
2	KITLG KIT ligand: SCF/MGF SCF_Human	Agonist plays a role as antianaemic. Secreted molecule might be a more potent agonist for the receptor. Soluble form might also be used as an antagonist and thus prevent proliferation of blood cells in hematopoietic cancers.	Skipping exon 8	Truncating C-ter including TM and ICD. Unique sequence might add an alternative TM. But may be soluble.	73	92, 342
2	KIT KIT_Human	Agonist plays a role as antianaemic. Soluble receptor might be used as an antagonist and thus prevent proliferation of blood cells in hematopoietic cancers.	Skipping exon 8	Truncation creates Soluble receptor	74	93, 343
2	ErbB2 Receptor Tyrosine Kinase ERB2_Human	Might serve as a diagnostic marker for HER2 overexpressing cancer types. Might be used as an antagonist.	Skipping exon 6	Truncation reduces Protein Kinase	75	94, 344
2	ErbB3 Receptor Tyrosine Kinase ERB3_Human	Since exon 15 and 18 skipping variants encode soluble receptors which include the ligand binding domain, it is suggested that such proteins may serve as antagonists for all EGFR family genes which undergo heterodimerization as part of their activation.	Skipping exon 4	Truncation of most C-ter (leaving one L-domain and reduced furin-like domain) - Soluble	76	95, 345
2	ErbB4 Receptor Tyrosine Kinase ERB4_Human	Especially skipping exon 14 might serve as a good antagonist for all EGFR family genes. Might serve as ERBB2 antagonist (also for EGFR, ERBB3 and ERBB4)	Skipping exon 14	Reducing distance L-domain - furin	77	96, 346
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Skipping exon 5	Soluble ECD (reduced 2 nd furin) – Soluble receptor Reducing 2 nd furin like domain	78	97, 347
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- β 2, Skipping exon 8	(Known in some isoforms, but not in others): Deletion Reduces distance between EGF – Ig like domain.	79	98, 348
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- β 1 Skipping exon 9	Truncation abolishes NRG family domain. (Truncates HGR- β 1 to be like the shorter isoforms).	80	99, 349
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Skipping exon 7	Truncation abolishes NRG family domain. (Truncates HGR- β 1 to be like the shorter isoforms).	81	100, 350
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	NDF43 Skipping exon 12	Truncation abolishes NRG and EGF domains (In NDF43 adds a long unique).	82	101, 351
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- β 1 Skipping exon 9	Truncation abolishes NRG family domain. (Truncates HGR- β 1 to be like the shorter isoforms).	83	102, 352
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Skipping exon 7	Truncation abolishes NRG and EGF domains (In NDF43 adds a long unique).	84	103, 353
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Skipping exon 12	Truncation abolishes NRG and EGF domains (In NDF43 adds a long unique).	85	104, 354
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Skipping exon 7	Truncation abolishes NRG and EGF domains (In NDF43 adds a long unique).	86	105, 355
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Skipping exon 12	Truncation abolishes NRG and EGF domains (In NDF43 adds a long unique).	87	106, 356
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Skipping exon 7	Truncation abolishes NRG and EGF domains (In NDF43 adds a long unique).	88	107, 357
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- β 2, Skipping exon 8	Truncation abolishes NRG family domain. (Truncates HGR- β 1 to be like the shorter isoforms).	89	108, 358
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- β 1 Skipping exon 9	Truncation abolishes NRG family domain. (Truncates HGR- β 1 to be like the shorter isoforms).	90	109, 359
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Skipping exon 7	Truncation abolishes NRG and EGF domains (In NDF43 adds a long unique).	91	110, 360
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Skipping exon 12	Truncation abolishes NRG and EGF domains (In NDF43 adds a long unique).	92	111, 361
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Skipping exon 7	Truncation abolishes NRG and EGF domains (In NDF43 adds a long unique).	93	112, 362
2	NRG1 incl forms: HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Neuregulin Variants NRG1_Human	As many of the NRG1 isoforms serve as ErbB1/3/4 (EGFR family) ligands. Most variants might be used as partial/full antagonists of these cancer related receptors. The indication might therefore be (in some of the cases) for cancer treatment and diagnosis. In some cases, some forms could serve as agonists, to enhance cell proliferation (especially for wound healing).	HGR- α , HGR- β 1, HGR- β 2, HGR- β 3, HGR- γ , HGR-GGF, NDF43 Skipping exon 12	Truncation abolishes NRG and EGF domains (In NDF43 adds a long unique).	94	113, 363

			<i>HGR-β I Skipping exon 8</i>	Truncates and adds a long unique sequence which is identical to the HGR-β isoform, and recreates the NRG domain. Reduces distance between EGF and NRG.	95	114, 364
2 9	JAG1 Jagged- regulator of Angiogenesis JAG1_Human	Has a known indication for atherosclerotic diseases. JAG1 antagonist (especially Soluble receptor) might serve in preventing/treating cardiovascular diseases and cancer.	<i>Skipping exon 10</i> <i>12</i> <i>18</i> <i>22</i>	Deletion of 4th EGF domain Deletion of 5th & 6th EGF domains Deletion of 12th EGF domain (extention creates a soluble receptor, but is known) Truncation creates a soluble receptor with a long unique sequence..	96 97 98 99	115, 365 116, 366 117, 367 118, 368
3 0	NOTCH2 Neurogenic locus notch homolog protein NTC2_Human	NOTCH agonists are indicated for AntiAsthma and immunosuppressants. Might also be diagnostic markers for mental illnesses.	<i>Skipping exon 9 – seeFig. 2e</i> <i>12</i>	abolishes one EGF-like repeat. abolishes one EGF-like repeat.	100 101	119, 369 120, 370
3 1	NOTCH3 Neurogenic locus notch homolog protein NTC3_Human	NOTCH agonists are indicated for AntiAsthma and immunosuppressants. Might also be diagnostic markers for mental illnesses.	<i>Skipping exon 2</i>	Truncates entire protein leaving only SP with a long different, unique, AA sequence.	102	121, 371
3 2	NOTCH4 Neurogenic locus notch homolog protein NTC4_Human	NOTCH agonists are indicated for AntiAsthma and immunosuppressants. Might also be diagnostic markers for mental illnesses.	<i>Skipping exon 8</i>	abolishes two EGF-like repeats	103	122, 372
3 3	NTRK2 BDNF/NT-3 growth factor receptor TRKB_HUMAN	Agonist/partial agonist might play a role in CNS related diseases such as Parkinson, Alzheimer and other disorders. As well as a memory enhancer and neuroprotective. Antagonist might also be a mental treatment.	<i>Skipping exon 14 Fig. 2g</i>	In-frame deletion, Doesn't affect a domain – Validated by sequencing.	104	123, 373
3 4	NTRK3 NT-3 growth factor receptor TRKC_HUMAN	Agonist/partial agonist might play a role in CNS related diseases such as Parkinson, Alzheimer and other disorders. As well as a memory enhancer and neuroprotective. Antagonist might also be a mental treatment.	<i>Skipping exon 5</i> <i>16</i>	Deletion abolishes two short LRRs Truncation reduces the PK domain	105 106	124, 374 125, 375
3 5	GFRA1 RET ligand GDNF receptor GDNR_HUMAN	Agonist might serve as a neuroprotective agent. Thus might have a role in preventing Parkinson and other CNS related disorders.	<i>Skipping exon 4 (3 in CDs)</i>	Reduces GDNF receptor family	107	126, 376
3 6	GFRA2 RET ligand GDNF receptor NRTR_Human	Agonist might serve as a neuroprotective agent. Thus might have a role in preventing Parkinson and other CNS related disorders.	<i>Skipping exon 3</i>	Reduces GDNF receptor family	108	127, 377
3 7	IL16 – Long Interleukin 16 long variant IL16 human	Both agonist and antagonist might have a role in treating cancer and inflammation, antagonist would be used for Asthma.	<i>Skipping exon 5</i> <i>18 (5 in</i>	Truncates the protein, leaving no domains Deletion reduces 3rd	109 110	128, 378 129, 379

			<i>shorter isoform)</i>	(1st) PDZ domain		
3 8	IGFBP4 Insulin Growth factor binding protein IBP4_Human	Might serve as an enhancer for Insulin growth factor. Might thus have an affect as a Growth hormone and on diseases such as: Osteoporosis and MS.	Skipping exon 3	Deletion reduces Thyroglobulin type-1 repeat domain	111	130, 380
3 9	NRP1 Neuropilin-1 precursor NRP1_HUMAN	Much like VEGF and VEGFR genes, indication for preventing angiogenesis (for treatment of cancer) and inducing angiogenesis (for cardiovascular and ischemia diseases).	Skipping exon 5	Deletion reduces the CUB domain	112	131, 381
4 0	FGF9 Fibroblast growth factor FGF9_Human	The soluble form might be used as FGFR agonist/antagonist. Might be used for treatment of Cancer, cardiovascular diseases and as a growth factor. Deletion might cause Antagonist effect, and thus be used for treatment of cancer as well as diabetes and respiratory conditions.	Skipping exon 2	Truncation reduces FGF domain (creating a unique putative hydrophilic tail)	113	132, 382
4 1	FGF10 Fibroblast growth factor FGFA_Human	The soluble form might be used as FGFR agonist/antagonist. Might be used for treatment of Cancer, cardiovascular diseases and as a growth factor. Deletion might cause Antagonist effect, and thus be used for treatment of cancer as well as diabetes and respiratory conditions.	Skipping exon 2	Truncation reduces FGF domain (creating a unique putative hydrophilic tail)	114	133, 383
4 2	FGF18 Fibroblast growth factor FGFI_Human	The soluble form might be used as FGFR agonist/antagonist. Might be used for treatment of Cancer, cardiovascular diseases and as a growth factor. Deletion might cause Antagonist effect, and thus be used for treatment of cancer as well as diabetes and respiratory conditions.	Skipping exon 2 4	Truncated protein Truncation reducing FGF domain (creating a unique putative hydrophilic tail)	115 116	134, 384 135, 385
4 3	ANGPT1 Angiopoietin-1 AGP1_HUMAN	Agonist of Angiopoietin might serve for therapy of cardiovascular diseases as well as cancer.	Skipping exon 5 6 8 (in long isoform)	Truncation of the Fibrinogen-C terminal domain Deletion reduces Fibrinogen-C terminal domain Truncation reduces Fibrinogen-C terminal domain	117 118 119	136, 386 137, 387 138, 388
4 5	EDNRB Endothelin B receptor ETBR_human	Antagonist would have a role in cardiovascular diseases.	Skipping exon 4	reduction in the 7 transmembrane receptor (rhodopsin family) domain	128	139, 389
4 6	ECE1 Endothelin converting Enzyme ECE1_HUMAN	Antagonist would be useful in respiratory diseases, it might have diuretic effect and thus be used for hypertension and cardiovascular diseases.	Skipping exon 2	Deletion would convert Signal Peptide to a Signal anchor.	129	140, 390
4 7	ECE2 Endothelin converting Enzyme ECE2_HUMAN	Antagonist would be useful in respiratory diseases, it might have diuretic effect and thus be used for hypertension and cardiovascular diseases.	Skipping exon 2 8 12 13	Deletion would convert Signal Peptide to a Signal anchor. (Known) Deletion reduces M13 peptidase N Deletion reduces M13 peptidase N Deletion reduces M13 peptidase N	130 131 132 133	141, 391 142, 392 143, 393 144, 394

			15	Deletion reduces M13 peptidase C	134	145, 395
4 8	ITGA2B Integrin alpha-IIb ITAB_HUMAN	Might be used as Integrin antagonist: Indicated for cardiovascular diseases.	Skipping exon 3	Truncation abolishes most of the protein including most of FG-GAP repeats (1 EST skips exons 2-4)	135	146, 396
4 9	MPL Thrombopoietin receptor TPOR_HUMAN	Might be used as a diagnostic agent for hematological diseases, as well as therapy as a growth factor and antiviral.	Skipping exon 2	Truncation of most of the protein	136	147, 397
5 0	CUL5 Cullin homolog 5 Vasopressin-activated calcium-mobilizing receptor VAC1_HUMAN	Variants might be used as Vasopressin antagonists for treatment of Diabetes, cardiovascular diseases (Diuretic for hypertension) and as an antidepressant.	Skipping exon 2 8	Truncation reduces the CULLIN domain Truncation reduces the CULLIN domain	137 or 138 139	148 or 149/398 150, 399
5 1	HPA Heparanase Q9Y251	As Agonist this protein might serve for treatment of Cystic Fibrosis. As antagonist it is indicated for Cancer (anti metastatic), cardiovascular and MS.	Skipping exon 10	Truncation slightly reduces Glycosyl hydrolase domain.	140	151, 400
5 2	HPSE2 Heparanase 2 Q8WWQ2 Q8WWQ1	As Agonist this protein might serve for treatment of Cystic Fibrosis. As antagonist it is indicated for Cancer (anti metastatic), cardiovascular and MS.	Skipping 5 6 7 8 9 10 11	Truncation reduces Glycosyl hydrolase domain Deletion reduces Glycosyl hydrolase domain Truncation reduces Glycosyl hydrolase domain Truncation reduces Glycosyl hydrolase domain Truncation reduces Glycosyl hydrolase domain Truncation reduces Glycosyl hydrolase domain Deletion doesn't affect Glycosyl hydrolase	141 142 143 144 145 146 147	152, 401 153, 402 154, 403 155, 404 156, 405 157, 406 158, 407
5 5	MME Neutral endopeptidase (Enkephalinase) NEP_HUMAN	As an antagonist, these variant might be used for treatment of Hypertension (a diuretic agent), as a cardiotonic, as antidepressant and for treatment of Migraine.	Skipping exon 4 7 9 11 12 16	Deletion reduces N-ter M13 peptidase Truncation reduces N-ter M13 peptidase and abolishes C-ter M13 peptidase. Deletion reduces N-ter M13 peptidase Truncation reduces N-ter M13 peptidase and abolishes C-ter M13 peptidase. Truncation reduces N-ter M13 peptidase and abolishes C-ter M13 peptidase. Truncation abolishes C-terminal M13 peptidase.	150 151 152 153 154 155	159, 408 160, 409 161, 410 162, 411 163, 412 164, 413
5 6	APBB1 Alzheimer's disease amyloid A4 binding protein ABBI_HUMAN	Antagonist to the amyloid 4a might be used as a neuroprotective agent, to help prevent/treat Alzheimer, Parkinson and other neurodegenerative diseases. It might also be used for hypertension, and as an anti-inflammatory agent.	Skipping exon 3 7	Truncation abolishes most of the protein (Extended EST) Deletion reduces 1st PID domain	156 157	165, 414 166, 415

			9 10 12	Deletion reduces 1st PID domain (Extended EST) Truncation abolishes 2 nd PID reduces 1st PID Domain Truncation abolishes 2 nd PID domain – Adds a Cys rich unique sequence.	158 159 160	167, 416 168, 417 169, 418
5 7	GDNF GDNF_HUMAN	Anti Parkinson.	Skipping exon 2	Unknown as exon 2 is last.		170, 419
5 8	SCTR Secretin receptor SCRC_HUMAN	Agonist has haemostatic affects (clotting) and some neurological functions.	Skipping exon 10	Truncation reduces 7 transmembrane receptor (Secretin family) (eliminates last two TM)	162	171, 420
5 9	RSU1 Ras suppressor protein 1 RSU1 Human	Might have anti-cancer affect. Might serve as a diagnostic marker.	Skipping exon 6	Truncation eliminates 3/7 LRR repeats.	163	172, 421
6 0	IL18R Interleukine 18 receptor IR18 Human	Antagonist has an anti-inflammatory effect, might be useful for arthritis and MS.	Skipping exon 9	Deletion abolishes all of TIR domain (NFkB activating)	164	173, 422
6 1	TGFB2 Transforming growth factor beta 2 TGF2 Human	Might only be used as a diagnostic marker as the variant is basically the Propeptide, Might be used for cancer or respiratory related diseases.	Skipping exon 5	Truncation abolishes TGFB peptide and slightly reduces pro-peptide.	165	174, 423
6 2	TIAF1 (TGFB1-induced anti-apoptotic factor 1) TIAF_HUMAN	An agonist might be used for anti cancer or as an immunosuppressant. An antagonist might be used for cancer, Asthma, MS, Cardiovascular diseases and respiratory.	Skipping exon 11 25 34	Deletion (4AA) reduces Myosin head (motor domain) Deletion doesn't affect a domain. Deletion doesn't affect a domain.	166 167 168	175, 424 176, 425 177, 426
6 3	IL1RAP IL-1 receptor accessory protein O14915	Many indications associated with IL1 and IL1 family proteins. The most prevalent indication is as an antagonist for anti-inflammatory purposes (Such as MS, Diabetes, Cancer and Arthritis). As both agonist and antagonist might be good for cancer, cardiovascular diseases and antiinflammatory.	Skipping exon 11	Deletion reduces TIR domain	169	178, 427
6 4	IL1RAPL1 IL-1 receptor accessory protein like 1 Q9UJ53	Many indications associated with IL1 and IL1 family proteins. The most prevalent indication is as an antagonist for anti-inflammatory purposes (Such as MS, Diabetes, Cancer and Arthritis). As both agonist and antagonist might be good for cancer, cardiovascular diseases and antiinflammatory.	Skipping exon 4 5 6 7 8	Truncation abolishes most of the protein Truncation abolishes most of the protein Deletion reduces distance:Ig2 - 3 Truncation abolishes ICD and 1 Ig (Soluble receptor) Truncation creates a soluble receptor with 3 Ig-like domains	170 171 172 173 174	179, 428 180, 429 181, 430 182, 431 183, 432
6 5	IL1RAPL2 IL-1 receptor accessory protein like 2 Q9NP60	Many indications associated with IL1 and IL1 family proteins. The most prevalent indication is as an antagonist for anti-inflammatory purposes (Such as MS, Diabetes, Cancer and Arthritis). As both agonist and antagonist might be good for cancer, cardiovascular diseases and antiinflammatory.	Skipping exon 4 5 6 7 8	Truncation abolishes most of the protein Truncation abolishes most of the protein Deletion reduces distance:Ig2 - 3 Truncation abolishes ICD and 1 Ig (Soluble receptor)	175 176 177 178 179	184, 433 185, 434 186, 435 187, 436 188, 437

6 6	THBS1 Thrombospondin 1 precursor TSP1_HUMAN	Can be used as an anticancer treatment both as antagonist and as agonist. Antagonist is useful against proliferation, and agonist as an anti-inflammatory.	Skipping exon 4 7 9 12	Truncation creates a soluble receptor with 3 Ig-like domains Truncation abolishes all domains but Thrombospondin N-terminal -like domain (reduced) Truncation abolishes all TSP and EGF domains leaving only the Thrombospondin N-terminal -like domain and a reduced VWC. A very long Unique tail. Deletion abolishes 1st TSP1 repeat. Deletion doesn't affect a domain.	180 181 182 183	189, 438 190, 439 191, 440 192, 441
6 7	THBS4 Thrombospondin 4 precursor TSP4_HUMAN	Can be used as an anticancer treatment both as antagonist and as agonist. Antagonist is useful against proliferation, and agonist as an anti-inflammatory.	Skipping exon 15	Truncation abolishes 6 TSP3 domain and the entire TSO – C domain. No Unique!	184	193, 442
6 8	PROS1 Vitamin K-dependent protein S precursor PTS_HUMAN	Indication for blood clotting – might serve as an antagonist for Fibrinogen, and as a stimulant for TPA (anti clotting).	Skipping exon 3	Truncation of most protein. Leaving only SP and 77 AA as reduced GLA Domain.	185	194, 443
6 9	VWF Von Willebrand factor precursor VWF_HUMAN	Could serve as agonist and/or antagonist for clotting factor VIII. As such might be used for hematodynamic indications, including anti-thrombosis and anti-bleeding.	Skipping exon 8 13 29	Deletion abolishes the 1st TIL domain. Trunction abolishes all C-terminus of the protein including all domains but two WWD domains and one TIL Deletion doesn't affect a domain.	186 187 188	195, 444 196, 445 197, 446
7 0	M17S2 Ovarian carcinoma antigen CA125 M172_HUMAN	A diagnostic marker for mostly Ovarian cancer. The variants could be indicated for other types of cancer.	Skipping exon 14 15 20	Truncation doesn't affect a domain. Deletion doesn't affect a domain. No Unique.	189 190 191	198, 447 199, 448 200, 449

EXAMPLE 4***Finding novel proteins using cross species homology***

Mouse expressed sequences were aligned to the human genome. Alignments were filtered by a minimal length criterion, and remaining alignments were used to generate "corrected" expressed sequences (by concatenating the fragments of human genomic sequence to which a mouse expressed sequence aligned). These corrected sequences were clustered together with human expressed sequences and the resulting clusters were assembled and subjected to a process of transcript prediction. Within the set of resulting transcripts, transcripts were identified, which cannot be predicted using only human expressed sequences.

Specifically, the following method was performed:

1. Human, mouse and rat ESTs and cDNAs were obtained from NCBI GenBank versions 136 (June 15, 2003) <ftp://ftp.ncbi.nih.gov/genbank/release.notes/gb136.release.notes>) and NCBI genome assembly of April 2003. Using the LEADS clustering and assembly system as described in Sorek et al. (2002), the expressed sequences were cleaned from repeats, vectors and immunoglobulins, and then aligned to the NCBI human genome reference build 33 (April 2003). The best genomic location was chosen for each human expressed sequence. The human sequences were clustered by genome location. Some clusters were separated in cases of suspected over-clustering or overlapping antisense clusters.
2. Mouse and rat expressed sequences may have more than one alignment to the human genome. All alignments were considered except those shorter than 50 base pairs and unspliced. For further analysis only alignments that overlap human clusters were selected.
3. Each mouse or rat alignment was replaced by the corresponding human DNA sequence, such that problems of low identity alignments do not interfere with the analysis.
4. Human expressed sequences were grouped in each cluster with all the mouse/rat-originated sequences overlapping it. These groups were then assembled to form new hybrid clusters, taking into account alternative splicing.

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5. A list of reliable transcripts was compiled for each of the clusters, filtering suspected intron contaminations and giving preference to canonical splice signals.
6. Alternative splicing events that are supported by non-human sequences only were searched. A list of the transcripts that contains these events was then compiled.
7. Proteins for these transcripts were predicted.

EXAMPLE 5

Annotation of computationally identified alternatively spliced sequences

Newly uncovered naturally occurring transcripts were annotated using the GeneCarta (Compugen, Tel-Aviv, Israel) platform. The GeneCarta platform includes a rich pool of annotations, sequence information (particularly of spliced sequences), chromosomal information, alignments, and additional information such as SNPs, gene ontology terms, expression profiles, functional analyses, detailed domain structures, known and predicted proteins and detailed homology reports.

Brief description of the methodology used to obtain annotative sequence information is summarized infra (for a detailed description see U.S. Pat. Appl. 10/426,002, filed on April 30, 2003 and owned in common with the present application, hereby incorporated by reference as if fully set forth herein).

The ontological annotation approach - An ontology refers to the body of knowledge in a specific knowledge domain or discipline such as molecular biology, microbiology, immunology, virology, plant sciences, pharmaceutical chemistry, medicine, neurology, endocrinology, genetics, ecology, genomics, proteomics, cheminformatics, pharmacogenomics, bioinformatics, computer sciences, statistics, mathematics, chemistry, physics and artificial intelligence.

An ontology includes domain-specific concepts – referred to, herein, as sub-ontologies. A sub-ontology may be classified into smaller and narrower categories. The ontological annotation approach is effected as follows.

First, biomolecular (i.e., polynucleotide or polypeptide) sequences are computationally clustered according to a progressive homology range, thereby generating a plurality of clusters each being of a predetermined homology of the homology range.

Progressive homology is used to identify meaningful homologies among biomolecular sequences and to thereby assign new ontological annotations to sequences, which share requisite levels of homologies. Essentially, a biomolecular sequence is assigned to a specific cluster if displays a predetermined homology to at least one member of the cluster (i.e., single linkage). A "progressive homology range" refers to a range of homology thresholds, which progress via predetermined increments from a low homology level (e.g. 35 %) to a high homology level (e.g. 99 %).

Following generation of clusters, one or more ontologies are assigned to each cluster. Ontologies are derived from an annotation preassociated with at least one biomolecular sequence of each cluster; and/or generated by analyzing (e.g., text-mining) at least one biomolecular sequence of each cluster thereby annotating biomolecular sequences.

Sequence annotations obtained using the above-described methodologies and other approaches are disclosed in a data table in the file AnnotationForPatent.txt of the enclosed CD-ROM 1.

EXAMPLE 6

Description of data

Following is a description of the data table in "AnnotationForPatent.txt" file, on the attached CD-ROM1. The data table shows a collection of annotations for biomolecular sequences, which were identified according to the teachings of the present invention using transcript data based on GenBank versions Genbank version 136 (June 15 2003 <ftp://ftp.ncbi.nih.gov/genbank/release.notes/gb136.release.notes>).

Each feature in the data table is identified by "#"

The sequences in this patent application are additional information to the Gencarta contigs. Therefore, all annotations that are in terms of Gencarta contigs were also assigned to the sequences in this patent that are derived from these contigs. Also, annotations that are applied by comparing proteins resulting from the same contig were adapted by comparing the sequences in this patent to the proteins from the original Gencarta contig.

#INDICATION – This field designates the indications and therapies that the polypeptide of the present invention can be utilized for. The indications state the

disorders/disease that the polypeptide can be used for and the therapy is the postulated mode of action of the polypeptide for the indication. For example, an indication can be "Cancer, general" while the therapy will be "Anticancer". Each Gencarta contig was assigned a SWISSPROT and/or TremBl human protein accession as described in section "Assignment of Swissprot/TremBl accessions to Gencarta contigs" hereinbelow. The information contained in this field is the indication concatenated to the therapies that were accumulated for the SWISSPROT and/or TremBl human protein from drug databases, such as PharmaProject (PJB Publications Ltd 2003 <http://www.pjbpubs.com/cms.asp?pageid=340>) and public databases, such as LocusLink (<http://www.genelynix.org/cgi-bin/resource?res=locuslink>) and Swissprot (<http://www.ebi.ac.uk/swissprot/index.html>). The field may comprise more than one term wherein a ";" separates each adjacent terms.

Example- #INDICATION Alopecia, general; Antianginal; Anticancer, immunological; Anticancer, other; Atherosclerosis; Buerger's syndrome; Cancer, general; Cancer, head and neck; Cancer, renal; Cardiovascular; Cirrhosis, hepatic; Cognition enhancer; Dermatological; Fibrosis, pulmonary; Gene therapy; Hepatic dysfunction, general; Hepatoprotective; Hypolipaemic/Antiatherosclerosis; Infarction, cerebral; Neuroprotective; Ophthalmological; Peripheral vascular disease; Radio/chemoprotective; Recombinant growth factor; Respiratory; Retinopathy, diabetic; Symptomatic antidiabetic; Urological;

Assignment of Swissprot/TremBl accessions to Gencarta contigs - Gencarta contigs were assigned a Swissprot/TremBl human accession as follows. Swissprot/TremBl data were parsed and for each Swissprot/TremBl accession (excluding Swissprot/TremBl that are annotated as partial or fragment proteins) cross-references to EMBL and Genbank were parsed. The alignment quality of the Swissprot/TremBl protein to their assigned mRNA sequences was checked by frame+p2n alignment analysis. A good alignment was considered as having the following properties:

- (i) For partial mRNAs (those that in the mRNA description have the phrase "partial.cds" or annotated as "3'" or "5'")- an overall identity of 97% and coverage of 80 % of the Swissprot/TremBl protein.
- (ii) All the rest were considered as full coding mRNAs and for them an overall identity of 97% identity and coverage of the Swissprot/TremBl protein of over 95%.

The mRNAs were searched in the LEADS database for their corresponding contigs, and the contigs that included these mRNA sequences were assigned the Swissprot/TremBl accession.

#PHARM- This field indicates possible pharmacological activities of the polypeptide. Each Gencarta polypeptide was assigned a SWISSPROT and/or TremBl human protein accession, as described above. The information contained in this field is the proposed pharmacological activity that was accumulated for the SWISSPROT and/or TremBl human protein from drug databases such as PharmaProject (PJB Publications Ltd 2003 <http://www.pjbpubs.com/cms.asp?pageid=340>) and public databases, such as LocusLink and Swissprot. Note that in some cases this field can include opposite terms in cases where the protein can have contradicting activities – such as:

- (i) Stimulant – inhibitor
- (ii) Agonist – antagonist
- (iii) Activator- inhibitor
- (iv) Immunosuppressant – Immunostimulant

In these cases the pharmacology was indicated as “modulator”.

As used herein the term “modulator” refers to a molecule which inhibits (i.e., antagonist, inhibitor, suppressor) or activates (i.e., agonist, stimulant, activator) a downstream molecule to thereby modulate its activity.

For example, if the predicted polypeptide has potential agonistic/antagonistic effects (e.g. Fibroblast growth factor agonist and Fibroblast growth factor antagonist) then the annotation for this code will be “Fibroblast growth factor modulator”.

A documented example for such contradicting activities has been described for the soluble tumor necrosis factor receptors [Mohler et al., J. Immunology 151, 1548-1561]. Essentially, Mohler and co-workers showed that soluble receptor can act both as a carrier of TNF (i.e., agonistic effect) and as an antagonist of TNF activity.

#THERAPEUTIC PROTEIN – This field predicts a therapeutic role for a protein represented by the contig. A contig was assigned this field if there was information in the drug database or the public databases (e.g., described hereinabove) that this protein, or part thereof, is used or can be used as a drug. This field is accompanied by the swissprot accession of the therapeutic protein which this contig most likely represents. Example: # THERAPEUTIC_PROTEIN UROK_HUMAN

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#DN represents information pertaining to transcripts, which contain altered functional interpro domains (further described hereinabove). The Interpro domain is either lacking in this protein (as compared to another expression product of the gene) or its score is decreased (i.e., includes sequence alteration within the domain when compared to another expression product of the gene). This field lists the description of the functional domain(s), which is altered in the respective splice variants.

As used herein the phrase "functional domain" refers to a region of a biomolecular sequence, which displays a particular function. This function may give rise to a biological, chemical, or physiological consequence which may be reversible or irreversible and which may include protein-protein interactions (e.g., binding interactions) involving the functional domain, a change in the conformation or a transformation into a different chemical state of the functional domain or of molecules acted upon by the functional domain, the transduction of an intracellular or intercellular signal, the regulation of gene or protein expression, the regulation of cell growth or death, or the activation or inhibition of an immune response.

Method: the proteins were compared to the proteins in the relevant Gencarta contig by BLASTP analysis against each other. All proteins were also analysed by Interpro domain analysis software (Interpro default parameters, the analyses that were run are HMMPfam, HMMSmart, ProfileScan, FprintScan, and BlastProdom). Each pair of proteins that shared at least 20 % coverage of one or the other with an identity of at least 80 % were analysed by domain comparison. If the proteins share a common domain (same domain accession) and in one of the proteins this domain has a decreased score (escore of 20 magnitude for HMMPfam, HMMSmart, BlastProdom, FprintScan or Pscore difference of ProfileScan of 5), or lacking the domain contained in another protein in the same contig, the protein with the reduced score or without the domain is annotated as having lost this interpro domain. This lack of domain can have a functional meaning in which the protein lacking it (or having some part of it missing) can either gain a function or lose a function (e.g., acting, at times, as dominant negative inhibitor of the respective protein). Interpro domains, which have no functional attributes, were omitted from this analysis. The domains that were omitted are:

IPR000694 Proline-rich region

IPR001611 Leucine-rich repeat

IPR001893 Cysteine rich repeat
IPR000372 Cysteine-rich flanking region, N-terminal
IPR000483 Cysteine-rich flanking region, C-terminal
IPR003591 Leucine-rich repeat, typical subtype
IPR003885 Leucine-rich repeat, cysteine-containing type
IPR006461 Uncharacterized Cys-rich domain
IPR006553 Leucine-rich repeat, cysteine-containing subtype
IPR007089 Leucine-rich repeat, cysteine-containing

The results of this analysis are denoted in terms of the Interpro domain that is missing or altered in the protein. Example: #DN IPR002110 Ankyrin.

A documented example is in an article describing two splice variant forms of guanylyl cyclase-B receptor (Tamura N and Garbers DL, J Biol Chem. 2003 Dec 5;278(49):48880-9. Epub 2003 Sep 26). One variant of this receptor has a 25 amino acid deletion in the kinase homology domain and therefore it binds the ligand but fails to activate the cyclase. The other variant includes part of the extracellular binding domain and hence it fails to bind the ligand. Both variants, when co-expressed with the wild-type receptor act as dominant negative isoforms.

#SECRETED_FORM_OF_MEMBRANAL_PROTEINS_BY_PROLOC

This field indicates if the indicated protein is a secreted form of a membranal protein. Method: the proteins were compared to the proteins in the relevant Gencarta by BLASTP analysis against each other. The Proloc algorithm was applied to all the proteins. Each pair of proteins that shared at least 20 % coverage of one or the other with an identity of at least 80 % was further examined. A protein was considered a soluble form of a membranal protein (i.e., cognate protein) if it was shown to be a secreted protein (as further described below) while the cognate partner was a membranal protein.

A protein was considered secreted or extracellular if it had at least one of the following properties.

- (i) Proloc's highest subcellular localization prediction is EXTRACELLULAR.
- (ii) Proloc's prediction of a signal peptide sequence is more reliable than the prediction of a lack of signal peptide sequence. Furthermore, no transmembrane

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regions are predicted in the non N-terminus part of the protein (following 30 N-terminal amino acids)

(iii) Proloc's prediction of only one transmembrane domain, which is localized to the N-terminus part of the protein (in a region less than the first 30 amino acids)

The cognate protein was considered to be a membranal protein if it obeyed at least one of the following rules:

(i) Proloc's highest subcellular localization prediction is either CELL_INTEGRAL_MEMBRANE, CELL_MEMBRAN_E_ANCHORI, or CELL_MEMBRANE_ANCHORII.

(ii) Proloc's prediction of at least one transmembrane domain which is not in the N-terminus part of the protein (in a region greater than the first 30 amino acids)

The header in this method will be
#SECRETED_FORM_OF_MEMBRANNEL_PROTEINS_BY_PROLOC.

Example:

#SECRETED_FORM_OF_MEMBRANNEL_PROTEINS_BY_PROLOC

Example:

AA290625_P2

#SECRETED_FORM_OF_MEMBRANNEL_PROTEINS

#MEMBRANE_FORM_OF_SOLUBLE_PROTEINS_BY_PROLOC – This field denotes if the indicated protein is a membranal form of a secreted protein.

Method: the proteins were compared to the proteins in the relevant Gencarta by BLASTP analysis against each other. The Proloc algorithm was applied to all the proteins. Each pair of proteins that shared at least 20 % coverage with an identity of at least 80 % was further examined. A protein was considered a membranal form of a secreted protein if it was shown to be (i.e., annotated) a membranal protein and the other protein it was compared to (i.e., cognate) was a secreted protein.

A protein is annotated membranal if it had at least one of the following properties:

(i) Proloc's highest subcellular localization prediction is either CELL_INTEGRAL_MEMBRANE, CELL_MEMBRAN_E_ANCHORI, or CELL_MEMBRANE_ANCHORII.

(ii) Proloc's prediction of at least one transmembrane domain which is not in the N-terminus part of the protein (in a region greater than the first N-terminal 30 amino acids)

The cognate protein is considered secreted if it obeyed at least one of the following rules:

(i) Proloc's highest subcellular localization prediction is EXTRACELLULAR.

(ii) Proloc's prediction of the existence of a signal peptide sequence is more reliable than the prediction of a lack of signal peptide sequence and no transmembrane regions are predicted in the non N-terminus part of the protein (after its N-terminal 30 amino acids)

(iii) Proloc's prediction of only one transmembrane domain which is in the N-terminus part of the protein (in a region less than the N-terminal 30

The annotation will be in the form of this header, example:

AA176800_P7 #MEMBRANE_FORM_OF_SOLUBLE_PROTEINS_BY
PROLOC.

GO annotations were predicted as described in "The ontological annotation approach" section hereinabove. Additions to the GO prediction, other than the GO engine will be described below. These additions are to the cellular component attribute and biological process.

Functional annotations of transcripts based on Gene Ontology (GO) are indicated by the following format.

"#GO_P", annotations related to Biological Process,

"#GO_F", annotations related to Molecular Function, and

"#GO_C", annotations related to Cellular Component.

Proloc was used for protein subcellular localization prediction that assigns GO cellular component annotation to the protein. The localization terms were assigned GO entries.

For this assignment two main approaches were used: (i) the presence of known extracellular domain/s in a protein (as appears in Table 4); (ii) calculating putative transmembrane segments, if any, in the protein and calculating 2 p-values for the existence of a signal peptide. The latest is done by a search for a signal peptide at the

N-terminal sequence of the protein generating a score. Running the program on real signal peptides and on N-terminal protein sequences that lack a signal peptide resulted in 2 score distributions: the first is the score distribution of the real signal peptides, and the second is the score distribution of the N-terminal protein sequences that lack the signal peptide. Given a new protein, ProLoc calculates its score and outputs the percentage of the scores that are higher than the current score, in the first distribution, as a first p-value (lower p-values mean more reliable signal peptide prediction) and the percentage of the scores that are lower than the current score, in the second distribution, as a second p-value (lower p-values mean more reliable non signal peptide prediction).

Assignment of an extracellular localization (#GO_Acc 5576 #GO_Desc extracellular) was also based on Interpro domains. A list of Interpro domains that characterize secreted proteins was compiled. A Gencarta protein that had a hit to at least one of these domains was annotated with an extracellular GO annotation. The list of secreted Interpro domains is depicted in Table 4.

Table 4 List of Interpro Domains of Secreted Proteins

IPR000874	Bombesin-like peptide
IPR001693	Calcitonin-like
IPR001651	Gastrin/cholecystokinin peptide hormone
IPR000532	Glucagon/GIP/secretin/VIP
IPR001545	Gonadotropin, beta chain
IPR004825	Insulin/IGF/relaxin
IPR000663	Natriuretic peptide
IPR001955	Pancreatic hormone
IPR001400	Somatotropin hormone
IPR002040	Tachykinin/Neurokinin
IPR006081	Alpha defensin
IPR001928	Endothelin-like toxin
IPR001415	Parathyroid hormone
IPR001400	Somatotropin hormone
IPR001990	Chromogranin/secretogranin
IPR001819	Chromogranin A/B
IPR002012	Gonadotropin-releasing hormone
IPR001152	Thymosin beta-4
IPR000187	Corticotropin-releasing factor, CRF
IPR001545	Gonadotropin, beta chain
IPR000476	Glycoprotein hormones alpha chain
IPR000476	Glycoprotein hormones alpha chain
IPR001323	Erythropoietin/thrombopoietin
IPR001894	Cathelicidin

IPR001894	Cathelicidin
IPR001483	Urotensin II
IPR006024	Opioid neuropeptide precursor
IPR000020	Anaphylatoxin/fibulin
IPR000074	Apolipoprotein A1/A4/E
IPR001073	Complement C1q protein
IPR000117	Kappa casein
IPR001588	Casein, alpha/beta
IPR001855	Beta defensin
IPR001651	Gastrin/cholecystokinin peptide hormone
IPR000867	Insulin-like growth factor-binding protein, IGFBP
IPR001811	Small chemokine, interleukin-8 like
IPR004825	Insulin/IGF/relaxin
IPR002350	Serine protease inhibitor, Kazal type
IPR000001	Kringle
IPR002072	Nerve growth factor
IPR001839	Transforming growth factor beta (TGFb)
IPR001111	Transforming growth factor beta (TGFb), N-terminal
IPR001820	Tissue inhibitor of metalloproteinase
IPR000264	Serum albumin family
IPR005817	Wnt superfamily

For each category the following features are optionally addressed:

"#GO_Acc" represents the accession number of the assigned GO entry, corresponding to the following "#GO_Desc" field.

"#GO_Desc" represents the description of the assigned GO entry, corresponding to the mentioned "#GO_Acc" field.

The assignment of Immune response GO annotation (#GO_Acc 6955 # GO_Desc immune response) to Gencarta transcripts and proteins was based on a homology to a viral protein, as described in U.S. Pat. Appl. No. 60/480,752.

"#CL" represents the confidence level of the GO assignment, when #CL1 is the highest and #CL5 is the lowest possible confidence level. This field appears only when the GO assignment is based on a Swissprot/TremBl protein accession or Interpro accession and (not on Proloc predictions or viral proteins predictions). Preliminary confidence levels were calculated for all public proteins as follows:

PCL 1: a public protein that has a curated GO annotation,

PCL 2: a public protein that has over 85 % identity to a public protein with a curated GO annotation,

PCL 3: a public protein that exhibits 50 - 85 % identity to a public protein with a curated GO annotation,

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PCL 4: a public protein that has under 50 % identity to a public protein with a curated GO annotation.

For each Gencarta protein a homology search against all public proteins was done. If the Gencarta protein has over 95 % identity to a public protein with PCL X than the Gencarta protein gets the same confidence level as the public protein. This confidence level is marked as "#CL X". If the Gencarta protein has over 85 % identity but not over 95 % to a public protein with PCL X than the Gencarta protein gets a confidence level lower by 1 than the confidence level of the public protein. If the Gencarta protein has over 70 % identity but not over 85 % to a public protein with PCL X than the Gencarta protein gets a confidence level lower by 2 than the confidence level of the public protein. If the Gencarta protein has over 50 % identity but not over 70 % to a public protein with PCL X than the Gencarta protein gets a confidence level lower by 3 than the confidence level of the public protein. If the Gencarta protein has over 30 % identity but not over 50 % to a public protein with PCL X than the Gencarta protein gets a confidence level lower by 4 than the confidence level of the public protein.

A Gencarta protein may get confidence level of 2 also if it has a true interpro domain that is linked to a GO annotation
<http://www.geneontology.org/external2go/interpro2go/>.

When the confidence level is above "1", GO annotations of higher levels of the GO hierarchy are assigned (e.g. for "#CL 3" the GO annotations provided, is as appears plus the 2 GO annotations above it in the hierarchy).

"#DB" marks the database on which the GO assignment relies on. The "sp", as in Example 10a, relates to SwissProt/TremBl Protein knowledgebase, available from <http://www.expasy.ch/sprot/>. "InterPro", as in Example 10c, refers to the InterPro combined database, available from <http://www.ebi.ac.uk/interpro/>, which contains information regarding protein families, collected from the following databases: SwissProt (<http://www.ebi.ac.uk/swissprot/>), Prosite (<http://www.expasy.ch/prosite/>), Pfam (<http://www.sanger.ac.uk/Software/Pfam/>), Prints (<http://www.bioinf.man.ac.uk/dbrowser/PRINTS/>), Prodom (<http://prodes.toulouse.inra.fr/prodom/>), Smart (<http://smart.embl-heidelberg.de/>) and Tigrfams (<http://www.tigr.org/TIGRFAMs/>). PROLOC means the method used was Proloc based on statistics Proloc uses for predicting the subcellular localization of

a protein. "#EN" represents the accession of the entity in the database (#DB), corresponding to the accession of the protein/domain why the GO was predicted. If the GO assignment is based on a protein from the SwissProt/TremBl Protein database this field will have the locus name of the protein. Examples, "#DB sp #EN NRG2_HUMAN" means that the GO assignment in this case was based on a protein from the SwissProt/Trembl database, while the closest homologue (that has a GO assignment) to the assigned protein is depicted in SwissProt entry "NRG2_HUMAN" "#DB interpro #EN IPR001609" means that GO assignment in this case was based on InterPro database, and the protein had an Interpro domain, IPR001609, that the assigned GO was based on. In Proloc predictions this field will have a Proloc annotation "#EN_Proloc". #GENE_SYMBOL – for each Gencarta contig a HUGO gene symbol was assigned in two ways:

- (i) After assigning a Swissprot/TremBl protein to each contig (see *Assignment of Swissprot/TremBl accessions to Gencarta contigs*) all the gene symbols that appear for the Swissprot entry were parsed and added as a Gene symbol annotation to the gene.
- (ii) LocusLink information- LocusLink was downloaded from NCBI <ftp://ftp.ncbi.nih.gov/refseq/LocusLink/> (files loc2acc, loc2ref, and LL.out_hs). The data was integrated producing a file containing the gene symbol for every sequence. Gencarta contigs were assigned a gene symbol if they contain a sequence from this file that has a gene symbol

Example: #GENE_SYMBOL MMP15

#DIAGNOSTICS- KGencarta contigs representing known diagnostic markers (such as listed in Table 5, below) and all transcripts and proteins deriving from this contig will be assigned to this field and will get the above mentioned annotation followed by "as indicated in the Diagnostic markers table".

Table 5

<i>Enzymes</i>	<i>Gencarta Contig</i>	<i>Comments</i>
<i>Test</i>		
GPT	R35137 (GPT glutamic-pyruvate transaminase (alanine aminotransferase)) Z24841 (GPT2 glutamic pyruvate transaminase (alanine aminotransferase) 2)	Also called ALT – alanine aminotransferase. Standard liver function test

GOT	M78228 (GOT1 glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)) M86145 (GOT2 glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2))	Also called AST - aspartate aminotransferase. Standard liver function test
GGT	<u>HUMGGTX</u> (GGT1: gamma-glutamyltransferase 1)	Liver disease
CPK	T05088 (CKB creatine kinase, brain) HUMCKMA (CKM creatine kinase, muscle) H20196 (CKMT1 creatine kinase, mitochondrial 1 (ubiquitous)) HUMSMCK (CKMT2 creatine kinase, mitochondrial 2 (sarcomeric))	Also called CK. Mostly used for muscle pathologies. The MB variant is heart specific and used in the diagnosis of myocardial infarction
CPK-MB	T05088 (CKB creatine kinase, brain) HUMCKMA (CKM creatine kinase, muscle)	Cardiac problems - hetero-dimer of CKB and CKM
Alkaline Phosphatase	HSAPHOL ALPL: alkaline phosphatase, liver/bone/kidney HUMALPHB ALPI: alkaline phosphatase, intestinal HUMALPP ALPP: alkaline phosphatase, placental (Regan isozyme)	Bone related syndromes and liver diseases, mostly with biliary involvement
Amylase	AA367524- (AMY1A: amylase, alpha 1A; salivary) T10898- (AMY2B: amylase, alpha 2B; pancreatic and 2A)	Blood/Urine. Pancreas related diseases
LDH	HSLDHAR (LDHA lactate dehydrogenase A) M77886 (LDHB lactate dehydrogenase B) HSU13680 (LDHC lactate dehydrogenase C) AA398148 (LDHL lactate dehydrogenase A-like) R09053 (LDHD lactate dehydrogenase D)	Lactate Dehydrogenase. Used for myocardial infarction diagnosis and neoplastic syndromes assessment.
G6PD	S58359 (G6PD glucose-6-phosphate dehydrogenase)	Glucose 6-phosphate dehydrogenase. Levels measured when deficiency is suspected (leading to susceptibility to hemolysis)
Alpha1 antiTrypsin	HUMA1ACM (SERPINA3 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3) T10891 (AGT angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8)) R83168 (SERPINA6 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6) HUMCINHP (SERPINAS5 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5) HSA1ATCA (SERPINA1 serine (or	Chronic lung diseases

	cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1) HUMKALLS (SERPINA4 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4). HUMTBG (SERPINA7 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 7) T60354 (SERPINA10 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10)	
Renin	HSRENK (REN renin)	Some hypertension syndromes
Acid Phosphatase	HUMAAPA (ACP1: acid phosphatase 1, soluble) T48863 (ACP2: acid phosphatase 2, lysosomal) HSMRACP5 (ACP5: acid phosphatase 5, tartrate resistant) T85211 (ACP6: lysophosphatidic acid phosphatase) HSPROSAP (ACPP: acid phosphatase, prostate) AA005037 (ACPT: acid phosphatase, testicular)	Used to differentiate multiple myeloma with other monoclonal gammopathies of uncertain significance
Beta glucuronidase	T11069 (GUSB glucuronidase, beta)	Used to differentiate multiple myeloma with other monoclonal gammopathies of uncertain significance
Aldolase	HSALDAR (ALDOA aldolase A, fructose-bisphosphate) HSALDOBR (ALDOB aldolase B, fructose-bisphosphate) M62176 (ALDOC aldolase C, fructose-bisphosphate)	Glycogen storage diseases
Choline esterase	HUMCHEF (BCHE butyrylcholinesterase) F00931 (ACHE acetylcholinesterase (YT blood group))	Probably used for organophosphates/"nerve gases" intoxications
Pepsinogen	HUMPGCA PGC: progastricsin (pépsinogen C)	(in the stomach), high in gastritis, low in pernicious anemia[
ACE	HSACE (ACE: angiotensin I converting enzyme (peptidyl-dipeptidase A) 1) AA397955 (ACE2: angiotensin I converting enzyme (peptidyl-dipeptidase A) 2)	Angiotensin-converting enzyme. Sarcoidosis
<i>Miscellaneous</i>		
Test	<i>Gencarta Contig</i>	<i>Comments</i>
Prion Protein	HUMPRP0A (PRNP prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)) W73057 (PRND prion protein 2 (dublet))	BSE diagnosis

Myelin basic protein	M78010 (MBP myelin basic protein) R13982 (MOBP myelin-associated oligodendrocyte basic protein)	In CSF. In Multiple sclerosis
Albumin	HSALB1 (ALB albumin)	Mostly liver function and failure of intestine absorption
Prealbumin	HSALB1 (ALB albumin)	early diagnosis of malabsorption
Ferritin	HUMFERLS (FTL ferritin, light polypeptide) HUMFERHA (FTH1 ferritin, heavy polypeptide 1)	Iron deficiency anemia
Transferrin	S95936 (TF transferrin)	Iron deficiency anemia
Haptoglobin	HUMHPA1B (HP haptoglobin)	Used in anemia states and neoplastic syndromes
CRP	HSCREACT (CRP C-reactive protein, pentraxin-related)	C reactive protein. Associated with active inflammation
AFP	D11581 (AFP alpha-fetoprotein)	Alpha Feto Protein. Used in pregnancy for abnormalities screening and as a cancer marker.
C3	T40158 (C3 complement component 3)	Various auto-immune and allergy syndromes
C4	HSCOC4 (C4A complement component 4A; C4B complement component 4B)	Various auto-immune and allergy syndromes
Ceruloplasmin	HSCP2 (CP ceruloplasmin (ferroxidase))	Wilson's disease (liver disease)
Myoglobin	T11628 (MB myoglobin)	Rhabdomyolysis, Myocardial infarction
FABP	S67314 (FABP3: fatty acid binding protein 3, muscle and heart) D11754 (FABP1 liver- L-FABP- fatty acid binding protein 1) AW605378 (FABP2: fatty acid binding protein 2, intestinal) HUMALBP (FABP4: fatty acid binding protein 4, adipocyte) T06152 (FABP5: fatty acid binding protein 5 (psoriasis-associated) HSI15PGN1 (FABP6: fatty acid binding protein 6, ileal (gastrotropin) R60348 (FABP7: fatty acid binding protein 7, brain)	myoglobin and Fatty Acid Binding
Troponin I	HUMTROPNIN (TNNI2 troponin I, skeletal, fast) Z25083 (TNNI1 troponin I, skeletal, slow) HUMTROPIA (TNNI3 troponin I, cardiac)	Acute myocardial infarction
Beta-2-microglobulin	HSB2MMU (B2M beta-2-microglobulin)	
Macroglobulin	M62177 (A2M: alpha-2-macroglobulin)	Elevated in inflammation
Alpha-1 glycoprotein	T72188 (A1BG: alpha-1-B glycoprotein)	Elevated in inflammation and tumors,
Apo A-I	HUMAPOAIP (APOA1: apolipoprotein A-I)	Risk for coronary artery disease

Apo B-100	<u>HSAPOBR2</u> (APOB: apolipoprotein B (including Ag(x) antigen))	Atherosclerotic heart disease
Apo E	<u>T61627</u> (APOE: apolipoprotein E)	diagnosis of Type III hyperlipoproteinemia, evaluate a possible genetic component to atherosclerosis, or to help confirm a diagnosis of late onset AD
CF gene	<u>HUMCFTRM</u> (CFTR: cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7))	Cystic fibrosis disease (a DNA test – blood sample)
PSEN1 gene	<u>T89701</u> (PSEN1: presenilin 1 (Alzheimer disease 3))	Early onset of familial AD (a DNA test – blood sample)
Hormones		
Test	Gencarta Contig	Comments
Erythropoietin	<u>HSERPR</u> (EPO erythropoietin)	Hardly used for diagnosis. Used as treatment
GH	<u>HSGROW1</u> (GH1 growth hormone 1) <u>HUMCS2</u> (GH2 growth hormone 2)	Growth Hormone. Endocrine syndromes
TSH	<u>AV745295</u> (TSHB thyroid stimulating hormone, beta)	Part of thyroid functions tests
betaHCG	<u>R27266</u> (CGB5 chorionic gonadotropin, beta polypeptide 5)	Pregnancy, malignant syndromes in men and women
LH	<u>HUMCGBB50</u> (LHB luteinizing hormone beta polypeptide)	Part of standard hormonal profile for fertility, gynecological syndromes and endocrine syndromes
FSH	<u>AV754057</u> (FSHB follicle stimulating hormone, beta polypeptide)	Part of standard hormonal profile for fertility, gynecological syndromes and endocrine syndromes
TBG	<u>S40807</u> (TG thyroglobulin)	Thyroxin binding globulin. Thyroid syndromes
Prolactin	<u>HSLACT</u> (PRL prolactin)	Various endocrine syndromes
Thyroglobulin	<u>S40807</u> (TG thyroglobulin)	Follow up of thyroid cancer patients
PTH	<u>HSTHYR</u> (PTH parathyroid hormone)	Parathyroid Hormone. Syndromes of calcium management
Insulin/Pre Insulin	<u>HSPP1</u> (INS insulin)	Diabetes
Gastrin	<u>HSGAST</u> (GAS gastrin)	Peptic ulcers
Oxytocin	<u>HUMOTCB</u> (OXT oxytocin, prepro-(neurophysin I))	Endocrine syndromes related to lactation
AVP	<u>HUMVPC</u> (AVP arginine vasopressin (neurophysin II, antidiuretic hormone, diabetes insipidus, neurohypophyseal))	Arginine Vasopressin. Endocrine syndromes related to the osmotic pressure of body fluids
ACTH	<u>HUMPOMCMTC</u> (POMC: proopiomelanocortin (adrenocorticotropin/ beta-lipotropin/ alpha-melanocyte stimulating hormone/ beta-melanocyte stimulating hormone/ beta-endorphin))	Secreted from the anterior pituitary gland. Regulation of cortisol. Abnormalities are indicative of Cushing's disease, addison's disease and adrenal tumors
BNP	<u>HUMNATPEP</u> (NPB: natriuretic peptide precursor B)	Heart failure
Blood Clotting		
Test	Gencarta Contig	Comments
Protein C	<u>S50739</u> (PROC protein C (inactivator of coagulation factors Va and VIIIa))	Inherited Clotting disorders

Protein S	HSSPROTR (PROS1 protein S (alpha))	Inherited Clotting disorders
Fibrinogen	D1:1940 (FGA: fibrinogen, A alpha polypeptide) HUMFBRB (FGB: fibrinogen, B beta polypeptide). T24021 (FGG: fibrinogen, gamma polypeptide)	Clotting disorders
Factors 2, 5, 7, 9, 10, 11, 12, 13	HUMPTHROM (F2 coagulation factor II (thrombin)) HUMTFPC (F3 coagulation factor III (thromboplastin, tissue factor)) HUMF5A (F5 coagulation factor V (proaccelerin, labile factor)) M78203 (F7 coagulation factor VII (serum prothrombin conversion accelerator)) HUMF8C (F8 coagulation factor VIII, procoagulant component (hemophilia A)) HUMCFIX (F9 coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B)) HUMCFX (F10: coagulation factor X) HUMFXI (F11 coagulation factor XI (plasma thromboplastin antecedent)) HUMCFXIIA (F12 coagulation factor XII (Hageman factor)) HUMFXIIIA (F13A1 coagulation factor XIII, A1 polypeptide) R28976 (F13B coagulation factor XIII, B polypeptide)	Inherited Clotting disorders
vWF	HUMVWF (VWF von Willebrand factor)	Von Willebrand factor. Inherited Clotting disorders
Antithrombin III	T62060 (SERPINC1 serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1)	Inherited Clotting disorders
Cancer Markers		
<i>Test</i>	<i>Gencarta Contig</i>	<i>Comments</i>
AFP	D11581 (AFP alpha-fetoprotein)	Pregnancy, testicular cancer and hepatocellular cancer
CA125	HSIAI3B (M17S2 membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125))	Ovarian cancer
CA-15-3	HSMUC1A (MUC1 mucin 1, transmembrane)	Breast cancer
CA-19-9	HSAFUTF (FUT3: fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included))	Gastrointestinal cancer, pancreatic cancer
CEA	T10888 HUMCEA (CEACAM3 carcinoembryonic antigen-related cell adhesion molecule 3)	Carcinoembryonic Antigen: Colorectal cancer
PSA	HSCDN9 (KLK3: kallikrein 3, (prostate specific antigen))	
PSMA	HUMPSM (FOLH1: folate hydrolase (prostate-specific membrane antigen) 1)	
TPA, TATI, OVX1, LASA	HSPSTI (SPINK1: serine protease inhibitor, Kazal type 1)	Ovarian cancer

CA54/81		
BRCA 1	<u>H90415</u> (BRCA1: breast cancer 1, early onset)	
BRCA 2	<u>H47777</u> (BRCA2: breast cancer 2, early onset)	Breast cancer (ovarian cancer)
HER2/Neu	<u>S57296</u> (ERBB2: v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian))	Breast cancer
Estrogen receptor	<u>HSERG5UTA</u> (ESR1: estrogen receptor 1) <u>HSRNLNAERB</u> (ESR2: estrogen receptor 2 (ER beta))	Breast cancer
Progesterone receptor	<u>T09102</u> (PGRMC1: progesterone receptor membrane component 1) <u>Z32891</u> (PGRMC2: progesterone receptor membrane component 2)	Breast cancer

Note:

- (i) Small portion of these "markers" are also drug targets, whether already for approved drugs (such as alpha1 antiTrypsin) or under development (e.g., GOT).
- (ii) Some of these "markers" are also used as therapeutic proteins (e.g., Erythropoietin).
- (iii) All markers are found in the blood/serum unless otherwise specified.

1. #DISEASE RELATED CLINICAL PHENOTYPE – This field denotes the possibility of using biomolecular sequences of the present invention for the diagnosis and/or treatment of genetic diseases such as listed in the following URL: <http://www.geneclinics.org/servlet/access?id=8888891&key=X9D790O5re1Az&db=genetests&res=&fcn=b&grp=g&genesearch=true&testtype=both&ls=1&type=e&qry=&submit=Search> and in Table 6, below. This list includes genetic diseases and genes which may be used for the detection and/or treatment thereof. As such, newly uncovered variants of these genes, including novel SNPs or mutations, may be used for improved diagnosis and/or treatment when used singly or in combination with the previously described genes. For example, in genetic diseases where the diseased phenotype has a different splice variant profile than the healthy phenotype, like that seen in Thalasemia and in Duchenne Muscular Dystrophy, the novel splice variants might discriminate between healthy and diseased phenotype.

Another example is in cases of autosomal recessive genetic diseases. Some of the sequences in genebank were sequenced from malfunctioning alleles derived from healthy carriers of the disease, and therefore contain the mutation that leads to the

disease. Identification of novel SNPs predicted based on sequence alignment can assist in identifying disease-causing mutations.

Table 6

<i>Gencarta Contig</i>	<i>Gene Symbol</i>	<i>Disease</i>
HSCFTRMA	CFTR	Congenital Bilateral Absence of the Vas Deferens ;Cystic Fibrosis
HUMCFTRM	CFTR	Congenital Bilateral Absence of the Vas Deferens ;Cystic Fibrosis
HUMFGFR3	FGFR3	Achondroplasia ;Crouzon Syndrome with Acanthosis Nigricans ;FGFR-Related Craniosynostosis Syndromes ;Hypochondroplasia ;Muenke Syndrome ;Severe Achondroplasia with Developmental Delay and Acanthosis Nigricans (SADDAN) ;Thanatophoric Dysplasia
HSU11690	FGD1	Aarskog Syndrome
HSCA1III	COL3A1	Ehlers-Danlos Syndrome, Vascular Type
HUMCOL2A1B	COL2A1	Achondrogenesis Type 2 ;Kniest Dysplasia ;Spondyloepimetaphyseal Dysplasia, Strudwick Type ;Spondyloepiphyseal Dysplasia, Congenita. ;Stickler Syndrome ;Stickler Syndrome Type I
R68817	APRT	Adenine Phosphoribosyltransferase Deficiency
HUMAMPD1	AMPD1	Adenosine Monophosphate Deaminase 1
M62124	PXR1	Zellweger Syndrome Spectrum
HSXLALDA	ABCD1	Adrenoleukodystrophy, X-Linked
T28718	BTK	X-Linked Agammaglobulinemia
R91110	IL2RG	X-Linked Severe Combined Immunodeficiency
HUMPEDG	OCA2	Oculocutaneous Albinism Type 2
HSU01873	TYR	Oculocutaneous Albinism Type 1
HSOA1MRNA	OA1	Ocular Albinism, X-Linked
R14843	TYRP1	Oculocutaneous Albinism Type 3 (TRP1 Related)
HSALDAR	ALDOA	Aldolase A Deficiency
T40633	HBA1	Alpha-Thalassemia
T40633	HBA2	Alpha-Thalassemia ;Hemoglobin Constant Spring
HSU09820	ATRX	Alpha-Thalassemia X-Linked Mental Retardation Syndrome
HUMCOL4A5	COL4A5	Alport Syndrome ;Alport Syndrome, X-Linked
T61627	APOE	Apolipoprotein E Genotyping ;Familial Combined Hyperlipidemia ;Hyperlipoproteinemia Type III
T89701	PSEN1	Alzheimer Disease Type 3 ;Early-Onset Familial Alzheimer Disease
R05822	PSEN2	Alzheimer Disease Type 4 ;Early-Onset Familial Alzheimer Disease
HSTTRM	TTR	Transthyretin Amyloidosis
T23978	SOD1	Amyotrophic Lateral Sclerosis
HUMANDREC	AR	Androgen Insensitivity Syndrome ;Spinal and Bulbar Muscular Atrophy
Z19491	UBE3A	Angelman Syndrome
HUMPAX6AN	PAX6	Aniridia ;Anophthalmia ;Isolated Aniridia ;Peters Anomaly ;Peters Anomaly with Cataract ;Wilms Tumor-Aniridia-Genital Anomalies-Retardation Syndrome

HUMKGFRA	FGFR2	Apert Syndrome ;Beare-Stevenson Syndrome ;Crouzon Syndrome ;FGFR-Related Craniosynostosis Syndromes ;Jackson-Weiss Syndrome ;Pfeiffer Syndrome Type 1, 2, and 3
HSU03272	FBN2	Congenital Contractural Arachnodactyly
Z19459	AMCD1	Arthrogryposis Multiplex Congenita, Distal, Type I
T88756	ATM	Ataxia-Telangiectasia
H30056	BBS1	Bardet-Biedl Syndrome
Z25009	BBS2	Bardet-Biedl Syndrome
T64876	BBS4	Bardet-Biedl Syndrome
N27125	PTCH	Nevvoid Basal Cell Carcinoma Syndrome
N31453	VMD2	Best Vitelliform Macular Dystrophy
HUMHBB3E	HBB	Beta-Thalassemia ;Hemoglobin E ;Hemoglobin S Beta-Thalassemia ;Hemoglobin SC ;Hemoglobin SD ;Hemoglobin SO ;Hemoglobin SS ;Sickle Cell Disease
H53763	BLM	Bloom Syndrome
N22283	EYA1	Branchiootorenal Syndrome
H90415	BRCA1	BRCA1 and BRCA2 Hereditary Breast/Ovarian Cancer ;BRCA1 Hereditary Breast/Ovarian Cancer
H47777	BRCA2	BRCA1 and BRCA2 Hereditary Breast/Ovarian Cancer ;BRCA2 Hereditary Breast/Ovarian Cancer
Z33575	SOX9	Campomelic Dysplasia
S67156	ASPA	Canavan Disease
TS2465	CPS1	Carbamoylphosphate Synthetase I Deficiency
HSVD3HYD	CYP27A1	Cerebrotendinous Xanthomatosis
S66705	MPZ	Charcot-Marie-Tooth Neuropathy Type 1 ;Charcot-Marie-Tooth Neuropathy Type 1B ;Congenital Hypomyelination
HSGAS3MR	PMP22	Charcot-Marie-Tooth Neuropathy Type 1 ;Charcot-Marie-Tooth Neuropathy Type 1A ;Charcot-Marie-Tooth Neuropathy Type 1E ;Hereditary Neuropathy with Liability to Pressure Palsies
T93208	PMP22	Charcot-Marie-Tooth Neuropathy Type 1 ;Charcot-Marie-Tooth Neuropathy Type 1A ;Charcot-Marie-Tooth Neuropathy Type 1E ;Hereditary Neuropathy with Liability to Pressure Palsies
HSGAPJR	GJB1	Charcot-Marie-Tooth Neuropathy Type X
HSXCGD	CYBB	Chronic Granulomatous Disease
S67289	CYBB	Chronic Granulomatous Disease
HSASD	ASS	Citrullinemia
HUMPAX2A	PAX2	Anophthalmia ;Renal-Coloboma Syndrome
HUMP45C21	CYP21A2	21-Hydroxylase Deficiency
S74720	NR0B1	Complex Glycerol Kinase Deficiency ;Dosage-Sensitive Sex Reversal ;Isolated X-Linked Adrenal Hypoplasia Congenita ;X-Linked Adrenal Hypoplasia Congenita
HSKERTRNS	TGM1	Autosomal Recessive Congenital Ichthyosis
BF928311	CPO	Hereditary Coproporphyria
HSCPPOX	CPO	Hereditary Coproporphyria
HUMTGFBIG	TGFB1	Avellino Corneal Dystrophy ;Granular Corneal Dystrophy ;Lattice Corneal Dystrophy Type I
R08437	MSX2	Craniosynostosis Type II ;Parietal Foramina 1
HUMPRP0A	PRNP	Prion Diseases
T08652	DRPLA	DRPLA
Z46151	DRPLA	DRPLA

HSWT1	WT1	Denys-Drash Syndrome ;Wilms Tumor ;Wilms Tumor-Aniridia-Genital Anomalies-Retardation Syndrome ;WT1-Related Disorders
HUMWT1X	WT1	Denys-Drash Syndrome ;Wilms Tumor ;Wilms Tumor-Aniridia-Genital Anomalies-Retardation Syndrome ;WT1-Related Disorders
M78080	ATP2A2	Darier Disease
Z30219	DCR	Down Syndrome Critical Region
T11279	DKC1	Dyskeratosis Congenita
T08131	DYT1	Early-Onset Primary Dystonia (DYT1)
T50729	ED1	Hypohidrotic Ectodermal Dysplasia ;Hypohidrotic Ectodermal Dysplasia, X-Linked
HUMPA1V	COL5A1	Ehlers-Danlos Syndrome, Classic Type
HUMLYSYL	PLOD	Ehlers-Danlos Syndrome, Kyphoscoliotic Form
HSCOLIA	COL1A2	Ehlers-Danlos Syndrome, Arthrochalasia Type ;Osteogenesis Imperfecta
HUMCG1PA1	COL1A1	Ehlers-Danlos Syndrome, Arthrochalasia Type ;Osteogenesis Imperfecta
Z30171	TAZ	3-Methylglutaconic Aciduria Type 2 ;Cardiomyopathy ;Dilated Cardiomyopathy ;Endocardial Fibroelastosis ;Familial Isolated Noncompaction of Left Ventrical Myocardium
Z39302	TAZ	3-Methylglutaconic Aciduria Type 2 ;Cardiomyopathy ;Dilated Cardiomyopathy ;Endocardial Fibroelastosis ;Familial Isolated Noncompaction of Left Ventrical Myocardium
HUMKERK5A	KRT5	Epidermolysis Bullosa Simplex
R72295	KRT14	Epidermolysis Bullosa Simplex
HUMKTEP2A	KRT1	Epidermolytic Hyperkeratosis ;Nonepidermolytic Palmoplantar Hyperkeratosis
HUMK10A	KRT10	Epidermolytic Hyperkeratosis
M78482	CHS1	Chediak-Higashi Syndrome
HSTCD1	CHM	Choroideremia
HSAGALAR	GLA	Fabry Disease
T79651	GLA	Fabry Disease
HUMF5A	F5	Factor V Leiden Thrombophilia ;Factor V R2 Mutation Thrombophilia
HUMFXI	F11	Factor XI Deficiency
M79108	APC	Colon Cancer (APC I1307K related) ;Familial Adenomatous Polyposis
T10619	IKBKAP	Familial Dysautonomia
HUMFMR1	FMR1	Fragile X Syndrome
M78417	FMR2	FRAXE Syndrome
R06415	FRDA	Friedreich Ataxia
HSALDOBR	ALDOB	Hereditary Fructose Intolerance
HUMALFUC	FUCA1	Fucosidosis
M85904	FH	Fumarate Hydratase Deficiency
H85361	ABCA4	Age-Related Macular Degeneration ;Retinitis Pigmentosa, Autosomal Recessive ;Stargardt Disease 1
R31596	GALK1	Galactokinase Deficiency
T53762	GALT	Galactosemia
HUMGCB	GBA	Gaucher Disease
T48672	GBA	Gaucher Disease

HSGCRAR	NR3C1	Glucocorticoid Resistance
S58359	G6PD	Glucose-6-Phosphate Dehydrogenase Deficiency
HSGKTS1	GK	Glycerol Kinase Deficiency
HSRNAGLK	GK	Glycerol Kinase Deficiency
U01120	G6PC	Glycogen Storage Disease Type Ia
HUMGAAA	GAA	Glycogen Storage Disease Type II
F00985	AGL	Glycogen Storage Disease Type III
HUMHGBE	GBE1	Glycogen Storage Disease Type IV
HSPHOSR1	PYGM	Glycogen Storage Disease Type V
D12179	PYGL	Glycogen Storage Disease Type VI
HSHMPFK	PFKM	Glycogen Storage Disease Type VII
HUMGLI3A	GLI3	GLI3-Related Disorders ;Greig Cephalopolysyndactyly Syndrome ;Pallister-Hall Syndrome
F09335	ATP2C1	Hailey-Hailey Disease
M62210	CCM1	Angiokeratoma Corporis Diffusum with Arteriovenous Fistulas ;Familial Cerebral Cavernous Malformation
T59431	HFE	HFE- Associated Hereditary Hemochromatosis
HSALK1A	ACVRL1	Hereditary Hemorrhagic Telangiectasia
HUMENDO	ENG	Hereditary Hemorrhagic Telangiectasia
HUMF8C	F8	Hemophilia A
HUMFVIII	F8	Hemophilia A
HUMCFIX	F9	Hemophilia B
HSU03911	MSH2	Hereditary Non-Polyposis Colon Cancer
Z24775	MLH1	Hereditary Non-Polyposis Colon Cancer
HSRETTT	RET	Hirschsprung Disease ;Multiple Endocrine Neoplasia Type 2
HUMSHH	SHH	Holoprosencephaly 3
N81026	TBX5	Holt-Oram Syndrome
M78262	CBS	Homocystinuria
T06035	IDS	Mucopolysaccharidosis Type II
T03828	HD	Huntington Disease
H27612	IDUA	Mucopolysaccharidosis Type I
M62205	GFAP	Alexander Disease
HUMCD40L	TNFSF5	Hyper IgM Syndrome, X-Linked
HUMPTHROM	F2	Prothrombin G20210A Thrombophilia
T61466	MTHFR	MTHFR Deficiency ;MTHFR Thermolabile Variant
HUMSKM1A	SCN4A	Hyperkalemic Periodic Paralysis Type 1 ;Hypokalemic Periodic Paralysis ;Hypokalemic Periodic Paralysis Type 2 ;Myotonia Congenita, Dominant ;Paramyotonia Congenita
HSU09784	CACNA1S	Hypokalemic Periodic Paralysis ;Hypokalemic Periodic Paralysis Type 1 ;Malignant Hyperthermia Susceptibility
HUMPLAА	LPL	Familial Lipoprotein Lipase Deficiency
HUMPEX	PHEX	Hypophosphatemic Rickets, X-Linked Dominant
M78626	STS	Ichthyosis, X-Linked
R56102	IKBKG	Incontinentia Pigmenti
Z39843	IVD	Isovaleric Acidemia
S60085S1	KAL1	Kallmann Syndrome, X-Linked
T55061	KEL	Kell Antigen Genotyping
HUMGALC	GALC	Krabbe Disease
HUMZFPSREB	ZNF9	Myotonic Dystrophy Type 2
Z19342	KIF1B	Charcot-Marie-Tooth Neuropathy Type 2
T11351	NPC2	Niemann-Pick Disease Type C
Z39096	NDRG1	Charcot-Marie-Tooth Neuropathy Type 4

AA984421	PRX	Charcot-Marie-Tooth Neuropathy Type 4 ;Charcot-Marie-Tooth Neuropathy Type 4F
HUMRETGC	GUCY2D	Leber Congenital Amaurosis
HSU18991	RPE65	Leber Congenital Amaurosis ;Retinitis Pigmentosa, Autosomal Recessive
C16899	MTND6	Leber Hereditary Optic Neuropathy ;Mitochondrial Disorders ;Mitochondrial DNA-Associated Leigh Syndrome and NARP
AA069417	MTND4	Leber Hereditary Optic Neuropathy ;Mitochondrial Disorders ;Mitochondrial DNA-Associated Leigh Syndrome and NARP
HUMCYP3A	MTND4	Leber Hereditary Optic Neuropathy ;Mitochondrial Disorders ;Mitochondrial DNA-Associated Leigh Syndrome and NARP
HSCPCH22	MTND1	Leber Hereditary Optic Neuropathy ;Mitochondrial Disorders ;Mitochondrial DNA-Associated Leigh Syndrome and NARP
HUMHPRT	HPRT1	Lésch-Nyhan Syndrome
HUMLHHCGR	LHCGR	Leydig Cell Hypoplasia/Agenesis ;Male-Limited Precocious Puberty
HSP53	TP53	Li-Fraumeni Syndrome
Z19198	HADHB	Long Chain 3-Hydroxyacyl-CoA Dehydrogenase Deficiency
M79018	HADHA	Long Chain 3-Hydroxyacyl-CoA Dehydrogenase Deficiency
W93500	KCNQ1	Atrial Fibrillation ;Jervell and Lange-Nielsen Syndrome ;LQT 1 ;Romano-Ward Syndrome
S62085	OCRL	Lowe Syndrome
T48981	FBN1	Marfan Syndrome
HUMASFB	ARSB	Mucopolysaccharidosis Type VI
M62202	GNAS	Albright Hereditary Osteodystrophy ;McCune-Albright Syndrome ;Osseus Heteroplasia, Progressive
N46342	SACS	ARSACS
T81605	FANCD2	Fanconi Anemia
H47777	FANCD1	Fanconi Anemia
T23877	ACADM	Medium Chain Acyl-Coenzyme A Dehydrogenase Deficiency
AA906866	PARK2	Parkin Type of Juvenile Parkinson Disease
BE140729	GJB4	Erythrokeratoderma Variabilis
HSU26727	CDKN2A	Familial Malignant Melanoma
T47218	SPINK5	Netherton Syndrome
HSMNKMBP	ATP7A	ATP7A-Related Copper Transport Disorders
R37821	SHFM4	Ectrodactyly
M78183	GSN	Amyloidosis V
HSARYA	ARSA	Chromosome 22q13.3 Deletion Syndrome ;Metachromatic Leukodystrophy
S68531	COL10A1	Metaphyseal Chondrodysplasia, Schmid Type
T59742	CACNA1A	Episodic Ataxia Type 2 ;Familial Hemiplegic Migraine ;Spinocerebellar Ataxia Type 6
HSCP2	HPS3	Hermansky-Pudlak Syndrome ;Hermansky-Pudlak Syndrome 3
R21301	HPS3	Hermansky-Pudlak Syndrome ;Hermansky-Pudlak Syndrome 3
HUMBGALRP	GLB1	GM1 Gangliosidosis ;Mucopolysaccharidosis Type

		IVB
HSU12507	KCNJ2	Andersen Syndrome
R28488	MEN1	Multiple Endocrine Neoplasia Type 1
HUMCOMP	COMP	COMP-Related Multiple Epiphyseal Dysplasia ;Multiple Epiphyseal Dysplasia, Dominant ;Pseudoachondroplasia
H30258	COL9A2	Multiple Epiphyseal Dysplasia, Dominant
T48133	EXT1	Hereditary Multiple Exostoses ;Multiple Exostoses, Type I
T06129	EXT2	Hereditary Multiple Exostoses ;Multiple Exostoses, Type II
T05624	LAMA2	Congenital Muscular Dystrophy with Merosin Deficiency
HSDYSTIA	DMD	Duchenne/Becker Muscular Dystrophy ;Dystrophinopathies ;X-Linked Dilated Cardiomyopathy
HSSTA	EMD	Emery-Dreifuss Muscular Dystrophy, X-Linked
HSU20165	BMPR2	Primary Pulmonary Hypertension
M79239	CAPN3	Calpainopathy ;Limb-Girdle Muscular Dystrophies, Autosomal Recessive
HSU34976	SGCG	Gamma-Sarcoglycanopathy ;Limb-Girdle Muscular Dystrophies, Autosomal Recessive ;Sarcoglycanopathies
HUMADHA	SGCA	Alpha-Sarcoglycanopathy ;Limb-Girdle Muscular Dystrophies, Autosomal Recessive ;Sarcoglycanopathies
Z25374	SGCB	Beta-Sarcoglycanopathy ;Limb-Girdle Muscular Dystrophies, Autosomal Recessive ;Sarcoglycanopathies
N29439	SGCD	Delta-Sarcoglycanopathy ;Dilated Cardiomyopathy ;Limb-Girdle Muscular Dystrophies, Autosomal Recessive ;Sarcoglycanopathies
N56180	CASQ2	Catecholaminergic Ventricular Tachycardia, Autosomal Recessive
T23560	CHRNBT2	Nocturnal Frontal Lobe Epilepsy, Autosomal Dominant
HSCHRNA44	CHRNA4	Nocturnal Frontal Lobe Epilepsy, Autosomal Dominant
M78654	CHRNA4	Nocturnal Frontal Lobe Epilepsy, Autosomal Dominant
T86329	CDH23	Usher Syndrome Type 1
D11677	PABPN1	Oculopharyngeal Muscular Dystrophy
AW449267	PCDH15	Usher Syndrome Type 1
HUMCLC	CLCN1	Myotonia Congenita, Dominant ;Myotonia Congenita, Recessive
S86455	DMPK	Myotonic Dystrophy Type 1
T70260	MTM1	Myotubular Myopathy, X-Linked
T12579	LMX1B	Nail-Patella Syndrome
HSTRKT1	TPM3	Nemaline Myopathy
HUMTROPCK	TPM3	Nemaline Myopathy
Z19248	NEB	Nemaline Myopathy
AF030626	AVPR2	Nephrogenic Diabetes Insipidus ;Nephrogenic Diabetes Insipidus, X-Linked
AA780862	NPHS1	Congenital Finnish Nephrosis
T08860	ABCC8	ABCC8-Related Hyperinsulinism ;Familial Hyperinsulinism
AA679741	KCNJ11	Familial Hyperinsulinism ;KCNJ11-Related Hyperinsulinism

M77935	NF1	Neurofibromatosis 1
HSMEORPRA	NF2	Neurofibromatosis 2
T08995	CLN3	CLN3-Related Neuronal Ceroid-Lipofuscinosis ;Neuronal Ceroid-Lipofuscinoses
T72120	CLN2	CLN2-Related Neuronal Ceroid-Lipofuscinosis ;Neuronal Ceroid-Lipofuscinoses
T41059	GRHPR	Hyperoxaluria, Primary, Type 2
HUMGCRFC	FCGR3A	Neutrophil Antigen Genotyping
R21657	NPC1	Niemann-Pick Disease Type C ;Niemann-Pick Disease Type C1
M77961	SMPD1	Niemann-Pick Disease Due to Sphingomyelinase Deficiency
T87256	SUOX	Sulfocysteinuria
D79813	SOST	SOST-Related Sclerosing Bone Dysplasias
T94707	MATN3	Multiple Epiphyseal Dysplasia, Dominant
HSCOL9AL	COL9A1	Multiple Epiphyseal Dysplasia, Dominant
S69208	TNNI1	Nemaline Myopathy
Z19459	TPM2	Nemaline Myopathy
D11793	SLC2A1	Glucose Transporter Type 1 Deficiency Syndrome
HSCHRX	NDP	Norrie Disease
T62791	OPA1	Optic Atrophy 1
Z24812	OFD1	Oral-Facial-Digital Syndrome Type I
HUMOTC	OTC	Ornithine Transcarbamylase Deficiency
R66505	MKKS	Bardet-Biedl Syndrome ;McKusick-Kaufman Syndrome
Z19438	CHAC	Choreoacanthocytosis
HUMRDSA	RDS	Patterned Dystrophy of Retinal Pigment Epithelium ;Retinitis Pigmentosa, Autosomal Dominant
Z30072	PLP1	Hereditary Spastic Paraparesis, X-Linked ;PLP-Related Disorders
HSFGR1IG	FGFR1	FGFR-Related Craniostenosis Syndromes ;Pfeiffer Syndrome Type 1, 2, and 3
HUMPHH	PAH	Phenylalanine Hydroxylase Deficiency
HSKITCR	KIT	Gastrointestinal Stromal Tumor ;Piebaldism
HSGROW1	GH1	Pituitary Dwarfism I
F00079	GHR	Pituitary Dwarfism II
HSPIT1	POU1F1	Pituitary-Specific Transcription Factor Defects (PIT1)
T58874	SDHD	Familial Nonchromaffin Paragangliomas
HUMINTB3	ITGB3	Integrin, Beta 3 ;Platelet Antigen Genotyping
T09245	PKD1	Polycystic Kidney Disease 1, Autosomal Dominant ;Polycystic Kidney Disease, Autosomal Dominant
T55657	PKD2	Polycystic Kidney Disease 2, Autosomal Dominant ;Polycystic Kidney Disease, Autosomal Dominant
T77325	PKD2	Polycystic Kidney Disease 2, Autosomal Dominant ;Polycystic Kidney Disease, Autosomal Dominant
W27963	PKD2	Polycystic Kidney Disease 2, Autosomal Dominant ;Polycystic Kidney Disease, Autosomal Dominant
R05352	PKHD1	Polycystic Kidney Disease, Autosomal Recessive
M77871	PCLD	Polycystic Liver Disease
M78097	UROD	Porphyria Cutanea Tarda
HUMPBG	HMBS	Acute Intermittent Porphyria
HUMRODSA	UROS	Congenital Erythropoietic Porphyria
T10891	AGT	Angiotensinogen
T67463	CTSK	Pycnodysostosis
M77954	PDHA1	Pyruvate Dehydrogenase Deficiency, X-linked

Z19400	PHYH	Refsum Disease, Adult
R07476	PEX1	Zellweger Syndrome Spectrum
Z24965	RCA1	Renal Cell Carcinoma
H37900	RHO	Retinitis Pigmentosa, Autosomal Dominant ;Retinitis Pigmentosa, Autosomal Recessive
T24020	RB1	Retinoblastoma
Z44098	RS1	X-Linked Juvenile Retinoschisis
HSRH30A	RHCE	Rh C Genotyping ;Rh E Genotyping
S57971	RHCE	Rh C Genotyping ;Rh E Genotyping
T89255	RHCE	Rh C Genotyping ;Rh E Genotyping
R60192	PEX7	Refsum Disease, Adult ;Rhizomelic Chondrodysplasia Punctata Type 1
HUMMLC1AA	MLC1	Megalencephalic Leukoencephalopathy with Subcortical Cysts
M79106	MLC1	Megalencephalic Leukoencephalopathy with Subcortical Cysts
T64905	PITX2	Anophthalmia ;Peters Anomaly ;Rieger Syndrome
Z41163	CREBBP	Rubinstein-Taybi Syndrome
HSBHLH	TWIST1	Saethre-Chotzen Syndrome
F00367	EIF2B1	Childhood Ataxia with Central Nervous System Hypomyelination/Vanishing White Matter
Z20030	EIF2B2	Childhood Ataxia with Central Nervous System Hypomyelination/Vanishing White Matter
Z41323	EIF2B3	Childhood Ataxia with Central Nervous System Hypomyelination/Vanishing White Matter
Z17882	EIF2B4	Childhood Ataxia with Central Nervous System Hypomyelination/Vanishing White Matter
R13846	EIF2B5	Childhood Ataxia with Central Nervous System Hypomyelination/Vanishing White Matter ;Cree Leukoencephalopathy
T03917	HEXB	Sandhoff Disease
HUMSRYA	SRY	XX Male Syndrome ;XY Gonadal Dysgenesis
HUMSCAD	ACADS	Short Chain Acyl-CoA Dehydrogenase Deficiency
HSALAS2R	ALAS2	Sideroblastic Anemia, X-Linked
T47846	GPC3	Simpson-Golabi-Behmel Syndrome
T11069	GUSB	Mucopolysaccharidosis Type VII
T08813	SPG3A	Hereditary Spastic Paraparesis, Dominant ;SPG 3
Z40639	SPG3A	Hereditary Spastic Paraparesis, Dominant ;SPG 3
M77964	SPG4	Hereditary Spastic Paraparesis, Dominant ;SPG 4
N36808	SMN1	Spinal Muscular Atrophy
Z38265	SMN1	Spinal Muscular Atrophy
T06490	SCA1	Spinocerebellar Ataxia Type 1
T55469	SCA2	Spinocerebellar Ataxia Type 2
Z41764	SCA2	Spinocerebellar Ataxia Type 2
T61453	MJD	Spinocerebellar Ataxia Type 3
HUMELASF	ELN	Cutis Laxa, Autosomal Dominant ;Supravalvular Aortic Stenosis
T05970	HEXA	Hexosaminidase A Deficiency
M79184	THRΒ	Thyroid Hormone Resistance
Z20729	TCOF1	Treacher Collins Syndrome
R48739	TRPS1	Trichorhinophalangeal Syndrome Type I
T77655	TSC1	Tuberous Sclerosis 1 ;Tuberous Sclerosis Complex
M78940	TSC2	Tuberous Sclerosis 2 ;Tuberous Sclerosis Complex
HSFAA	FAH	Tyrosinemia Type I
T39510	TBX3	Ulnar-Mammary Syndrome

HUMM7AA	MYO7A	Usher Syndrome Type 1
W22160	USH1C	Usher Syndrome Type 1
T08506	ACADVL	Very Long Chain Acyl-CoA Dehydrogenase Deficiency
HUMHPLIND	VHL	Von Hippel-Lindau Syndrome
HUMVWF	VWF	Von Willebrand Disease
HSU02368	PAX3	Waardenburg Syndrome Type I
H80461	WRN	Werner Syndrome
HUMWND	ATP7B	Wilson Disease
T40645	WAS	WAS-Related Disorders
HSLAL	LIPA	Wolman Disease
HSASL1	ASL	Argininosuccinicaciduria
HSAGAGENE	AGA	Aspartylglycosaminuria
T88756	ATD	Asphyxiating Thoracic Dystrophy
Z19164	ASAHI	Farber Disease
HUMALD	FBP1	Fructose 1,6 Bisphosphatase Deficiency
HSLDHAR	LDHA	Lactate Dehydrogenase Deficiency
M77886	LDHB	Lactate Dehydrogenase Deficiency
HSU13680	LDHC	Lactate Dehydrogenase Deficiency
Z46189	MAN2B1	Alpha-Mannosidosis
M79249	MANBA	Beta-Mannosidosis
H26723	GALNS	Mucopolysaccharidosis Type IVA
H23053	SLC26A4	DFNB 4 ;Enlarged Vestibular Aqueduct Syndrome ;Nonsyndromic Hearing Loss and Deafness, Autosomal Recessive ;Pendred Syndrome
HSPGK1	PGK1	Phosphoglycerate Kinase Deficiency
HSU08818	MET	Papillary Renal Carcinoma
M79231	PRCC	Papillary Renal Carcinoma
T08200	GNS	Mucopolysaccharidosis Type IIID
HUMNAGB	NAGA	Schindler Disease
T08881	NEU1	Mucolipidosis I
R81783	SLC17A5	Free Sialic Acid Storage Disorders
HUMAUTONH	MTATP6	Mitochondrial Disorders ;Mitochondrial DNA-Associated Leigh Syndrome and NARP
F09306	SCA7	Spinocerebellar Ataxia Type 7
AF248482	DAZ	Y Chromosome Infertility
HSU21663	DAZ	Y Chromosome Infertility
T47024	JAG1	Alagille Syndrome
HSRYRRM1	RBMY1A1	Y Chromosome Infertility
HSRYRRM2	RBMY1A1	Y Chromosome Infertility
HSVD3R	VDR	Osteoporosis ;Rickets-Alopecia Syndrome
T40157	FMO3	Trimethylaminuria
HUMPHOSLIP	PPGB	Galactosialidosis
HUMPPR	PPGB	Galactosialidosis
H22222	FANCC	Fanconi Anemia
D12009	RPS6KA3	Coffin-Lowry Syndrome
M78282	PTEN	PTEN Hamartoma Tumor Syndrome (PHTS)
M78802	FY	Duffy Antigen Genotyping
HSU04270	KCNH2	LQT 2 ;Romano-Ward Syndrome
T19733	SCNSA	Brugada Syndrome ;LQT 3 ;Romano-Ward Syndrome
HSTFIIDX	TBP	Spinocerebellar Ataxia Type17
HUMKCHA	KCNA1	Episodic Ataxia Type 1
HSU78110	NRTN	Hirschsprung Disease
HSET3AA	EDN3	Hirschsprung Disease
Z17351	ECE1	Hirschsprung Disease
T47284	DHCR7	Smith-Lemli-Opitz Syndrome

HUMXIHB	HBZ	Alpha-Thalassemia
HSCP2	CP	Aceruloplasminemia
N25320	CLN6	CLN6-Related Neuronal Ceroid-Lipofuscinosis ;Neuronal Ceroid-Lipofuscinoses
T11340	NBS1	Nijmegen Breakage Syndrome
Z40114	NBS1	Nijmegen Breakage Syndrome
HSU03688	CYP1B1	Glaucoma, Recessive (Congenital) ;Peters Anomaly
D62980	MYOC	Glaucoma, Dominant (Juvenile Onset)
T98453	NAGLU	Mucopolysaccharidosis Type III B
AA779817	RUNX2	Cleidocranial Dysplasia
HUMCBFA	RUNX2	Cleidocranial Dysplasia
HSMARENO	MEFV	Familial Mediterranean Fever
F02180	PHKB	Phosphorylase Kinase Deficiency of Liver and Muscle
D11905	HPS1	Hermansky-Pudlak Syndrome ;Hermansky-Pudlak Syndrome 1
R95987	CRX	Retinitis Pigmentosa, Autosomal Dominant
T05762	EVC	Ellis-van Creveld Syndrome
T12126	FLNA	Frontometaphyseal Dysplasia ;Melnick-Needles Syndrome ;Otopalatodigital Syndrome ;Periventricular Heterotopia, X-Linked
T60913	EBP	Chondrodysplasia Punctata, X-Linked Dominant
HSHNF4	HNF4A	Maturity-Onset Diabetes of the Young Type I
HUMBGLUKIN	GCK	Familial Hyperinsulinism ;GCK-Related Hyperinsulinism ;Maturity-Onset Diabetes of the Young Type II
M62026	GCK	Familial Hyperinsulinism ;GCK-Related Hyperinsulinism ;Maturity-Onset Diabetes of the Young Type II
R94860	CIAS1	Chronic Infantile Neurological Cutaneous and Articular Syndrome ;Familial Cold Urticaria ;Muckle-Wells Syndrome
T08221	SMARCAL1	Schimke Immunoosseous Dysplasia
T95621	SLC25A15	Hyperornithinemia-Hyperammonemia-Homocitrullinuria Syndrome
HUMOATC	OAT	Ornithine Aminotransferase Deficiency
R08989	MLYCD	Malonyl-CoA Decarboxylase Deficiency
T20008	PMM2	Congenital Disorders of Glycosylation
HSRPMI	MPI	Congenital Disorders of Glycosylation
HSSRECV6	MGAT2	Congenital Disorders of Glycosylation
T91755	MGAT2	Congenital Disorders of Glycosylation
HSCPTI	CPT1A	Carnitine Palmitoyltransferase IA (liver) Deficiency
HUMCPT	CPT2	Carnitine Palmitoyltransferase II Deficiency
HSA1ATCA	SERPINA1	Alpha-1-Antitrypsin Deficiency
N36808	SMN2	Spinal Muscular Atrophy
Z38265	SMN2	Spinal Muscular Atrophy
HUMACADL	ACADL	Long Chain Acyl-CoA Dehydrogenase Deficiency
Z25247	CACT	Carnitine-Acylcarnitine Translocase Deficiency
HUMETFA	ETFA	Glutaricacidemia Type 2
HSETFB	ETFB	Glutaricacidemia Type 2
S69232	ETFDH	Glutaricacidemia Type 2
T09377	MEB	Muscle-Eye-Brain Disease
Z40427	G6PT1	Glycogen Storage Disease Type Ib
AI002801	SLC14A1	Kidd Genotyping
Z19313	SLC14A1	Kidd Genotyping
HUMPGAMM	PGAM2	Phosphoglycerate Mutase Deficiency
H86930	MPP4	Retinitis Pigmentosa, Autosomal Recessive

HSU14910	RGR	Retinitis Pigmentosa, Autosomal Recessive
AA775466	CARD15	Crohn Disease
AA306952	GAN	Giant Axonal Neuropathy
T99245	CLCN5	Dent Disease
T23537	NR3C2	Pseudohypoadosteronism Type 1, Dominant
HSLASNA	SCNN1A	Pseudohypoadosteronism Type 1, Recessive
H26938	SCNN1B	Pseudoaldosteronism ;Pseudohypoadosteronism Type 1, Recessive
HUMGAMM	SCNN1G	Pseudoaldosteronism ;Pseudohypoadosteronism Type 1, Recessive
HSP450AL	CYP11B2	Familial Hyperaldosteronism Type 1 ;Familial Hypoaldosteronism Type 2
HUMCYPADA	CYP11B1	Familial Hyperaldosteronism Type 1
AF017089	COL11A1	Stickler Syndrome ;Stickler Syndrome Type II
HUMCA1XIA	COL11A1	Stickler Syndrome ;Stickler Syndrome Type II
HUMA2XICOL	COL11A2	Stickler Syndrome
S61523	PIGA	Paroxysmal Nocturnal Hemoglobinuria
T58881	PHKA2	Glycogen Storage Disease Type IX
Z39614	DHAPAT	Rhizomelic Chondrodysplasia Punctata Type 2
N89899	SH2D1A	Lymphoproliferative Disease, X-Linked
HUMUGT1FA	UGT1A1	Gilbert Syndrome
HUMNC1A	COL7A1	Epidermolysis Bullosa Dystrophica, Bart Type ;Epidermolysis Bullosa Dystrophica, Cockayne-Touraine Type ;Epidermolysis Bullosa Dystrophica, Hallopeau-Siemens Type ;Epidermolysis Bullosa Dystrophica, Pasini Type ;Epidermolysis Bullosa, Pretibial
T49684	ITGB4	Epidermolysis Bullosa Letalis with Pyloric Atresia
S66196	ITGA6	Epidermolysis Bullosa Letalis with Pyloric Atresia
T10988	LAMC2	Epidermolysis Bullosa Junctional, Herlitz-Pearson Type
HUMLAMAA	LAMA3	Epidermolysis Bullosa Junctional, Herlitz-Pearson Type
Z24848	LAMA3	Epidermolysis Bullosa Junctional, Herlitz-Pearson Type
T10484	LAMB3	Epidermolysis Bullosa Junctional, Disentis Type ;Epidermolysis Bullosa Junctional, Herlitz-Pearson Type
HUMMPBP180AA	COL17A1	Epidermolysis Bullosa Junctional, Disentis Type
M78889	PLEC1	Epidermolysis Bullosa with Muscular Dystrophy
Z38659	SLC22A5	Carnitine Deficiency, Systemic
T85099	CTNS	Cystinosis
W27253	CNGA3	Achromatopsia ;Achromatopsia 2
HSU66088	SLC5A5	Thyroid Hormonogenesis Defect I
HUMTEKRPTK	TEK	Venous Malformation, Multiple Cutaneous and Mucosal
R69741	SLC26A2	Achondrogenesis Type 1B ;Atelosteogenesis Type 2 ;Diastrophic Dysplasia ;Multiple Epiphyseal Dysplasia, Recessive
Z46092	PEX10	Zellweger Syndrome Spectrum
S55790	COL4A3	Alport Syndrome ;Alport Syndrome, Autosomal Recessive
HSCOL4A4	COL4A4	Alport Syndrome ;Alport Syndrome, Autosomal Recessive
T10559	SHFM3	Ectrodactyly
T93670	FANCA	Fanconi Anemia

H47777	FANCB	Fanconi Anemia
AA542822	FANCE	Fanconi Anemia
HUMPSPB	PSAP	Metachromatic Leukodystrophy
HUMSAPA1	PSAP	Metachromatic Leukodystrophy
S69686	PSAP	Metachromatic Leukodystrophy
AA252786	NCF1	Chronic Granulomatous Disease
HUMNCF1A	NCF1	Chronic Granulomatous Disease
HSTGFB1	TGFB1	Camurati-Engelmann Disease
R24242	CYBA	Chronic Granulomatous Disease
HUMNOXF	NCF2	Chronic Granulomatous Disease
S41458	PDE6B	Retinitis Pigmentosa, Autosomal Recessive
R21727	DYSF	Dysferlinopathy ;Limb-Girdle Muscular Dystrophies, Autosomal Recessive
AF055580	USH2A	Usher Syndrome Type 2 ;Usher Syndrome Type 2A
N36632	MITF	Waardenburg Syndrome Type II ;Waardenburg Syndrome Type IIA
M78027	MYH9	DFNA 17 ;Epstein Syndrome ;Fechtner Syndrome ;May-Hegglin Anomaly ;Sebastian Syndrome
Z40194	HPS4	Hermansky-Pudlak Syndrome
AA333774	GP1BA	Platelet Antigen Genotyping
M79110	GP1BB	Platelet Antigen Genotyping
HUMGPIIBA	ITGA2B	Platelet Antigen Genotyping
T29174	ITGA2	Glycoprotein 1a Deficiency ;Platelet Antigen Genotyping
HSGST4	GSTM1	Lung Cancer
AA338271	CHEK2	Li-Fraumeni Syndrome
T78869	CHEK2	Li-Fraumeni Syndrome
T03839	SH3BP2	Cherubism
T67412	IRF6	IRF6-Related Disorders
AB037973	FGF23	Hypophosphatemic Rickets, Dominant
T60199	FBLN5	Cutis Laxa, Autosomal Recessive
T03890	ARX	ARX-Related Disorders
M79175	NSD1	Sotos Syndrome
T07860	NSD1	Sotos Syndrome
M79181	COH1	Cohen Syndrome
MIHS75KDA	NDUFS1	Leigh Syndrome (nuclear DNA mutation) ;Mitochondrial Respiratory Chain Complex I Deficiency
T09312	NDUFV1	Leigh Syndrome (nuclear DNA mutation) ;Mitochondrial Respiratory Chain Complex I Deficiency
AA399371	SALL4	Acrorenoocular Syndrome ;Okihiro Syndrome
HUMA8SEQ	TIMP3	Pseudoinflammatory Fundus Dystrophy
Z40623	GDAP1	Charcot-Marie-Tooth Neuropathy Type 4 ;Charcot-Marie-Tooth Neuropathy Type 4A
AA128030	FOXL2	Blepharophimosis, Epicanthus Inversus, Ptosis
HUMCRTR	SLC6A8	Creatine Deficiency Syndrome, X-Linked
T08882	JPH3	Huntington Disease-Like 2
T07283	SNRPN	Autistic Disorder ;Pervasive Developmental Disorders
Z38837	SPR	Sepiapterin Reductase Deficiency (SR)
HUMANTIR	AGTR1	Angiotensin II Receptor, Type 1
T46961	SEPN1	Congenital Muscular Dystrophy with Early Spine Rigidity ;Multiminicore Disease
Z43954	TRIM32	Limb-Girdle Muscular Dystrophies, Autosomal Recessive
Z19219	TTID	Limb-Girdle Muscular Dystrophies, Autosomal

		Dominant
HSECADH	CDH1	Hereditary Diffuse Gastric Cancer
Z41199	WFS1	Nonsyndromic Low-Frequency Sensorineural Hearing Loss ;Wolfram Syndrome
HUMLORAA	LOR	Progressive Symmetric Erythrokeratoderma
Z38324	HR	Alopecia Universalis ;Papular Atrichia
T09039	RYR1	Central Core Disease of Muscle ;Malignant Hyperthermia Susceptibility ;Multiminicore Disease
T10442	GALE	Galactose Epimerase Deficiency
D82541	PDB2	Paget Disease of Bone
HSU20759	CASR	Autosomal Dominant Hypocalcemia ;Familial Hypocalciuric Hypercalcemia, Type I ;Familial Isolated Hypoparathyroidism ;Neonatal Severe Primary Hyperparathyroidism
AA071082	SALL1	Townes-Brocks Syndrome
T81692	EDAR	Hypohidrotic Ectodermal Dysplasia ;Hypohidrotic Ectodermal Dysplasia, Autosomal
HUMHPA1B	HP	Anhaptoglobinemia
HSU01922	TIMM8A	Deafness-Dystonia-Optic Neuronopathy Syndrome
HUMHSD1	HSD3B2	Prostate Cancer
HSU05659	HSD17B3	Prostate Cancer
Z38915	NPHP4	Nephronophthisis 4 ;Senior-Loken Syndrome
HSC1INHR	SERPING1	Hereditary Angioneurotic Edema
D62739	BBS7	Bardet-Biedl Syndrome
T64266	SLC7A7	Lysinuric Protein Intolerance
S52028	CTH	Cystathioninuria
Z30254	EFEMP1	Doyne Honeycomb Retinal Dystrophy ;Patterned Dystrophy of Retinal Pigment Epithelium
D59254	ELOVL4	Stargardt Disease 3
S43856	GCH1	Dopa-Responsive Dystonia ;GTP Cyclohydrolase 1-Deficient DRD ;GTP Cyclohydrolase-1 Deficiency (GTPCH)
M78468	PAFAH1B1	17-Linked Lissencephaly
M78473	PAFAH1B1	17-Linked Lissencephaly
S51033	MID1	Opitz Syndrome, X-Linked
Z40343	MID1	Opitz Syndrome, X-Linked
HUM6PTHS	PTS	Pyruvoyltetrahydropterin Synthase Deficiency
M62103	CIRH1A	North American Indian Childhood Cirrhosis
HSDHPR	QDPR	Dihydropteridine Reductase Deficiency (DHPR)
T23665	FKRP	Congenital Muscular Dystrophy Type 1C ;Limb-Girdle Muscular Dystrophies, Autosomal Recessive
T60498	LRPPRC	Leigh Syndrome, French-Canadian Type
HSACHRA	CHRNA1	Congenital Myasthenic Syndromes
HSACHRB	CHRNB1	Congenital Myasthenic Syndromes
HSACHRG	CHRND	Congenital Myasthenic Syndromes
HSACCTR	CHRNE	Congenital Myasthenic Syndromes
HSACRAP	RAPSN	Congenital Myasthenic Syndromes
M78334	COLQ	Congenital Myasthenic Syndromes
S56138	CHAT	Congenital Myasthenic Syndromes
D11584	SDHC	Familial Nonchromaffin Paragangliomas
HSPSTI	SPINK1	Hereditary Pancreatitis
HSSPROTR	PROS1	Protein S Heerlen Variant
HUMLAP	ITGB2	Leukocyte Adhesion Deficiency, Type 1
T12572	ADAMTS13	Familial Thrombotic Thrombocytopenia Purpura

HUMCOMIIP	SDHB	Carotid Body Tumors and Multiple Extraadrenal Pheochromocytomas
NM005912	MC4R	Obesity
HUMPAX8A	PAX8	Congenital Hypothyroidism
AA037119	FOXE1	Bamforth-Lazarus Syndrome ;Congenital Hypothyroidism
AV754057	FSHB	Isolated Follicle Stimulating Hormone Deficiency
HUMHOMEOA	PCBD	Pterin-4a Carbinolamine Dehydratase Deficiency (PCD)
HSTHR	TH	Dopa-Responsive Dystonia ;Tyrosine Hydroxylase-Deficient DRD
AA219596	ZIC3	Heterotaxy Syndrome
HSU20324	CSRP3	Dilated Cardiomyopathy
HUMPHLAM	PLN	Dilated Cardiomyopathy
F10219	ALMS1	Alstrom Syndrome
T06612	VCL	Dilated Cardiomyopathy
AF388366	USH3A	Usher Syndrome Type 3
Z40797	SGCE	Myoclonus-Dystonia
T08448	RAB7	Charcot-Marie-Tooth Neuropathy Type 2
D12383	GARS	Charcot-Marie-Tooth Neuropathy Type 2
Z36734	HRPT2	HRPT2-Related Disorders
H19914	EDARADD	Hypohidrotic Ectodermal Dysplasia ;Hypohidrotic Ectodermal Dysplasia, Autosomal
T08852	PPT1	Neuronal Ceroid-Lipofuscinoses ;PPT1-Related Neuronal Ceroid-Lipofuscinosis
HUMDRA	SLC26A3	Familial Chloride Diarrhea
R16324	AGPAT2	Berardinelli-Seip Congenital Lipodystrophy
Z38569	BSCL2	Berardinelli-Seip Congenital Lipodystrophy
W28410	OPN1MW	Blue-Mono-Cone-Monochromatic Type Colorblindness
T27896	OPN1LW	Blue-Mono-Cone-Monochromatic Type Colorblindness
AI469991	PHOX2A	Congenital Fibrosis of Extraocular Muscles
HSFSTHR	FSHR	Premature Ovarian Failure, Autosomal Recessive
HSLPH	LCT	Hypolactasia, Adult Type
Z41000	BCS1L	Gracile Syndrome ;Mitochondrial Respiratory Chain Complex III Deficiency
HSCGJP	GJA1	Oculodentodigital Dysplasia
HSPERFP1	PRF1	Familial Hemophagocytic Lymphohistiocytosis 2
M78112	GLUD1	Familial Hyperinsulinism ;GLUD1-Related Hyperinsulinism
W79230	RAX	Anophthalmia
AF041339	PITX3	Anophthalmia
AA151708	HESX1	Anophthalmia
HSSOXB	SOX3	Anophthalmia ;Mental Retardation, X-Linked, with Growth Hormone Deficiency
HUMHMGBOX	SOX2	Anophthalmia
HSGM2APA	GM2A	GM2 Activator Deficiency
Z19280	GLC1E	Glaucoma, Dominant (Adult Onset)
T20165	PHF6	Borjeson-Forssman-Lehmann Syndrome
Z40394	CMT4B2	Charcot-Marie-Tooth Neuropathy Type 4
HUMIHH	IHH	Brachydactyly Type A1
HUMCDPK	CDK4	Familial Malignant Melanoma
T39355	SBDS	Shwachman-Diamond Syndrome
HSHMPLK	MPL	Amegakaryocytic Thrombocytopenia, Congenital
Z38860	TRIM37	Mulibrey Nanism

M62027	DTNA	Familial Isolated Noncompaction of Left Ventrical Myocardium
Z39175	DDB2	Xeroderma Pigmentosum
T09329	MUTYH	MYH-Associated Polyposis
HUMAPA	APP	Alzheimer Disease Type 1 ;Early-Onset Familial Alzheimer Disease
M79090	GSS	5-Oxoprolinuria
Z26981	OXCT	3-Oxoacid CoA Transferase
D12046	PMS1	Hereditary Non-Polyposis Colon Cancer
T08186	PMS2	Hereditary Non-Polyposis Colon Cancer
R00471	MSH6	Hereditary Non-Polyposis Colon Cancer
T60457	NDUFS4	Leigh Syndrome (nuclear DNA mutation) ;Mitochondrial Respiratory Chain Complex I Deficiency
D30864	NDUFS8	Leigh Syndrome (nuclear DNA mutation)
M78107	SDHA	Leigh Syndrome (nuclear DNA mutation)
R15290	NDUFS7	Leigh Syndrome (nuclear DNA mutation)
HUMPCBA	PC	Pyruvate Carboxylase Deficiency
W32719	AASS	Hyperlysinemia
T23789	PEX3	Zellweger Syndrome Spectrum
T09086	STK11	Peutz-Jeghers Syndrome
T87335	HAL	Histidinemia
Z19082	ALDH4A1	Hyperprolinemia, Type II
Z25227	MADH4	Juvenile Polyposis Syndrome
M78130	XPB	Xeroderma Pigmentosum
T08987	XPD	Xeroderma Pigmentosum
D81449	XPF	Xeroderma Pigmentosum
HSXPGAA	XPG	Xeroderma Pigmentosum
HSAUHMR	AUH	3-Methylglutaconic Aciduria Type 1
T19530	MMAB	Methylmalonicaciduria
Z40169	MMAA	Methylmalonicaciduria
T93695	BCAT1	Hyperleucine-Isoleucinemia
Z41266	BCAT2	Hyperleucine-Isoleucinemia
HSU03506	SLC1A1	Dicarboxylicaminoaciduria
R88591	PRODH	Hyperprolinemia, Type I
T05380	EPM2A	Progressive Myoclonus Epilepsy, Lafora Type
T27227	FANCF	Fanconi Anemia
Z41736	FANCG	Fanconi Anemia
R66178	ED4	Ectodermal Dysplasia, Margarita Island Type
L25197	KCNE1	Jervell and Lange-Nielsen Syndrome ;LQT 5 ;Romano-Ward Syndrome
HUMUMOD	UMOD	Familial Nephropathy with Gout ;Medullary Cystic Kidney Disease 2
HSU66583	CRYGD	Cataract, Crystalline Aculeiform
HSPHR	PTHR1	Chondrodysplasia, Blomstrand Type
T97980	MTRR	Homocystinuria-Megaloblastic Anemia
S60710	ADSL	Adenylosuccinase deficiency
Z38216	SLC25A19	Amish Lethal Microcephaly
T11501	DBH	Dopamine Beta-Hydroxylase Deficiency
H11439	NLGN3	Autistic Disorder ;Pervasive Developmental Disorders
R12551	NLGN4	Autistic Disorder ;Pervasive Developmental Disorders
M78212	ATP1A2	Familial Hemiplegic Migraine
T96957	SPCH1	Severe Speech Delay
AI266171	PHOX2B	Congenital Central Hypoventilation Syndrome
BG723199	DSG4	Localized Autosomal Recessive Hypotrichosis
T46918	HSD11B2	Apparent Mineralocorticoid Excess Syndrome

HUMFERLS	FTL	Hyperferritinemia Cataract Syndrome
HUMCKRASA	KRAS2	Familial Pancreatic Cancer
S39383	PTPN11	LEOPARD Syndrome ;Noonan Syndrome
HUMSTAR	STAR	Cholesterol Desmolase Deficiency
Z20453	STAR	Cholesterol Desmolase Deficiency
HUMVPC	AVP	Neurohypophyseal Diabetes Insipidus
M62144	MECP2	Rett Syndrome
HSCA2VR	COL5A2	Ehlers-Danlos Syndrome, Classic Type
HUMGENX	TNXB	Ehlers-Danlos-like Syndrome Due to Tenascin-X Deficiency
R02385	TNXB	Ehlers-Danlos-like Syndrome Due to Tenascin-X Deficiency
T39901	LITAF	Charcot-Marie-Tooth Neuropathy Type 1
AA621310	FOXE3	Anophthalmia
H18132	CFC1	Heterotaxy Syndrome
R36719	EBAF	Heterotaxy Syndrome
HSACTIIRE	ACVR2B	Heterotaxy Syndrome
T52017	CRELD1	Heterotaxy Syndrome
D11851	LMNA	Dilated Cardiomyopathy ;Emery-Dreifuss Muscular Dystrophy, Autosomal Dominant ;Familial Partial Lipodystrophy, Dunnigan Type ;Hutchinson-Gilford Progeria Syndrome ;Limb-Girdle Muscular Dystrophies, Autosomal Dominant ;Mandibuloacral Dysplasia
D12062	DSP	Cardiomyopathy, Dilated, with Woolly Hair and Keratoderma ;Keratosis Palmoplantaris Striata
H99382	MSH3	Hereditary Non-Polyposis Colon Cancer
AW205295	NOG	Multiple Synostoses Syndrome
AA135181	GJB3	Erythrokeratoderma Variabilis
F10278	PEO1	Mitochondrial DNA Deletion Syndromes
M62022	MASS1	Febrile Seizures
Z42549	UQCRCB	Mitochondrial Respiratory Chain Complex III Deficiency
HUMEGR2A	EGR2	Charcot-Marie-Tooth Neuropathy Type 1 ;Charcot-Marie-Tooth Neuropathy Type 1D ;Charcot-Marie-Tooth Neuropathy Type 4 ;Charcot-Marie-Tooth Neuropathy Type 4E
HSFLT4X	FLT4	Milroy Congenital Lymphedema
Z28459	PEX26	Zellweger Syndrome Spectrum
HUMRPS24A	RPS19	Diamond-Blackfan Anemia
T11633	RPS19	Diamond-Blackfan Anemia
HSACMHCP	MYH7	Dilated Cardiomyopathy ;Familial Hypertrophic Cardiomyopathy
Z25920	TNNT2	Dilated Cardiomyopathy ;Familial Hypertrophic Cardiomyopathy
HUMTRO	TPM1	Dilated Cardiomyopathy ;Familial Hypertrophic Cardiomyopathy
Z18303	MYBPC3	Dilated Cardiomyopathy ;Familial Hypertrophic Cardiomyopathy
HSU09466	COX10	Leigh Syndrome (nuclear DNA mutation)
S72487	ECGF1	Mitochondrial Neurogastrointestinal Encephalopathy Syndrome
M62196	KIF5A	Hereditary Spastic Paraplegia, Dominant
T07578	KIF5A	Hereditary Spastic Paraplegia, Dominant
D11648	HSPD1	Hereditary Spastic Paraplegia, Dominant

T47330	SOX18	Hypotrichosis-Lymphedema-Telangiectasia Syndrome
AA448334	CAV3	Caveolinopathy ;Limb-Girdle Muscular Dystrophies, Autosomal Dominant
AW071529	ALX4	Parietal Foramina 2
M61973	CD2AP	Focal Segmental Glomerulosclerosis
W21801	NR2E3	Enhanced S-Cone Syndrome
Z20305	TREM2	PLOS1
T05421	ANK2	LQT 4 ;Romano-Ward Syndrome
HUMROR2A	ROR2	ROR2-Related Disorders
Z25920	CMD1D	Dilated Cardiomyopathy
AA887962	HLXB9	Currarino Syndrome
R00281	ALDH5A1	Succinic Semialdehyde Dehydrogenase Deficiency
HSPCCAR	PCCA	Propionic Acidemia
N43992	DLL3	Spondylocostal Dysostosis, Autosomal Recessive ;Syndactyly, Type IV
Z39790	MUT	Methylmalonicaciduria
HUMARGL	ARG1	Argininemia
HUMRENBAT	SLC3A1	Cystinuria
T80665	SLC7A9	Cystinuria
T27286	HGD	Alkaptonuria
HUMBCKDH	BCKDHA	Maple Syrup Urine Disease
HUMBCKDHA	BCKDHB	Maple Syrup Urine Disease
HSTRANSP	DBT	Maple Syrup Urine Disease
Z44722	HLCS	Holocarboxylase Synthetase Deficiency
Z38396	BTD	Biotinidase Deficiency
T48178	POMT1	Walker-Warburg Syndrome
T28737	GJB2	DFNA 3 Nonsyndromic Hearing Loss and Deafness ;DFNB 1 Nonsyndromic Hearing Loss and Deafness ;GJB2-Related DFNA 3 Nonsyndromic Hearing Loss and Deafness ;GJB2-Related DFNB 1 Nonsyndromic Hearing Loss and Deafness ;Nonsyndromic Hearing Loss and Deafness, Autosomal Dominant ;Nonsyndromic Hearing Loss and Deafness, Autosomal Recessive ;Vohwinkel Syndrome
T05861	COCH	DFNA 9 (COCH) ;Nonsyndromic Hearing Loss and Deafness, Autosomal Dominant
HSBRN4	POU3F4	DFN 3
HSU21938	TTPA	Ataxia with Vitamin E Deficiency (AVED)
T93783	KIAA1985	Charcot-Marie-Tooth Neuropathy Type 4
BE735997	SANS	Usher Syndrome Type 1
AA548783	HOXD13	Syndactyly, Type II
R33750	HOXA13	Hand-Foot-Uterus Syndrome
HUMPP	GLDC	GLDC-Related Glycine Encephalopathy ;Glycine Encephalopathy
F04230	AMT	AMT-Related Glycine Encephalopathy ;Glycine Encephalopathy
T54795	DECR	2,4-Dienoyl-CoA Reductase Deficiency
R07295	ACAT1	Ketothiolase Deficiency
S70578	ACAT1	Ketothiolase Deficiency
HUMMEVKIN	MVK	Hyper IgD Syndrome ;Mevalonicaciduria
T11245	HMGCL	3-Hydroxy-3-Methylglutaryl-Coenzyme A Lyase Deficiency
Z41427	GCDH	Glutaricacidemia Type 1
HSSHOXA	SHOX	Langer Mesomelic Dwarfism ;Leri-Weill Dyschondrosteosis ;Short Stature

HUMDOPADC	DDC	Aromatic L-Amino Acid Decarboxylase Deficiency
HSCOL3A4	COL6A3	Limb-Girdle Muscular Dystrophies, Autosomal Dominant
HSCOL1A4	COL6A1	Limb-Girdle Muscular Dystrophies, Autosomal Dominant
HSCOL2C2	COL6A2	Limb-Girdle Muscular Dystrophies, Autosomal Dominant
H16770	RECQL4	Rothmund-Thomson Syndrome
H11473	SGSH	Mucopolysaccharidosis Type IIIA
H67137	MCCC1	3-Methylcrotonyl-CoA Carboxylase Deficiency
R88931	MCCC2	3-Methylcrotonyl-CoA Carboxylase Deficiency
Z24865	TCAP	Dilated Cardiomyopathy ;Limb-Girdle Muscular Dystrophies, Autosomal Recessive
M86030	DCX	DCX-Related Malformations
HUMACTASK	ACTA1	Nemaline Myopathy
HSDGIGLY	DSG1	Keratosis Palmoplantaris Striata
HSRETSAA	SAG	Retinitis Pigmentosa, Autosomal Recessive
HSAPHOL	ALPL	Hypophosphatasia
N73784	XPA	Xeroderma Pigmentosum
T28958	XPC	Xeroderma Pigmentosum
N69543	POLH	Xeroderma Pigmentosum
T54103	POLH	Xeroderma Pigmentosum
H56484	CKN1	Cockayne Syndrome
Z38185	ERCC6	Cockayne Syndrome
F07041	PI12	Familial Encephalopathy with Neuroserpin Inclusion Bodies
AA633404	KCNE2	LQT 6 ;Romano-Ward Syndrome
HSTITINC2	CMD1G	Dilated Cardiomyopathy
N99115	NPHP1	Nephronophthisis 1 ;Senior-Loken Syndrome
HUMELANAA	ELA2	ELA2-Related Neutropenia
S67325	PCCB	Propionic Acidemia
HSGA7331	M1S1	Corneal Dystrophy, Gelatinous Drop-Like
HSACE	ACE	Angiotensin I Converting Enzyme 1
S49816	TSHR	Congenital Hypothyroidism ;Familial Non-Autoimmune Hyperthyroidism
Z30221	VMGLOM	Multiple Glomus Tumors
H88042	COL9A3	Multiple Epiphyseal Dysplasia, Dominant
M78119	ADA	Adenosine Deaminase Deficiency
T55785	GAMT	Guanidinoacetate Methyltransferase Deficiency
HUMCST4BA	CSTB	Myoclonic Epilepsy of Unverricht and Lundborg
S73196	AQP2	Nephrogenic Diabetes Insipidus ;Nephrogenic Diabetes Insipidus, Autosomal
HSU76388	NR5A1	XY Sex Reversal with Adrenal Failure
HSCPBC22	MTRNR1	MTRNR1-Related Hearing Loss and Deafness
H21596	PPARG	Diabetes Mellitus with Acanthosis Nigricans and Hypertension
D56550	FOXC1	Anophthalmia ;Rieger Syndrome
M78868	AP3B1	Hermansky-Pudlak Syndrome
T47068	NOTCH3	CADASIL
HSHMF1C	TCF1	Maturity-Onset Diabetes of the Young Type III
AF049893	IPF1	Maturity-Onset Diabetes of the Young Type IV
HSU30329	IPF1	Maturity-Onset Diabetes of the Young Type IV
HSVHNF1	TCF2	Maturity-Onset Diabetes of the Young Type V
HUMLDLRFMT	LDLR	Familial Hypercholesterolemia
HSAPOBR2	APOB	Familial Hypercholesterolemia Type B
T78010	ABCB7	Sideroblastic Anemia and Ataxia

		PROP1-Related Deficiency	Combined	Pituitary	Hormone
AF076215	PROP1				
S99468	ALAD	Acute Hepatic Porphyria			
T61818	ABCC2	Dubin-Johnson Syndrome			
HUMLCAT	LCAT	Lecithin Cholesterol Acyltransferase Deficiency			
Z38510	HADHSC	Short Chain 3-Hydroxyacyl-CoA Dehydrogenase Deficiency, Liver			
AF041240	PPOX	Variegate Porphyria			
T77011	PPOX	Variegate Porphyria			
Z40014	ALDH10	Sjogren-Larsson Syndrome			
S79867	KRT16	Nonepidermolytic Pachyonychia Congenita ;Pachyonychia Congenita	Palmoplantar Hyperkeratosis		
HUMKER56K	KRT6A	Pachyonychia Congenita			
HSKERELP	KRT17	Pachyonychia Congenita ;Steatocystoma Multiplex			
R11850	KRT6B	Pachyonychia Congenita			
S69510	KRT9	Epidermolytic Palmoplantar Keratoderma			
HSCYTK	KRT13	White Sponge Nevus of Cannon			
T92918	KRT4	White Sponge Nevus of Cannon			
S54769	SPG7	Hereditary Spastic Paraparesis, Recessive ;SPG 7			
T50707	FECH	Erythropoietic Protoporphyrina			
HUMPOMM	PXMP3	Zellweger Syndrome Spectrum			
R05392	PEX6	Zellweger Syndrome Spectrum			
Z38759	PEX12	Zellweger Syndrome Spectrum			
R14480	PEX16	Zellweger Syndrome Spectrum			
R10031	PEX13	Zellweger Syndrome Spectrum			
R13532	PXF	Zellweger Syndrome Spectrum			
Z30136	AGPS	Rhizomelic Chondrodyplasia Punctata Type 3			
HSU07866	ACOX	Pseudoneonatal Adrenoleukodystrophy			
N63143	ALG6	Congenital Disorders of Glycosylation			
HSTNFR1A	TNFRSF1A	Familial Hibernian Fever			
AA018811	RP1	Retinitis Pigmentosa, Autosomal Dominant			
HSG11	RP1	Retinitis Pigmentosa, Autosomal Dominant			
T07942	RP1	Retinitis Pigmentosa, Autosomal Dominant			
H28658	PRPF31	Retinitis Pigmentosa, Autosomal Dominant			
T07062	PRPF8	Retinitis Pigmentosa, Autosomal Dominant			
T05573	RP18	Retinitis Pigmentosa, Autosomal Dominant			
HUMNRLGP	NRL	Retinitis Pigmentosa, Autosomal Dominant			
T87786	CRB1	Retinitis Pigmentosa, Autosomal Recessive			
H92408	TULP1	Retinitis Pigmentosa, Autosomal Recessive			
S42457	CNGA1	Retinitis Pigmentosa, Autosomal Recessive			
H30568	PDE6A	Retinitis Pigmentosa, Autosomal Recessive			
M78192	RLBP1	Retinitis Pigmentosa, Autosomal Recessive ;Retinitis Pigmentosa, Autosomal Recessive, Bothnia Type			
T10761	SLC4A4	Proximal Renal Tubular Acidosis with Ocular Abnormalities			
N64339	GJB6	DFNA 3 Nonsyndromic Hearing Loss and Deafness ;DFNB 1 Nonsyndromic Hearing Loss and Deafness ;GJB6-Related DFNB 1 Nonsyndromic Hearing Loss and Deafness ;GJB6-Related DFNA 3 Nonsyndromic Hearing Loss and Deafness ;Hidrotic Ectodermal Dysplasia 2 ;Nonsyndromic Hearing Loss and Deafness, Autosomal Dominant ;Nonsyndromic Hearing Loss and Deafness, Autosomal Recessive			
T67968	MAT1A	Isolated Persistent Hypermethioninemia			
HUMUMPS	UMPS	Oroticaciduria			

HSPNP	NP	Purine Nucleoside Phosphorylase Deficiency
AB006682	AIRE	Autoimmune Polyendocrinopathy Syndrome Type 1
BE871354	JUP	Naxos Disease
T08214	JUP	Naxos Disease
F00120	DES	Dilated Cardiomyopathy
R28506	MOCS1	Molybdenum Cofactor Deficiency
T70309	MOCS2	Molybdenum Cofactor Deficiency
T08212	SNCA	Parkinson Disease
R99091	ABCC6	Pseudoxanthoma Elasticum
T69749	ABCC6	Pseudoxanthoma Elasticum
AA207040	PRG4	Arthropathy Camptodactyly Syndrome
T07189	PRG4	Arthropathy Camptodactyly Syndrome
F07016	OPPG	Osteoporosis Pseudoglioma Syndrome
H27782	SCO2	Fatal Infantile Cardioencephalopathy due to COX Deficiency
S54705S1	PRKAR1A	Carney Complex
Z25903	SCA10	Spinocerebellar Ataxia Type 10
AA592984	WISP3	Progressive Pseudorheumatoid Arthropathy of Childhood
Z39666	MCOLN1	Mucolipidosis IV
HSEM1X2	EMX2	Familial Schizencephaly
HUMSP18A	SFTPB	Pulmonary Surfactant Protein B Deficiency
T10596	ATP8B1	Benign Recurrent Intrahepatic Cholestasis ;Progressive Familial Intrahepatic Cholestasis ;Progressive Familial Intrahepatic Cholestasis 1
U46845	CYP27B1	Pseudovitamin D Deficiency Rickets
Z21585	MAPT	Frontotemporal Dementia with Parkinsonism-17
HSPPD	HPD	Tyrosinemia Type III
HUMUGT1FA	UGT1A	Crigler-Najjar Syndrome
R20880	SLC19A2	Thiamine-Responsive Megaloblastic Anemia Syndrome
H42203	TFAP2B	Char Syndrome
Z30126	RYR2	Catecholaminergic Ventricular Tachycardia, Autosomal Dominant
HSSPYRAT	AGXT	Hyperoxaluria, Primary, Type 1
T80758	SEDL	Spondyloepiphyseal Dysplasia Tarda, X-Linked
T89449	SEDL	Spondyloepiphyseal Dysplasia Tarda, X-Linked
AA373083	FOXC2	Lymphedema with Distichiasis
HUMPROP2AB	SCA12	Spinocerebellar Ataxia Type 12
Z30145	ACTC	Dilated Cardiomyopathy
HS1900	GDNF	Hirschsprung Disease
M62223	NEFL	Charcot-Marie-Tooth Neuropathy Type 1F/2E ;Charcot-Marie-Tooth Neuropathy Type 2 ;Charcot-Marie-Tooth Neuropathy Type 2E/1F
T10920	SERPINE1	Plasminogen Activator Inhibitor I
HSNCAMLI	L1CAM	Hereditary Spastic Paraparesis, X-Linked ;L1 Syndrome
T11074	L1CAM	Hereditary Spastic Paraparesis, X-Linked ;L1 Syndrome
HUMHPROT	GCSH	Glycine Encephalopathy
HSTATR	TAT	Tyrosinemia Type II
Z19514	CPT1B	Carnitine Palmitoyltransferase IB (muscle) Deficiency
HSALK3A	BMPRIA	Juvenile Polyposis Syndrome
T78581	CLN5	CLN5-Related Neuronal Ceroid-Lipofuscinosis ;Neuronal Ceroid-Lipofuscinoses
N32269	CLN8	CLN8-Related Neuronal Ceroid-Lipofuscinosis ;Neuronal Ceroid-Lipofuscinoses

HSU44128	SLC12A3	Gitelman Syndrome
AI590292	NPHS2	Focal Segmental Glomerulosclerosis ;Steroid-Resistant Nephrotic Syndrome
M62209	ACTN4	Focal Segmental Glomerulosclerosis
H53423	CNGB3	Achromatopsia ;Achromatopsia 3
HSEPAR	HCI	Hemangioma, Hereditary
R14741	ZIC2	Holoprosencephaly 5
H84264	SIX3	Anophthalmia ;Holoprosencephaly 2
T10497	TGIF	Holoprosencephaly 4
Z30052	USP9Y	Y Chromosome Infertility
N85185	DBY	Y Chromosome Infertility
T11164	SPTLC1	Hereditary Sensory Neuropathy Type I
T68440	GNE	GNE-Related Myopathies ;Sialuria, French Type
HSPROPERD	PFC	Properdin Deficiency, X-Linked
T46865	SURF1	Leigh Syndrome (nuclear DNA mutation)
AI015025	VAX1	Anophthalmia
BM727523	VAX1	Anophthalmia
AA310724	SIX6	Anophthalmia
R37821	TP63	TP63-Related Disorders
AF091582	ABCB11	Progressive Familial Intrahepatic Cholestasis
HUMHOX7	MSX1	Hypodontia, Autosomal Dominant ;Tooth-and-Nail Syndrome
R15034	CACNB4	Episodic Ataxia Type 2
T52100	TYROBP	PLOSL
F09012	MTMR2	Charcot-Marie-Tooth Neuropathy Type 4
T08510	APTX	Ataxia with Oculomotor Apraxia ;Ataxia with Oculomotor Apraxia 1
HUMHAAC	HF1	Hemolytic-Uremic Syndrome
C16899	MTND5	Leber Hereditary Optic Neuropathy ;Mitochondrial DNA-Associated Leigh Syndrome and NARP

#DRUG_DRUG_INTERACTION: refers to proteins involved in a biological process which mediates the interaction between at least two consumed drugs. Novel splice variants of known proteins involved in interaction between drugs may be used, for example, to modulate such drug-drug interactions. Examples of proteins involved in drug-drug interactions are presented in Table 7 together with the corresponding internal gene contig name, enabling to allocate the new splice variants within the data files “proteins.fasta” and “transcripts.fasta” in the attached CD-ROM1 and “proteins” and “transcripts” files in the attached CD-ROM2.

Table 7

Contig	Gene Symbol	Description
HUMANTLA	SLC3A2	4f2 cell-surface antigen heavy chain
Z43093	HTR6	5-hydroxytryptamine 6 receptor
HSXLALDA	ABCD1	Adrenoleukodystrophy protein
R35137	GPT	Alanine aminotransferase
D11683	ALDH1	Aldehyde dehydrogenase, cytosolic
T53833	AOX1	Aldehyde oxidase
HUMAGP1A	ORM1	Alpha-1-acid glycoprotein 1
HUMAGP1A	ORM2	Alpha-1-acid glycoprotein 2

HUMABPA	ABP1	Amiloride-sensitive amine oxidase [copper-containing]
S62734	MAOB	Amine oxidase [flavin-containing] b
AA526963	SLC6A14	Amino acid transporter b0+
HSAE2	SLC4A2	Anion exchange protein 2
M78110	SLC4A3	Anion exchange protein 3
M78052	ABCB2	Antigen peptide transporter 1
HUMMHCIIB	ABCB3	Antigen peptide transporter 2
F02693	APOD	Apolipoprotein d
M62234	ASNA1	Arsenical pump-driving ATPase
HUMNORTR	NAT1	Arylamine n-acetyltransferase 1
T67129	NAT1	Arylamine n-acetyltransferase 1
AI262683	NAT2	Arylamine n-acetyltransferase 2
Z39550	ABCB9	ATP-binding cassette protein abc9
Z44377	ABCA1	ATP-binding cassette, sub-family a, member 1
M78056	ABCA2	ATP-binding cassette, sub-family a, member 2
M85498	ABCA3	ATP-binding cassette, sub-family a, member 3
T79973	ABCB6	ATP-binding cassette, sub-family b, member 6, mitochondrial
T78010	ABCB7	ATP-binding cassette, sub-family b, member 7, mitochondrial
R89046	ABCB8	ATP-binding cassette, sub-family b, member 8, mitochondrial
H64439	ABCD2	ATP-binding cassette, sub-family d, member 2
M85760	ABCD3	ATP-binding cassette, sub-family d, member 3
Z21904	ABCD4	ATP-binding cassette, sub-family d, member 4
Z39977	ABCG1	ATP-binding cassette, sub-family g, member 1
Z45628	ABCG2	ATP-binding cassette, sub-family g, member 2
T80665	SLC7A9	B(0,+) -type amino acid transporter 1
AF091582	ABCB11	Bile salt export pump
Z38696	BLMH	Bleomycin hydrolase
T08127	BNPI	Brain-specific na-dependent inorganic phosphate cotransporter
F00545	SLC12A2	Bumetanide-sensitive sodium-(potassium)-chloride cotransporter 2
HSU07969	CDH17	Cadherin-17
T10238	SLC25A12	Calcium-binding mitochondrial carrier protein aralar1
Z40674	SLC25A13	Calcium-binding mitochondrial carrier protein aralar2
T61818	ABCC2	Canalicular multispecific organic anion transporter 1
T39953	ABCC3	Canalicular multispecific organic anion transporter 2
HUMCRE	CBR1	Carbonyl reductase [nadph] 1
AA320697	CBR3	Carbonyl reductase [nadph] 3
F03362	COMT	Catechol o-methyltransferase, membrane-bound form
T11004	COMT	Catechol o-methyltransferase, membrane-bound form
T39368	SLC7A4	Cationic amino acid transporter-4
S74445	RBP5	Cellular retinol-binding protein iii
T55952	RBP5	Cellular retinol-binding protein iii
HSU39905	SLC18A1	Chromaffin granule amine transporter
R52371	SLC35A1	Cmp-sialic acid transporter
D20754	CNT3	Concentrative nucleoside transporter 3
HSMNKMBP	ATP7A	Copper-transporting ATPase 1
HUMWND	ATP7B	Copper-transporting ATPase 2
HUMCFTRM	ABCC7	Cystic fibrosis transmembrane conductance regulator
F10774	SLC7A11	Cystine/glutamate transporter
HUMCYPADA	CYP11B1	Cytochrome P450 11B1, mitochondrial
HUMARM	CYP19	Cytochrome P450 19
HUMCYP145	CYP1A1	Cytochrome P450 1A1
R21282	CYP26	Cytochrome P450 26
AF209774	CYP2A13	Cytochrome P450 2A13
HSC45B2C	CYP2A6	Cytochrome P450 2A6
HSC45B2C	CYP2A7	Cytochrome P450 2A7
HSP452B6	CYP2B6	Cytochrome P450 2B6
HUM2C18	CYP2C18	Cytochrome P450 2C18

HSCP450	CYP2C19	Cytochrome P450 2C19
HUM2C18	CYP2C19	Cytochrome P450 2C19
HUMCYPAX	CYP2C8	Cytochrome P450 2C8
HSCP450	CYP2C9	Cytochrome P450 2C9
HSP450	CYP2D6	Cytochrome P450 2D6
M77918	CYP2E1	Cytochrome P450 2E1
HUMCYP1F	CYP2F1	Cytochrome P450 2F1
H09076	CYP2J2	Cytochrome P450 2J2
R07010	CYP39A1	Cytochrome P450 39A1
HUMCYPHLP	CYP3A3	Cytochrome P450 3A3
HUMCYPHLP	CYP3A4	Cytochrome P450 3A4
AA416822	CYP3A43	Cytochrome P450 3A43
HUMCYP3A	CYP3A5	Cytochrome P450 3A5
T82801	CYP3A7	Cytochrome P450 3A7
HSCYP4AA	CYP4A11	Cytochrome P450 4A11
S67580	CYP4A11	Cytochrome P450 4A11
HUMCP45IV	CYP4B1	Cytochrome P450 4B1
T98002	CYP4F12	Cytochrome P450 4F12
AA377259	CYP4F2	Cytochrome P450 4F2
AI400898	CYP4F8	Cytochrome P450 4F8
HSU09178	DPYD	Dihydropyrimidine dehydrogenase [nadp+]
W03174	DPYD	Dihydropyrimidine dehydrogenase [nadp+]
HUMFMO1	FMO1	Dimethylamine monooxygenase [n-oxide forming] 1
HSFLMON2R	FMO2	Dimethylamine monooxygenase [n-oxide forming] 2
T64494	FMO2	Dimethylamine monooxygenase [n-oxide forming] 2
T40157	FMO3	Dimethylamine monooxygenase [n-oxide forming] 3
HSFLMON2R	FMO4	Dimethylamine monooxygenase [n-oxide forming] 4
D12220	FMO5	Dimethylamine monooxygenase [n-oxide forming] 5
H25503	HET	Efflux transporter like protein
T12485	HET	Efflux transporter like protein
M78151	EPHX1	Epoxide hydrolase 1
T66884	SLC29A1	Equilibrative nucleoside transporter 1
HSHNP36	SLC29A2	Equilibrative nucleoside transporter 2
T08444	SLC1A3	Excitatory amino acid transporter 1
HSU01824	SLC1A2	Excitatory amino acid transporter 2
HSU03506	SLC1A1	Excitatory amino acid transporter 3
F07883	SLC1A6	Excitatory amino acid transporter 4
N39099	SLC1A7	Excitatory amino acid transporter 5
F00548	SLC2A9	Facilitative glucose transporter family member glut9
T95337	SLC27A1	Fatty acid transport protein
Z44099	SLC27A1	Fatty acid transport protein
HUMALBP	FABP4	Fatty acid-binding protein, adipocyte
S67314	FABP3	Fatty acid-binding protein, heart
AW605378	FABP2	Fatty acid-binding protein, intestinal
L25227	SLC19A1	Folate transporter 1
HSI15PGN1	FABP6	Gastrotropin
Z40427	G6PT1	Glucose 6-phosphate transporter
D11793	SLC2A1	Glucose transporter type 1, erythrocyte/brain
N27535	SLC2A10	Glucose transporter type 10
T52633	SLC2A11	Glucose transporter type 11
HUMLGTPA	SLC2A2	Glucose transporter type 2, liver
HUMLGTPA	SLC2A2	Glucose transporter type 2, liver
T07239	SLC2A3	Glucose transporter type 3, brain
HUMIRGT	SLC2A4	Glucose transporter type 4, insulin-responsive.
M62105	SLC2A5	Glucose transporter type 5, small intestine
T59518	SLC2A8	Glucose transporter type 8
HUMLGTH1	GSTA1	Glutathione s-transferase a1

HUMLGTH1	GSTA2	Glutathione s-transferase a2
T98291	GSTA3	Glutathione s-transferase a3-3
Z21581	GSTA4	Glutathione s-transferase a4-4
HSGST4	GSTM1	Glutathione s-transferase mu 1
D31291	GSTM2	Glutathione s-transferase mu 2
HSGST4	GSTM2	Glutathione s-transferase mu 2
T08311	GSTM3	Glutathione s-transferase mu 3
HUMGSTM4B	GSTM4	Glutathione s-transferase mu 4
HUMGSTM5	GSTM5	Glutathione s-transferase mu 5
T05391	GSTP1	Glutathione s-transferase p
Z32822	GSTT1	Glutathione s-transferase theta 1
R08187	GSTT2	Glutathione s-transferase theta 2
Z25318	GSTK1	Glutathione s-transferase, mitochondrial
H03163	SLC37A1	Glycerol-3-phosphate transporter
AA363955	SLC5A7	High affinity choline transporter
HSRRMRNA	SLC7A1	High-affinity cationic amino acid transporter-1
R22196	SLC31A1	High-affinity copper uptake protein 1
AA918012	SLC10A2	Ileal sodium/bile acid transporter
F00840	SLC7A5	Large neutral amino acid transporter small subunit 1
M79133	SLC7A5	Large neutral amino acid transporter small subunit 1
Z38621	SLC7A8	Large neutral amino acids transporter small subunit 2
HUMCARAA	CES1	Liver carboxylesterase
S52379	CES1	Liver carboxylesterase
T55488	SLC21A6	Liver-specific organic anion transporter
W78748	SLC5A4	Low affinity sodium-glucose cotransporter
T54842	SLC7A2	Low-affinity cationic amino acid transporter-2
T87799	ABCA7	Macrophage abc transporter
Z17844	LRP	Major vault protein
Z24885	GSTZ1	Maleylacetoacetate isomerase
T39939	MT1A	Metallothionein-IA
R99207	MT1B	Metallothionein-IB
T39939	MT1E	Metallothionein-IE
D11725	MT1F	Metallothionein-IF
S68949	MT1G	Metallothionein-JG
S68954	MT1G	Metallothionein-JG
HSFMET	MT1H	Metallothionein-IH
S52379	MT2A	Metallothionein-II
M78846	MT3	Metallothionein-III
AA570216	MT1K	Metallothionein-IK
S68954	MT1K	Metallothionein-IK
D11725	MT1L	Metallothionein-IL
HSPP15	MT1L	Metallothionein-IL
HSPP15	MT1R	Metallothionein-IR
NM032935	MT4	Metallothionein-IV
HUMGST	MGST1	Microsomal glutathione s-transferase 1
H59104	MGST2	Microsomal glutathione s-transferase 2
T47062	MGST3	Microsomal glutathione s-transferase 3
SSMPCP	SLC25A3	Mitochondrial phosphate carrier protein
H39996	SULT1A3	Monoamine-sulfating phenol sulfotransferase
HUMARYTRAB	SULT1A3	Monoamine-sulfating phenol sulfotransferase
M62141	SLC16A1	Monocarboxylate transporter 1
H90048	SLC16A6	Monocarboxylate transporter 2
F02520	SLC16A2	Monocarboxylate transporter 3
AI005004	SLC16A8	Monocarboxylate transporter 4
T59354	SLC16A3	Monocarboxylate transporter 5
R22416	SLC16A4	Monocarboxylate transporter 6
T78890	SLC16A5	Monocarboxylate transporter 7

F01173	SLC16A7	Monocarboxylate transporter 8
Z41819	ABCB1	Multidrug resistance protein 1
HUMMDR3	ABCB4	Multidrug resistance protein 3
SATHRMRP	ABCC1	Multidrug resistance-associated protein 1
R00050	ABCC4	Multidrug resistance-associated protein 4
M78673	ABCC5	Multidrug resistance-associated protein 5
R99091	ABCC6	Multidrug resistance-associated protein 6
T69749	ABCC6	Multidrug resistance-associated protein 6
D11495	DIA4	Nad(p)h dehydrogenase [quinone] 1
HUMNRAMP	SLC11A1	Natural resistance-associated macrophage protein 1
Z38360	SLC11A2	Natural resistance-associated macrophage protein 2
HUMASCT1A	SLC1A4	Neutral amino acid transporter a
T10696	SLC1A5	Neutral amino acid transporter b(0)
HUMRENBAT	SLC3A1	Neutral and basic amino acid transport protein rbat
HSU08021	NNMT	Nicotinamide n-methyltransferase
T87759	SLC22A4	Novel organic cation transporter 1
Z41935	SLC15A2	Oligopeptide transporter, kidney isoform
HSU21936	SLC15A1	Oligopeptide transporter, small intestine isoform
M62053	OAT1	Organic anion transporter 1
H18607	OAT3	Organic anion transporter 3
R16970	OAT4	Organic anion transporter 4
T39111	SLC21A9	Organic anion transporter b
Z41576	SLC21A11	Organic anion transporter oATP-d
T23657	SLC21A12	Organic anion transporter oATP-e
Z21041	SLC21A14	Organic anion transporting polypeptide 14
H75435	SLC21A8	Organic anion transporting polypeptide 8
HSU77086	SLC22A1	Organic cation transporter 1
HSOCTK	SLC22A2	Organic cation transporter 2
T53187	SLC22A3	Organic cation transporter 3
H30224	ORCTL4	Organic cation transporter like 4
H25503	ORCTL2	Organic cation transporter-like 2
Z38659	SLC22A5	Organic cation/carnitine transporter 2
AB010438	ORCTL3	Organic-cation transporter like 3
T95621	ORNT1	Ornithine transporter
AA398593	ORNT2	Ornithine transporter 2
R79412	NTT5	Orphan sodium- and chloride-dependent neurotransmitter transporter ntt5
H82347	NTT73	Orphan sodium- and chloride-dependent neurotransmitter transporter ntt73
Z43484	NTT73	Orphan sodium- and chloride-dependent neurotransmitter transporter ntt73
Z44749	SLC25A17	Peroxisomal membrane protein pmp34
HUMARYLSUL	SULT1A1	Phenol-sulfating phenol sulfotransferase 1
HUMARYLSUL	SULT1A2	Phenol-sulfating phenol sulfotransferase 2
D12243	RBP4	Plasma retinol-binding protein
HUMATPAD	ATP12A	Potassium-transporting ATPase alpha chain 2
Z40030	ATP8A1	Potential phospholipid-transporting ATPase ia
T10596	FIC1	Potential phospholipid-transporting ATPase ic
T86800	SLC31A2	Probable low-affinity copper uptake protein 2
Z41717	PTGIS	Prostacyclin synthase
S78220	PTGS1	Prostaglandin g/h synthase 1
HUMENDOSYN	PTGS2	Prostaglandin g/h synthase 2
T85296	SLC21A2	Prostaglandin transporter
M62053	SLC22A6	Renal organic anion transport protein 1
HSU26209	SLC13A2	Renal sodium/dicarboxylate cotransporter
Z40774	SLC13A2	Renal sodium/dicarboxylate cotransporter
HSNAPI1	SLC17A1	Renal sodium-dependent phosphate transport protein 1

HUMNAPI3X	SLC34A1	Renal sodium-dependent phosphate transport protein 2
H85361	ABCA4	Retinal-specific ATP-binding cassette transporter
S74445	CRABP1	Retinoic acid-binding protein i, cellular
HUMCRABP	CRABP2	Retinoic acid-binding protein ii, cellular
HUMCRBP	RBP1	Retinol-binding protein i, cellular
S57153	RBP1	Retinol-binding protein i, cellular
T07054	RBP2	Retinol-binding protein ii, cellular
T63266	RBP2	Retinol-binding protein ii, cellular
HUMBGT1R	SLC6A12	Sodium- and chloride-dependent betaine transporter
HUMCRT	SLC6A8	Sodium- and chloride-dependent creatine transporter 1
R20043	SLC6A13	Sodium- and chloride-dependent gaba transporter 2
S70609	SLC6A9	Sodium- and chloride-dependent glycine transporter 1
AA625644	SLC6A5	Sodium- and chloride-dependent glycine transporter 2
M78677	SLC6A6	Sodium- and chloride-dependent taurine transporter
T10761	SLC4A4	Sodium bicarbonate cotransporter nbc1
AA452802	NBC4	Sodium bicarbonate cotransporter nbc4a
HUMCNC	SLC8A1	Sodium/calcium exchanger 1
R20720	SLC8A2	Sodium/calcium exchanger 2
T07666	SLC8A3	Sodium/calcium exchanger 3
T07666	SLC8A3	Sodium/glucose cotransporter 1
HUMSGLCT	SLC5A2	Sodium/glucose cotransporter 2
S83549	SLC9A2	Sodium/hydrogen exchanger 2
HSU66088	SLC5A5	Sodium/iodide cotransporter
HSU62966	SLC28A1	Sodium/nucleoside cotransporter 1
AA358822	SLC28A2	Sodium/nucleoside cotransporter 2
HUMNTCP	SLC10A1	Sodium/taurocholate cotransporting polypeptide
HSGAT1MR	SLC6A1	Sodium-and chloride-dependent gaba transporter 1
F05686	SLC6A11	Sodium-and chloride-dependent gaba transporter 3
AA604857	SVCT1	Sodium-dependent vitamin c transporter 1
T27309	SVCT2	Sodium-dependent vitamin c transporter 2
S44626	SLC6A3	Sodium-dependent dopamine transporter
Z39412	NADC3	Sodium-dependent high-affinity dicarboxylate transporter
T77525	SLC5A6	Sodium-dependent multivitamin transporter
HUMNORTR	SLC6A2	Sodium-dependent noradrenaline transporter
HSZ83953	SLC17A3	Sodium-dependent phosphate transport protein 3
R06460	SLC17A3	Sodium-dependent phosphate transport protein 3
HSZ83953	SLC17A4	Sodium-dependent phosphate transport protein 4
R09122	SLC17A4	Sodium-dependent phosphate transport protein 4
H40741	SLC6A7	Sodium-dependent proline transporter
HSsert	SLC6A4	Sodium-dependent serotonin transporter
T64950	SLC21A3	Sodium-independent organic anion transporter
M79233	EPHX2	Soluble epoxide hydrolase
Z39813	SLC25A18	Solute carrier
HUMSTAR	STAR	Steroidogenic acute regulatory protein
Z20453	STAR	Steroidogenic acute regulatory protein
R69741	SLC26A2	Sulfate transporter
T08860	ABCC8	Sulfonylurea receptor 1
R73927	ABCC9	Sulfonylurea receptor 2
T84623	SULT1C1	Sulfotransferase 1C1
R58632	SULT1C2	Sulfotransferase 1C2
HSVMT	SLC18A2	Synaptic vesicle amine transporter
AF080246	TRAG3	Taxol-resistant associated protein 3
R20880	SLC19A2	Thiamine transporter 1
HSU44128	SLC12A3	Thiazide-sensitive sodium-chloride cotransporter
S62904	TPMT	Thiopurine S-methyltransferase
HSPBX2	G17	Transporter protein
T62038	G17	Transporter protein

R53836	SLC35A3	UDP N-acetylglucosamine transporter
T60594	SLC35A2	UDP-galactose translocator
HUMUGT1FA	UGT1	UDP-glucuronosyltransferase 1-1, microsomal
HUMUGT1FA	UGT1A10	UDP-glucuronosyltransferase 1A10
HUMUGT1FA	UGT1A7	UDP-glucuronosyltransferase 1A7
HUMUGT1FA	UGT1A8	UDP-glucuronosyltransferase 1A8
HUMUGT1FA	UGT1A9	UDP-glucuronosyltransferase 1A9
HSUGT2BIO	UGT2B10	UDP-glucuronosyltransferase 2B10, microsomal
HSUDPGT	UGT2B11	UDP-glucuronosyltransferase 2B11, microsomal
N70316	UGT2B11	UDP-glucuronosyltransferase 2B11, microsomal
HSU08854	UGT2B15	UDP-glucuronosyltransferase 2B15, microsomal
T24450	UGT2B17	UDP-glucuronosyltransferase 2B17, microsomal
HSUDPGT	UGT2B4	UDP-glucuronosyltransferase 2B4, microsomal
HUMUDPGTA	UGT2B7	UDP-glucuronosyltransferase 2B7, microsomal
AI002801	SLC14A1	Urea transporter, erythrocyte
Z19313	SLC14A1	Urea transporter, erythrocyte
AI002801	SLC14A2	Urea transporter, kidney
HSU09210	SLC18A3	Vesicular acetylcholine transporter
HUMKCHB	KCNA4	Voltage-gated potassium channel protein kv1.4
R09608	XDH	Xanthine dehydrogenase/oxidase
T64266	SLC7A7	Y+1 amino acid transporter 1
T10628	SLC30A1	Zinc transporter 1
AA322641	SLC30A4	Zinc transporter 4

#EXONS_SKIPPED: This field details alternatively spliced exons identified according to the teachings of the present invention and their deletion to create the biomolecular sequences of the present invention. This field is marked by #EXONS_SKIPPED and thereafter the names of exons (for example: #EXONS_SKIPPED C15NT010194P1split49_294009_294072). C15NT010194P1split49_294009_294072 specifies the name of the exon of the present invention.

EXAMPLE 7

Proteins and diseases

The following sections list examples of proteins (subsection i), based on their molecular function, which participate in variety of diseases (listed in subsection ii), which diseases can be diagnosed/treated using the biomolecular sequences uncovered by the present invention.

The present invention is of biomolecular sequences, which can be classified to functional groups based on known activity of homologous sequences. This functional group classification, allows the identification of diseases and conditions, which may

be diagnosed and treated based on the novel sequence information and annotations of the present invention.

This functional group classification includes the following groups:

Proteins involved in Drug-Drug interactions:

The phrase "proteins involved in drug-drug interactions" refers to proteins involved in a biological process which mediates the interaction between at least two consumed drugs.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to modulate drug-drug interactions. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such drug-drug interactions.

Examples of these conditions include, but are not limited to the cytochrom P450 protein family, which is involved in the metabolism of many drugs. Examples of proteins, which are involved in drug-drug interactions are presented in Table 7.

Proteins involved in the metabolism of a pro-drug to a drug:

The phrase "proteins involved in the metabolism of a pro-drug to a drug" refers to proteins that activate an inactive pro-drug by chemically chaining it into a biologically active compound. Preferably, the metabolizing enzyme is expressed in the target tissue thus reducing systemic side effects.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to modulate the metabolism of a pro-drug into drug. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such conditions.

Examples of these proteins include, but are not limited to esterases hydrolyzing the cholesterol lowering drug simvastatin into its hydroxy acid active form.

MDR proteins:

The phrase "MDR proteins" refers to Multi Drug Resistance proteins that are responsible for the resistance of a cell to a range of drugs, usually by exporting these

drugs outside the cell. Preferably, the MDR proteins are ABC binding cassette proteins. Preferably, drug resistance is associated with resistance to chemotherapy.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the transport of molecules and macromolecules such as neurotransmitters, hormones, sugar etc. is abnormal leading to various pathologies. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of these proteins include, but are not limited to the multi-drug resistant transporter MDR1/P-glycoprotein, the gene product of MDR1, which belongs to the ATP-binding cassette (ABC) superfamily of membrane transporters and increases the resistance of malignant cells to therapy by exporting the therapeutic agent out of the cell.

Hydrolases acting on amino acids:

The phrase "hydrolases acting on amino acids" refers to hydrolases acting on a pair of amino acids.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the transfer of a glycosyl chemical group from one molecule to another is abnormal thus, a beneficial effect may be achieved by modulation of such reaction. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to reperfusion of clotted blood vessels by TPA (Tissue Plasminogen Activator) which converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single ARG-VAL bond in plasminogen.

Transaminases:

The term "transaminases" refers to enzymes transferring an amine group from one compound to another.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of

altering expression of such proteins, may be used to treat diseases in which the transfer of an amine group from one molecule to another is abnormal thus, a beneficial effect may be achieved by modulation of such reaction. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such transaminases include, but are not limited to two liver enzymes, frequently used as markers for liver function - SGOT (Serum Glutamic-Oxaloacetic Transaminase - AST) and SGPT (Serum Glutamic-Pyruvic Transaminase - ALT).

Immunoglobulins:

The term "immunoglobulins" refers to proteins that are involved in the immune and complement systems such as antigens and autoantigens, immunoglobulins, MHC and HLA proteins and their associated proteins.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases involving the immune system such as inflammation, autoimmune diseases, infectious diseases, and cancerous processes. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases and molecules that may be target for diagnostics include, but are not limited to members of the complement family such as C3 and C4 that their blood level is used for evaluation of autoimmune diseases and allergy state and C1 inhibitor that its absence is associated with angioedema. Thus, new variants of these genes are expected to be markers for similar events. Mutation in variants of the complement family may be associated with other immunological syndromes, such as increased bacterial infection that is associated with mutation in C3. C1 inhibitor was shown to provide safe and effective inhibition of complement activation after reperfused acute myocardial infarction and may reduce myocardial injury [Eur. Heart J. 2002, 23(21):1670-7], thus, its variant may have the same or improved effect.

Transcription factor binding:

The phrase "transcription factor binding" refers to proteins involved in transcription process by binding to nucleic acids, such as transcription factors, RNA and DNA binding proteins, zinc fingers, helicase, isomerase, histones, and nucleases.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins may be used to treat diseases involving transcription factors binding proteins. Such treatment may be based on transcription factor that can be used to for modulation of gene expression associated with the disease. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to breast cancer associated with ErbB-2 expression that was shown to be successfully modulated by a transcription factor [Proc. Natl. Acad. Sci. U.S.A. 2000, 97(4):1495-500]. Examples of novel transcription factors used for therapeutic protein production include, but are not limited to those described for Erythropoietin production [J. Biol. Chem. 2000, 275(43):33850-60; J. Biol. Chem. 2000, 275(43):33850-60] and zinc fingers protein transcription factors (ZFP-TF) variants [J. Biol. Chem. 2000, 275(43):33850-60].

Small GTPase regulatory/interacting proteins:

The phrase "Small GTPase regulatory/interacting proteins" refers to proteins capable of regulating or interacting with GTPase such as RAB escort protein, guanyl-nucleotide exchange factor, guanyl-nucleotide exchange factor adaptor, GDP-dissociation inhibitor, GTPase inhibitor, GTPase activator, guanyl-nucleotide releasing factor, GDP-dissociation stimulator, regulator of G-protein signaling, RAS interactor, RHO interactor, RAB interactor, and RAL interactor.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which G-proteases mediated signal-transduction is abnormal, either as a cause, or as a result of the disease. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to diseases related to prenylation. Modulation of prenylation was shown to affect therapy of diseases such as osteoporosis, ischemic heart disease, and inflammatory processes. Small GTPases regulatory/interacting proteins are major component in the prenylation post translation modification, and are required to the normal activity of prenylated proteins. Thus, their variants may be used for therapy of prenylation associated diseases.

Calcium binding proteins:

The phrase "calcium binding proteins" refers to proteins involve in calcium binding, preferably, calcium binding proteins, ligand binding or carriers, such as diacylglycerol kinase, Calpain, calcium-dependent protein serine/threonine phosphatase, calcium sensing proteins, calcium storage proteins.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat calcium involved diseases. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to diseases related to hypercalcemia, hypertension, cardiovascular disease, muscle diseases, gastro-intestinal diseases, uterus relaxing, and uterus. An example for therapy use of calcium binding proteins variant may be treatment of emergency cases of hypercalcemia, with secreted variants of calcium storage proteins.

Oxidoreductase:

The term "oxidoreductase" refers to enzymes that catalyze the removal of hydrogen atoms and electrons from the compounds on which they act. Preferably, oxidoreductases acting on the following groups of donors: CH-OH, CH-CH, CH-NH₂, CH-NH; oxidoreductases acting on NADH or NADPH, nitrogenous compounds, sulfur group of donors, heme group, hydrogen group, diphenols and related substances as donors; oxidoreductases acting on peroxide as acceptor, superoxide radicals as acceptor, oxidizing metal ions, CH₂ groups; oxidoreductases acting on reduced ferredoxin as donor; oxidoreductases acting on reduced flavodoxin as donor; and oxidoreductases acting on the aldehyde or oxo group of donors.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases caused by abnormal activity of oxidoreductases. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to malignant and autoimmune diseases in which the enzyme DHFR (DiHydroFolateReductase) that participates in folate metabolism and essential for *de novo* glycine and purine synthesis is the target for the widely used drug Methotrexate (MTX).

Receptors:

The term "receptors" refers to protein-binding sites on a cell's surface or interior, that recognize and binds to specific messenger molecule leading to a biological response, such as signal transducers, complement receptors, ligand-dependent nuclear receptors, transmembrane receptors, GPI-anchored membrane-bound receptors, various coreceptors, internalization receptors, receptors to neurotransmitters, hormones and various other effectors and ligands.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases caused by abnormal activity of receptors, preferably, receptors to neurotransmitters, hormones and various other effectors and ligands. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, chronic myelomonocytic leukemia caused by growth factor β receptor deficiency [Rao D. S., et al., (2001) Mol. Cell Biol., 21(22):7796-806], thrombosis associated with protease-activated receptor deficiency [Sambrano G. R., et al., (2001) Nature, 413(6851):26-7], hypercholesterolemia associated with low density lipoprotein receptor deficiency [Koivisto U. M., et al., (2001) Cell, 105(5):575-85], familial Hibernian fever associated with tumor necrosis factor receptor deficiency [Simon A., et al., (2001) Ned Tijdschr Geneesk; 145(2):77-8], colitis associated with immunoglobulin E receptor expression [Dombrowicz D., et al., (2001) J. Exp. Med., 193(1):25-34], and alagille syndrome

associated with Jagged1 [Stankiewicz P. et al., (2001) Am. J. Med. Genet., 103(2):166-71], breast cancer associated with mutated BRCA2 and androgen. Therapeutic applications of nuclear receptors variants may be based on secreted version of receptors such as the thyroid nuclear receptor that by binding plasma free thyroid hormone to reduce its levels may have a therapeutic effect in cases of thyrotoxicosis. A secreted version of glucocorticoid nuclear receptor, by binding plasma free cortisol, thus, reducing, may have a therapeutic effect in cases of Cushing's disease (a disease associated with high cortisole levels in the plasma).

Another example of a secreted variant of a receptor is a secreted form of the TNF receptor, which is used to treat conditions in which reduction of TNF levels is of benefit including Rheumatoid Arthritis, Juvenile Rheumatoid Arthritis, Psoriatic Arthritis and Ankylosing Spondylitis.

Protein serine/threonine kinases:

The phrase "protein serine/threonine kinases" refers to proteins which phosphorylate serine/threonine residues, mainly involved in signal transduction, such as transmembrane receptor protein serine/threonine kinase, 3-phosphoinositide-dependent protein kinase, DNA-dependent protein kinase, G-protein-coupled receptor phosphorylating protein kinase, SNF1A/AMP-activated protein kinase, casein kinase, calmodulin regulated protein kinase, cyclic-nucleotide dependent protein kinase, cyclin-dependent protein kinase, eukaryotic translation initiation factor 2 α kinase, galactosyltransferase-associated kinase, glycogen synthase kinase 3, protein kinase C, receptor signaling protein serine/threonine kinase, ribosomal protein S6 kinase, and I κ B kinase.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases ameliorated by a modulating kinase activity. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to schizophrenia. 5-HT(2A) serotonin receptor is the principal molecular target for LSD-like hallucinogens and atypical antipsychotic drugs. It has been shown that a major mechanism for the attenuation of this receptor signaling following agonist activation typically involves the

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phosphorylation of serine and/or threonine residues by various kinases. Therefore, serine/threonine kinases specific for the 5-HT(2A) serotonin receptor may serve as drug targets for a disease such as schizophrenia. Other diseases that may be treated through serine/threonine kinases modulation are Peutz-Jeghers syndrome (PJS, a rare autosomal-dominant disorder characterized by hamartomatous polyposis of the gastrointestinal tract and melanin pigmentation of the skin and mucous membranes [Hum. Mutat. 2000, 16(1):23-30], breast cancer [Oncogene. 1999, 18(35):4968-73], Type 2 diabetes insulin resistance [Am. J. Cardiol. 2002, 90(5A):11G-18G], and fanconi anemia [Blood. 2001, 98(13):3650-7].

Channel/pore class transporters:

The phrase "Channel/pore class transporters" refers to proteins that mediate the transport of molecules and macromolecules across membranes, such as α -type channels, porins, and pore-forming toxins.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the transport of molecules and macromolecules are abnormal, therefore leading to various pathologies. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to diseases of the nervous system such as Parkinson, diseases of the hormonal system, diabetes and infectious diseases such as bacterial and fungal infections. For example, α -hemolysin, is a protein product of *S. aureus* which creates ion conductive pores in the cell membrane, thereby diminishing its integrity.

Hydrolases, acting on acid anhydrides:

The phrase "hydrolases, acting on acid anhydrides" refers to hydrolytic enzymes that are acting on acid anhydrides, such as hydrolases acting on acid anhydrides in phosphorus-containing anhydrides or in sulfonyl-containing anhydrides, hydrolases catalyzing transmembrane movement of substances, and involved in cellular and subcellular movement.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of

altering expression of such proteins may be used to treat diseases in which the hydrolase-related activities are abnormal. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to glaucoma treated with carbonic anhydrase inhibitors (e.g. Dorzolamide), peptic ulcer disease treated with H(⁺)K(⁺)ATPase inhibitors that were shown to affect disease by blocking gastric carbonic anhydrase (e.g. Omeprazole).

Transferases, transferring phosphorus-containing groups:

The phrase "transferases, transferring phosphorus-containing groups" refers to enzymes that catalyze the transfer of phosphate from one molecule to another, such as phosphotransferases using the following groups as acceptors: alcohol group, carboxyl group, nitrogenous group, phosphate; phosphotransferases with regeneration of donors catalyzing intramolecular transfers; diphosphotransferases; nucleotidyltransferase; and phosphotransferases for other substituted phosphate groups.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins may be used to treat diseases in which the transfer of a phosphorous containing functional group to a modulated moiety is abnormal. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to acute MI [Ann. Emerg. Med. 2003, 42(3):343-50], Cancer [Oral. Dis. 2003, 9(3):119-28; J. Surg. Res. 2003, 113(1):102-8] and Alzheimer's disease [Am. J. Pathol. 2003, 163(3):845-58]. Examples for possible utilities of such transferases for drug improvement include, but are not limited to aminoglycosides treatment (antibiotics) to which resistance is mediated by aminoglycoside phosphotransferases [Front. Biosci. 1999, 1;4:D9-21]. Using aminoglycoside phosphotransferases variants or inhibiting these enzymes may reduce aminoglycosides resistance. Since aminoglycosides can be toxic to some patients, proving the expression of aminoglycoside phosphotransferases in a patient can deter from treating him with aminoglycosides and risking the patient in vain.

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Phosphoric monoester hydrolases:

The phrase "phosphoric monoester hydrolases" refers to hydrolytic enzymes that are acting on ester bonds, such as nuclease, sulfuric ester hydrolase, carboxylic ester hydrolase, thioester hydrolase, phosphoric monoester hydrolase, phosphoric diester hydrolase, triphosphoric monoester hydrolase, diphosphoric monoester hydrolase, and phosphoric triester hydrolase.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the hydrolytic cleavage of a covalent bond with accompanying addition of water (-H being added to one product of the cleavage and -OH to the other), is abnormal. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to diabetes and CNS diseases such as Parkinson and cancer.

Enzyme inhibitors:

The term "enzyme inhibitors" refers to inhibitors and suppressors of other proteins and enzymes, such as inhibitors of kinases, phosphatases, chaperones, guanylate cyclase, DNA gyrase, ribonuclease, proteasome inhibitors, diazepam-binding inhibitor, ornithine decarboxylase inhibitor, GTPase inhibitors, dUTP pyrophosphatase inhibitor, phospholipase inhibitor, proteinase inhibitor, protein biosynthesis inhibitors, and α -amylase inhibitors.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which beneficial effect may be achieved by modulating the activity of inhibitors and suppressors of proteins and enzymes. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to α -1 antitrypsin (a natural serine proteases, which protects the lung and liver from proteolysis) deficiency associated with emphysema, COPD and liver cirrhosis. α -1 antitrypsin is also used for

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diagnostics in cases of unexplained liver and lung disease. A variant of this enzyme may act as protease inhibitor or a diagnostic target for related diseases.

Electron transporters:

The term "Electron transporters" refers to ligand binding or carrier proteins involved in electron transport such as flavin-containing electron transporter, cytochromes, electron donors, electron acceptors, electron carriers, and cytochrome-c oxidases.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which beneficial effect may be achieved by modulating the activity of electron transporters. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to cyanide toxicity, resulting from cyanide binding to ubiquitous metalloenzymes rendering them inactive, and interfering with the electron transport. Novel electron transporters to which cyanide can bind may serve as drug targets for new cyanide antidotes.

Transferases, transferring glycosyl groups:

The phrase "transferases, transferring glycosyl groups" refers to enzymes that catalyze the transfer of a glycosyl chemical group from one molecule to another such as murein lytic endotransglycosylase E, and sialyltransferase.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the transfer of a glycosyl chemical group is abnormal. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Ligases, forming carbon-oxygen bonds:

The phrase "ligases, forming carbon-oxygen bonds" refers to enzymes that catalyze the linkage between carbon and oxygen such as ligase forming aminoacyl-tRNA and related compounds.

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Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the linkage between carbon and oxygen in an energy dependent process is abnormal. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Ligases:

The term "ligases" refers to enzymes that catalyze the linkage of two molecules, generally utilizing ATP as the energy donor, also called synthetase. Examples for ligases are enzymes such as β -alanyl-dopamine hydrolase, carbon-oxygen bonds forming ligase, carbon-sulfur bonds forming ligase, carbon-nitrogen bonds forming ligase, carbon-carbon bonds forming ligase, and phosphoric ester bonds forming ligase.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the joining together of two molecules in an energy dependent process is abnormal. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to neurological disorders such as Parkinson's disease [Science. 2003, 302(5646):819-22; J. Neurol. 2003, 250 Suppl. 3:III25-III29] or epilepsy [Nat. Genet. 2003, 35(2):125-7], cancerous diseases [Cancer Res. 2003, 63(17):5428-37; Lab. Invest. 2003, 83(9):1255-65], renal diseases [Am. J. Pathol. 2003, 163(4):1645-52], infectious diseases [Arch. Virol. 2003, 148(9):1851-62] and fanconi anemia [Nat. Genet. 2003, 35(2):165-70].

Hydrolases, acting on glycosyl bonds:

The phrase "hydrolases, acting on glycosyl bonds" refers to hydrolytic enzymes that are acting on glycosyl bonds such as hydrolases hydrolyzing N-glycosyl compounds, S-glycosyl compounds, and O-glycosyl compounds.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the

hydrolase-related activities are abnormal. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include cancerous diseases [J. Natl. Cancer Inst. 2003, 95(17):1263-5; Carcinogenesis. 2003, 24(7):1281-2; author reply 1283] vascular diseases [J. Thorac. Cardiovasc. Surg. 2003, 126(2):344-57], gastrointestinal diseases such as colitis [J. Immunol. 2003, 171(3):1556-63] or liver fibrosis [World J. Gastroenterol. 2002, 8(5):901-7].

Kinases:

The term "kinases" refers to enzymes which phosphorylate serine/threonine or tyrosine residues, mainly involved in signal transduction. Examples for kinases include enzymes such as 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase, NAD⁽⁺⁾ kinase, acetylglutamate kinase, adenosine kinase, adenylate kinase, adenylylsulfate kinase, arginine kinase, aspartate kinase, choline kinase, creatine kinase, cytidylate kinase, deoxyadenosine kinase, deoxycytidine kinase, deoxyguanosine kinase, dephospho-CoA kinase, diacylglycerol kinase, dolichol kinase, ethanolamine kinase, galactokinase, glucokinase, glutamate 5-kinase, glycerol kinase, glycerone kinase, guanylate kinase, hexokinase, homoserine kinase, hydroxyethylthiazole kinase, inositol/phosphatidylinositol kinase, ketohexokinase, mevalonate kinase, nucleoside-diphosphate kinase, pantothenate kinase, phosphoenolpyruvate carboxykinase, phosphoglycerate kinase, phosphomevalonate kinase, protein kinase, pyruvate dehydrogenase (lipoamide) kinase, pyruvate kinase, ribokinase, ribose-phosphate pyrophosphokinase, selenide, water dikinase, shikimate kinase, thiamine pyrophosphokinase, thymidine kinase, thymidylate kinase, uridine kinase, xylulokinase, 1D-myo-inositol-trisphosphate 3-kinase, phosphofructokinase, pyridoxal kinase, sphinganine kinase, riboflavin kinase, 2-dehydro-3-deoxygalactonokinase, 2-dehydro-3-deoxygluconokinase, 4-diphosphocytidyl-2C-methyl-D-erythritol kinase, GTP pyrophosphokinase, L-fuculokinase, L-ribulokinase, L-xylulokinase, isocitrate dehydrogenase (NADP⁺) kinase, acetate kinase, allose kinase, carbamate kinase, cobinamide kinase, diphosphate-purine nucleoside kinase, fructokinase, glycerate kinase, hydroxymethylpyrimidine kinase, hygromycin-B kinase, inosine kinase, kanamycin kinase, phosphomethylpyrimidine kinase, phosphoribulokinase, polyphosphate kinase, propionate kinase, pyruvate kinase, water

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dikinase, rhamnulokinase, tagatose-6-phosphate kinase, tetraacyldisaccharide 4'-kinase, thiamine-phosphate kinase, undecaprenol kinase, uridylate kinase, N-acylmannosamine kinase, D-erythro-sphingosine kinase.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases which may be ameliorated by a modulating kinase activity. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, acute lymphoblastic leukemia associated with spleen tyrosine kinase deficiency [Goodman P.A., et al., (2001) Oncogene, 20(30):3969-78], ataxia telangiectasia associated with ATM kinase deficiency [Boultwood J., (2001) J. Clin. Pathol., 54(7):512-6], congenital haemolytic anaemia associated with erythrocyte pyruvate kinase deficiency [Zanella A., et al., (2001) Br. J. Haematol., 113(1):43-8], mevalonic aciduria caused by mevalonate kinase deficiency [Houten S. M., et al., (2001) Eur. J. Hum. Genet., 9(4):253-9], and acute myelogenous leukemia associated with over-expressed death-associated protein kinase [Guzman M. L., et al., (2001) Blood, 97(7):2177-9].

Nucleotide binding:

The term "nucleotide binding" refers to ligand binding or carrier proteins, involved in physical interaction with a nucleotide, preferably, any compound consisting of a nucleoside that is esterified with [ortho]phosphate or an oligophosphate at any hydroxyl group on the glycoside moiety, such as purine nucleotide binding proteins.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases that are associated with abnormal nucleotide binding. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to Gout (a syndrome characterized by high urate level in the blood). Since urate is a breakdown metabolite

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of purines, reducing purines serum levels could have a therapeutic effect in Gout disease.

Tubulin binding:

The term "tubulin binding" refers to binding proteins that bind tubulin such as microtubule binding proteins.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases which are associated with abnormal tubulin activity or structure. Binding the products of the genes of this family, or antibodies reactive therewith, can modulate a plurality of tubulin activities as well as change microtubulin structure. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, Alzheimer's disease associated with t-complex polypeptide 1 deficiency [Schuller E., et al., (2001) Life Sci., 69(3):263-70], neurodegeneration associated with *apoE* deficiency [Masliah E., et al., (1995) Exp. Neurol., 136(2):107-22], progressive axonopathy associated with dysfunctional neurofilaments [Griffiths I. R., et al., (1989) Neuropathol. Appl. Neurobiol., 15(1):63-74], familial frontotemporal dementia associated with tau deficiency [astor P., et al., (2001) Ann. Neurol., 49(2):263-7], and colon cancer suppressed by APC [White R. L., (1997) Pathol. Biol. (Paris), 45(3):240-4]. An example for a drug whose target is tubulin is the anticancer drug - Taxol. Drugs having similar mechanism of action (interfering with tubulin polymerization) may be developed based on tubulin binding proteins.

Receptor signaling proteins:

The phrase "receptor signaling proteins" refers to receptor proteins involved in signal transduction such as receptor signaling protein serine/threonine kinase, receptor signaling protein tyrosine kinase, receptor signaling protein tyrosine phosphatase, aryl hydrocarbon receptor nuclear translocator, hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer, transmembrane receptor protein tyrosine kinase signaling protein, transmembrane receptor protein serine/threonine kinase signaling protein, receptor signaling protein serine/threonine kinase signaling protein, receptor signaling protein serine/threonine phosphatase signaling protein, small

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GTPase regulatory/interacting protein, receptor signaling protein tyrosine kinase signaling protein, and receptor signaling protein serine/threonine phosphatase.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the signal-transduction is abnormal, either as a cause, or as a result of the disease. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, complete hypogonadotropic hypogonadism associated with GnRH receptor deficiency [Kottler M. L., et al., (2000) J. Clin. Endocrinol. Metab., 85(9):3002-8], severe combined immunodeficiency disease associated with IL-7 receptor deficiency [Puel A. and Leonard W. J., (2000) Curr. Opin. Immunol., 12(4):468-7], schizophrenia associated N-methyl-D-aspartate receptor deficiency [Mohn A.R., et al., (1999) Cell, 98(4):427-36], Yesinia-associated arthritis associated with tumor necrosis factor receptor p55 deficiency [Zhao Y. X., et al., (1999) Arthritis Rheum., 42(8):1662-72], and Dwarfism of Sindh caused by growth hormone-releasing hormone receptor deficiency [aheshwari H. G., et al., (1998) J. Clin. Endocrinol. Metab., 83(11):4065-74].

Molecular function unknown:

The phrase "molecular function unknown" refers to various proteins with unknown molecular function, such as cell surface antigens.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which regulation of the recognition, or participation or bind of cell surface antigens to other moieties may have therapeutic effect. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, autoimmune diseases, various infectious diseases, cancer diseases which involve non cell surface antigens recognition and activity.

Enzyme activators:

The term "enzyme activators" refers to enzyme regulators such as activators of: kinases, phosphatases, sphingolipids, chaperones, guanylate cyclase, tryptophan hydroxylase, proteases, phospholipases, caspases, proprotein convertase 2 activator, cyclin-dependent protein kinase 5 activator, superoxide-generating NADPH oxidase activator, sphingomyelin phosphodiesterase activator, monophenol monooxygenase activator, proteasome activator, and GTPase activator.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which beneficial effect may be achieved by modulating the activity of activators of proteins and enzymes. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to all complement related diseases, as most complement proteins activate by cleavage other complement proteins.

Transferases, transferring one-carbon groups:

The phrase "transferases, transferring one-carbon groups" refers enzymes that catalyze the transfer of a one-carbon chemical group from one molecule to another such as methyltransferase, amidinotransferase, hydroxymethyl-, formyl- and related transferase, carboxyl- and carbamoyltransferase.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the transfer of a one-carbon chemical group from one molecule to another is abnormal so that a beneficial effect may be achieved by modulation of such reaction. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Transferases:

The term "transferases" refers to enzymes that catalyze the transfer of a chemical group, preferably, a phosphate or amine from one molecule to another. It includes enzymes such as transferases, transferring one-carbon groups, aldehyde or ketonic groups, acyl groups, glycosyl groups, alkyl or aryl (other than methyl) groups,

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nitrogenous, phosphorus-containing groups, sulfur-containing groups, lipoyltransferase, deoxycytidyl transferases.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the transfer of a chemical group from one molecule to another is abnormal. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to cancerous diseases such as prostate cancer [Urology. 2003, 62(5 Suppl 1):55-62] or lung cancer [Invest. New Drugs. 2003, 21(4):435-43; JAMA. 2003, 22;290(16):2149-58], psychiatric disorders [Am. J. Med. Genet. 2003, 15;123B(1):64-9], colorectal disease such as Crohn's disease [Dis. Colon Rectum. 2003, 46(11):1498-507] or celiac diseases [N Engl. J. Med. 2003, 349(17):1673-4; author reply 1673-4], neurological diseases such as Prkinson's disease [J. Chem Neuroanat. 2003, 26(2):143-51], Alzheimer disease [Hum. Mol. Genet. 2003 21] or Charcot-Marie-Tooth Disease [Mol. Biol. Evol. 2003 31].

Chaperones:

The term "chaperones" refers to functional classes of unrelated families of proteins that assist the correct non-covalent assembly of other polypeptide-containing structures *in vivo*, but are not components of these assembled structures when they are performing their normal biological function. The group of chaperones include proteins such as ribosomal chaperone, peptidylprolyl isomerase, lectin-binding chaperone, nucleosome assembly chaperone, chaperonin ATPase, cochaperone, heat shock protein, HSP70/HSP90 organizing protein, fimbrial chaperone, metallochaperone, tubulin folding, and HSC70-interacting protein.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases which are associated with abnormal protein activity, structure, degradation or accumulation of proteins. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

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Examples of such diseases include, but are not limited to neurological syndromes [J. Neuropathol. Exp. Neurol. 2003, 62(7):751-64; Antioxid Redox Signal. 2003, 5(3):337-48; J. Neurochem. 2003, 86(2):394-404], neurological diseases such as Parkinson's disease [Hum. Genet. 2003, 6; Neurol Sci. 2003, 24(3):159-60; J. Neurol. 2003, 250 Suppl. 3:III25-III29] ataxia [J. Hum. Genet. 2003;48(8):415-9] or Alzheimer diseases [J. Mol. Neurosci. 2003, 20(3):283-6; J. Alzheimers Dis. 2003, 5(3):171-7], cancerous diseases [Semin. Oncol. 2003, 30(5):709-16], prostate cancer [Semin. Oncol. 2003, 30(5):709-16] metabolic diseases [J Neurochem. 2003, 87(1):248-56], infectious diseases, such as prion infection [EMBO J. 2003, 22(20):5435-5445]. Chaperones may be also used for manipulating therapeutic proteins binding to their receptors therefore, improving their therapeutic effect.

Cell adhesion molecule:

The phrase "cell adhesion molecule" refers to proteins that serve as adhesion molecules between adjoining cells such as membrane-associated protein with guanylate kinase activity, cell adhesion receptor, neuroligin, calcium-dependent cell adhesion molecule, selectin, calcium-independent cell adhesion molecule, and extracellular matrix protein.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which adhesion between adjoining cells is involved, typically conditions in which the adhesion is abnormal. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to cancer in which abnormal adhesion may cause and enhance the process of metastasis and abnormal growth and development of various tissues in which modulation adhesion among adjoining cells can improve the condition. Leucocyte-endothelial interactions characterized by adhesion molecules involved in interactions between cells lead to a tissue injury and ischemia reperfusion disorders in which activated signals generated during ischemia may trigger an exuberant inflammatory response during reperfusion, provoking greater tissue damage than initial ischemic insult [Crit. Care Med. 2002, 30(5 Suppl):S214-9]. The blockade of leucocyte-endothelial adhesive interactions has the

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potential to reduce vascular and tissue injury. This blockade may be achieved using a soluble variant of the adhesion molecule.

States of septic shock and ARDS involve large recruitment of neutrophil cells to the damaged tissues. Neutrophil cells bind to the endothelial cells in the target tissues through adhesion molecules. Neutrophils possess multiple effector mechanisms that can produce endothelial and lung tissue injury, and interfere with pulmonary gas transfer by disruption of surfactant activity [Eur. J. Surg. 2002, 168(4):204-14]. In such cases, the use of soluble variant of the adhesion molecule may decrease the adhesion of neutrophils to the damaged tissues.

Examples of such diseases include, but are not limited to, Wiskott-Aldrich syndrome associated with WAS deficiency [Westerberg L., et al., (2001) Blood, 98(4):1086-94], asthma associated with intercellular adhesion molecule-1 deficiency [Tang M. L. and Fiscus L. C., (2001) Pulm. Pharmacol. Ther., 14(3):203-10], intra-atrial thrombogenesis associated with increased von Willebrand factor activity [Fukuchi M., et al., (2001) J. Am. Coll. Cardiol., 37(5):1436-42], junctional epidermolysis bullosa associated with laminin 5- β -3 deficiency [Robbins P. B., et al., (2001) Proc. Natl. Acad. Sci., 98(9):5193-8], and hydrocephalus caused by neural adhesion molecule L1 deficiency [Rolf B., et al., (2001) Brain Res., 891(1-2):247-52].

Motor proteins:

The term "motor proteins" refers to proteins that generate force or energy by the hydrolysis of ATP and that function in the production of intracellular movement or transportation. Examples of such proteins include microfilament motor, axonemal motor, microtubule motor, and kinetochore motor (dynein, kinesin, or myosin).

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which force or energy generation is impaired. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, malignant diseases where microtubules are drug targets for a family of anticancer drugs such as myodystrophies and myopathies [Trends Cell Biol. 2002, 12(12):585-91], neurological disorders [Neuron. 2003, 25:40(1):25-40; Trends Biochem. Sci. 2003, 28(10):558-65;

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Med. Genet. 2003, 40(9):671-5], and hearing impairment [Trends Biochem. Sci. 2003, 28(10):558-65].

Defense/immunity proteins:

The term "defense/immunity proteins" refers to proteins that are involved in the immune and complement systems such as acute-phase response proteins, antimicrobial peptides, antiviral response proteins, blood coagulation factors, complement components, immunoglobulins, major histocompatibility complex antigens and opsonins.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases involving the immunological system including inflammation, autoimmune diseases, infectious diseases, as well as cancerous processes or diseases which are manifested by abnormal coagulation processes, which may include abnormal bleeding or excessive coagulation. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, late (C5-9) complement component deficiency associated with opsonin receptor allotypes [Fijen C. A., et al., (2000) Clin. Exp. Immunol., 120(2):338-45], combined immunodeficiency associated with defective expression of MHC class II genes [Griscelli C., et al., (1989) Immunodefic. Rev. 1(2):135-53], loss of antiviral activity of CD4 T cells caused by neutralization of endogenous TNF α [Pavic I., et al., (1993) J. Gen. Virol., 74 (Pt 10):2215-23], autoimmune diseases associated with natural resistance-associated macrophage protein deficiency [Evans C. A., et al., (2001) Neurogenetics, 3(2):69-78], Epstein-Barr virus-associated lymphoproliferative disease inhibited by combined GM-CSF and IL-2 therapy [Baiocchi R. A., et al., (2001) J. Clin. Invest., 108(6):887-94], and sepsis in which activated protein C is a therapeutic protein itself.

Intracellular transporters:

The term "intracellular transporters" refers to proteins that mediate the transport of molecules and macromolecules inside the cell, such as intracellular

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nucleoside transporter, vacuolar assembly proteins, vesicle transporters, vesicle fusion proteins, type II protein secretors.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the transport of molecules and macromolecules is abnormal leading to various pathologies. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Transporters:

The term "transporters" refers to proteins that mediate the transport of molecules and macromolecules, such as channels, exchangers, and pumps. Transporters include proteins such as: amine/polyamine transporter, lipid transporter, neurotransmitter transporter, organic acid transporter, oxygen transporter, water transporter, carriers, intracellular transports, protein transporters, ion transporters, carbohydrate transporter, polyol transporter, amino acid transporters, vitamin/cofactor transporters, siderophore transporter, drug transporter, channel/pore class transporter, group translocator, auxiliary transport proteins, permeases, murein transporter, organic alcohol transporter, nucleobase, nucleoside, and nucleotide and nucleic acid transporters.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the transport of molecules and macromolecules such as neurotransmitters, hormones, sugar etc. is impaired leading to various pathologies. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, glycogen storage disease caused by glucose-6-phosphate transporter deficiency [Hiraiwa H., and Chou J. Y. (2001) DNA Cell Biol., 20(8):447-53], tangier disease associated with ATP-binding cassette transporter-1 deficiency [McNeish J., et al., (2000) Proc. Natl. Acad. Sci., 97(8):4245-50], systemic primary carnitine deficiency associated with organic cation transporter deficiency [Tang N. L., et al., (1999) Hum. Mol. Genet., 8(4):655-60], Wilson disease associated with copper-transporting ATPases deficiency [Payne A. S., et al.,

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(1998) Proc. Natl. Acad. Sci. 95(18):10854-9], and atelosteogenesis associated with diastrophic dysplasia sulphate transporter deficiency [Newbury-Ecob R., (1998) J. Med. Genet., 35(1):49-53], Central Nervous system diseases treated by inhibiting neurotransmitter transporter (e.g. Depression, treated with serotonin transporters inhibitors – Prozac), and Cystic fibrosis mediated by the chloride channel CFTR. Other transporter related diseases are cancer [Oncogene. 2003, 22(38):6005-12] and especially cancer resistant to treatment [Oncologist. 2003, 8(5):411-24; J. Med. Invest. 2003, 50(3-4):126-35], infectious diseases, especially fungal infections [Annu. Rev. Phytopathol. 2003, 41:641-67], neurological diseases, such as Parkinson [FASEB J. 2003, Sep 4 [Epub ahead of print]], and cardiovascular diseases, including hypercholesterolemia [Am. J. Cardiol. 2003, 92(4B):10K-16K].

There are about 30 membrane transporter genes linked to a known genetic clinical syndrome. Secreted versions of splice variants of transporters may be therapeutic as the case with soluble receptors. These transporters may have the capability to bind the compound in the serum they would normally bind on the membrane. For example, a secreted form ATP7B, a transporter involved in Wilson's disease, is expected to bind plasma Copper, therefore have a desired therapeutic effect in Wilson's disease.

Lyases:

The term "lyases" refers to enzymes that catalyze the formation of double bonds by removing chemical groups from a substrate without hydrolysis or catalyze the addition of chemical groups to double bonds. It includes enzymes such as carbon-carbon lyase, carbon-oxygen lyase, carbon-nitrogen lyase, carbon-sulfur lyase, carbon-halide lyase, and phosphorus-oxygen lyase.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the double bonds formation catalyzed by these enzymes is impaired. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, autoimmune diseases [JAMA. 2003, 290(13):1721-8; JAMA. 2003, 290(13):1713-20], diabetes [Diabetes. 2003, 52(9):2274-8], neurological disorders such as epilepsy [J. Neurosci. 2003, 23(24):8471-9], Parkinson [J. Neurosci. 2003, 23(23):8302-9; Lancet. 2003,

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362(9385):712] or Creutzfeldt-Jakob disease [Clin. Neurophysiol. 2003, 114(9):1724-8], and cancerous diseases [J. Pathol. 2003, 201(1):37-45; J. Pathol. 2003, 201(1):37-45; Cancer Res. 2003, 63(16):4952-9; Eur. J. Cancer. 2003, 39(13):1899-903].

Actin binding proteins:

The phrase "actin binding proteins" refers to proteins binding actin as actin cross-linking, actin bundling, F-actin capping, actin monomer binding, actin lateral binding, actin depolymerizing, actin monomer sequestering, actin filament severing, actin modulating, membrane associated actin binding, actin thin filament length regulation, and actin polymerizing proteins.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which actin binding is impaired. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, neuromuscular diseases such as muscular dystrophy [Neurology. 2003, 61(3):404-6], Cancerous diseases [Urology. 2003, 61(4):845-50; J. Cutan. Pathol. 2002, 29(7):430; Cancer. 2002, 94(6):1777-86; Clin. Cancer Res. 2001, 7(8):2415-24; Breast Cancer Res. Treat. 2001, 65(1):11-21], renal diseases such as glomerulonephritis [J. Am. Soc. Nephrol. 2002, 13(2):322-31; Eur. J. Immunol. 2001, 31(4):1221-7], and gastrointestinal diseases such as Crohn's disease [J. Cell Physiol. 2000, 182(2):303-9].

Protein binding proteins:

The phrase "protein binding proteins" refers to proteins involved in diverse biological functions through binding other proteins. Examples of such biological function include intermediate filament binding, LIM-domain binding, LLR-domain binding, clathrin binding, ARF binding, vinculin binding, KU70 binding, troponin C binding PDZ-domain binding, SH3-domain binding, fibroblast growth factor binding, membrane-associated protein with guanylate kinase activity interacting, Wnt-protein binding, DEAD/H-box RNA helicase binding, β -amyloid binding, myosin binding, TATA-binding protein binding DNA topoisomerase I binding, polypeptide hormone

binding, RHO binding, FH1-domain binding, syntaxin-1 binding, HSC70-interacting, transcription factor binding, metarhodopsin binding, tubulin binding, JUN kinase binding, RAN protein binding, protein signal sequence binding, importin α export receptor, poly-glutamine tract binding, protein carrier, β -catenin binding, protein C-terminus binding, lipoprotein binding, cytoskeletal protein binding protein, nuclear localization sequence binding, protein phosphatase 1 binding, adenylate cyclase binding, eukaryotic initiation factor 4E binding, calmodulin binding, collagen binding, insulin-like growth factor binding, lamin binding, profilin binding, tropomyosin binding, actin binding, peroxisome targeting sequence binding, SNARE binding, and cyclin binding.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases which are associated with impaired protein binding. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, neurological and psychiatric diseases [J. Neurosci. 2003, 23(25):8788-99; Neurobiol. Dis. 2003, 14(1):146-56; J. Neurosci. 2003, 23(17):6956-64; Am. J. Pathol. 2003, 163(2):609-19], and cancerous diseases [Cancer Res. 2003, 63(15):4299-304; Semin. Thromb. Hemost. 2003, 29(3):247-58; Proc. Natl. Acad. Sci. U S A. 2003, 100(16):9506-11].

Ligand binding or carrier proteins:

The phrase "ligand binding or carrier proteins" refers to proteins involved in diverse biological functions such as: pyridoxal phosphate binding, carbohydrate binding, magnesium binding, amino acid binding, cyclosporin A binding, nickel binding, chlorophyll binding, biotin binding, penicillin binding, selenium binding, tocopherol binding, lipid binding, drug binding, oxygen transporter, electron transporter, steroid binding, juvenile hormone binding, retinoid binding, heavy metal binding, calcium binding, protein binding, glycosaminoglycan binding, folate binding, odorant binding, lipopolysaccharide binding and nucleotide binding.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases which are associated

with impaired function of these proteins. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, neurological disorders [J. Med. Genet. 2003, 40(10):733-40; J. Neuropathol. Exp. Neurol. 2003, 62(9):968-75; J. Neurochem. 2003, 87(2):427-36], autoimmune diseases (N. Engl. J. Med. 2003, 349(16):1526-33; JAMA. 2003, 290(13):1721-8]; gastroesophageal reflux disease [Dig. Dis. Sci. 2003, 48(9):1832-8], cardiovascular diseases [J. Vasc. Surg. 2003, 38(4):827-32], cancerous diseases [Oncogene. 2003, 22(43):6699-703; Br. J. Haematol. 2003, 123(2):288-96], respiratory diseases [Circulation. 2003, 108(15):1839-44], and ophtalmic diseases [Ophthalmology. 2003, 110(10):2040-4; Am. J. Ophthalmol. 2003, 136(4):729-32].

ATPases:

The term "ATPases" refers to enzymes that catalyze the hydrolysis of ATP to ADP, releasing energy that is used in the cell. This group include enzymes such as plasma membrane cation-transporting ATPase, ATP-binding cassette (ABC) transporter, magnesium-ATPase, hydrogen-/sodium-translocating ATPase or ATPase translocating any other elements, arsenite-transporting ATPase, protein-transporting ATPase, DNA translocase, P-type ATPase, and hydrolase, acting on acid anhydrides involved in cellular and subcellular movement.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases which are associated with impaired conversion of the hydrolysis of ATP to ADP or resulting energy use. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, infectious diseases such as *helicobacter pylori* ulcers [BMC Gastroenterol. 2003, Nov 6], Neurological, muscular and psychiatric diseases [Int. J. Neurosci. 2003, 13(12):1705-1717; Int. J. Neurosci. 2003, 113(11):1579-1591; Ann. Neurol. 2003, 54(4):494-500], Amyotrophic Lateral Sclerosis [Other Motor Neuron Disord. 2003 4(2):96-9], cardiovascular diseases [J. Nippon. Med. Sch. 2003, 70(5):384-92; Endocrinology.

2003, 144(10):4478-83], metabolic diseases [Mol. Pathol. 2003, 56(5):302-4; Neurosci. Lett. 2003, 350(2):105-8], and peptic ulcer disease treated with inhibitors of the gastric H⁺-K⁺ ATPase (e.g. Omeprazole) responsible for acid secretion in the gastric mucosa.

Carboxylic ester hydrolases:

The phrase "carboxylic ester hydrolases" refers to hydrolytic enzymes acting on carboxylic ester bonds such as N-acetylglucosaminylphosphatidylinositol deacetylase, 2-acetyl-1-alkylglycerophosphocholine esterase, aminoacyl-tRNA hydrolase, arylesterase, carboxylesterase, cholinesterase, gluconolactonase, sterol esterase, acylesterase, carboxymethylenebutenolidase, protein-glutamate methylesterase, lipase, and 6-phosphogluconolactonase.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the hydrolytic cleavage of a covalent bond with accompanying addition of water (-H being added to one product of the cleavage and -OH to the other) is abnormal so that a beneficial effect may be achieved by modulation of such reaction. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, autoimmune neuromuscular disease Myasthenia Gravis, treated with cholinesterase inhibitors.

Hydrolase, acting on ester bonds:

The phrase "hydrolase, acting on ester bonds" refers to hydrolytic enzymes acting on ester bonds such as nucleases, sulfuric ester hydrolase, carboxylic ester hydrolases, thiolester hydrolase, phosphoric monoester hydrolase, phosphoric diester hydrolase, triphosphoric monoester hydrolase, diphosphoric monoester hydrolase, and phosphoric triester hydrolase.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the hydrolytic cleavage of a covalent bond with accompanying addition of water (-H being added to one product of the cleavage and -OH to the other), is abnormal. Antibodies and

polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Hydrolases:

The term "hydrolases" refers to hydrolytic enzymes such as GPI-anchor transamidase, peptidases, hydrolases, acting on ester bonds, glycosyl bonds, ether bonds, carbon-nitrogen (but not peptide) bonds, acid anhydrides, acid carbon-carbon bonds, acid halide bonds, acid phosphorus-nitrogen bonds, acid sulfur-nitrogen bonds, acid carbon-phosphorus bonds, acid sulfur-sulfur bonds.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the hydrolytic cleavage of a covalent bond with accompanying addition of water (-H being added to one product of the cleavage and -OH to the other) is abnormal. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, cancerous diseases [Cancer. 2003, 98(9):1842-8; Cancer. 2003, 98(9):1822-9], neurological diseases such as Parkinson diseases [J. Neurol. 2003, 250 Suppl 3:III15-III24; J. Neurol. 2003, 250 Suppl 3:III2-III10], endocrinological diseases such as pancreatitis [Pancreas. 2003, 27(4):291-6] or childhood genetic diseases [Eur. J. Pediatr. 1997, 156(12):935-8], coagulation diseases [BMJ. 2003, 327(7421):974-7], cardiovascular diseases [Ann. Intern. Med. 2003, Oct 139(8):670-82], autoimmunity diseases [J. Med. Genet. 2003, 40(10):761-6], and metabolic diseases [Am. J. Hum. Genet. 2001, 69(5):1002-12].

Enzymes:

The term "enzymes" refers to naturally occurring or synthetic macromolecular substance composed mostly of protein, that catalyzes, to various degree of specificity, at least one (bio)chemical reactions at relatively low temperatures. The action of RNA that has catalytic activity (ribozyme) is often also regarded as enzymatic. Nevertheless, enzymes are mainly proteinaceous and are often easily inactivated by heating or by protein-denaturing agents. The substances upon which they act are known as substrates, for which the enzyme possesses a specific binding or active site.

The group of enzymes include various proteins possessing enzymatic activities such as mannosylphosphate transferase, para-hydroxybenzoate:polyprenyltransferase,

rieske iron-sulfur protein, imidazoleglycerol-phosphate synthase, sphingosine hydroxylase, tRNA 2'-phosphotransferase, sterol C-24(28) reductase, C-8 sterol isomerase, C-22 sterol desaturase, C-14 sterol reductase, C-3 sterol dehydrogenase (C-4 sterol decarboxylase), 3-keto sterol reductase, C-4 methyl sterol oxidase, dihydronicotinamide riboside quinone reductase, glutamate phosphate reductase, DNA repair enzyme, telomerase, α -ketoacid dehydrogenase, β -alanyl-dopamine synthase, RNA editase, aldo-keto reductase, alkylbase DNA glycosidase, glycogen debranching enzyme, dihydropterin deaminase, dihydropterin oxidase, dimethylnitrosamine demethylase, ecdysteroid UDP-glucosyl/UDP glucuronosyl transferase, glycine cleavage system, helicase, histone deacetylase, mevaldate reductase, monooxygenase, poly(ADP-ribose) glycohydrolase, pyruvate dehydrogenase, serine esterase, sterol carrier protein X-related thiolase, transposase, tyramine- β hydroxylase, para-aminobenzoic acid (PABA) synthase, glu-tRNA(gln) amidotransferase, molybdopterin cofactor sulfurase, lanosterol 14- α -demethylase, aromatase, 4-hydroxybenzoate octaprenyltransferase, 7,8-dihydro-8-oxoguanine-triphosphatase, CDP-alcohol phosphotransferase, 2,5-diamino-6-(ribosylamino)-4(3H)-pyrimidonone 5'-phosphate deaminase, diphosphoinositol polyphosphate phosphohydrolase, γ -glutamyl carboxylase, small protein conjugating enzyme, small protein activating enzyme, 1-deoxyxylulose-5-phosphate synthase, 2'-phosphotransferase, 2-octoprenyl-3-methyl-6-methoxy-1,4-benzoquinone hydroxylase, 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, 3,4 dihydroxy-2-butanone-4-phosphate synthase, 4-amino-4-deoxychorismate lyase, 4-diphosphocytidyl-2C-methyl-D-erythritol synthase, ADP-L-glycero-D-manno-heptose synthase, D-erythro-7,8-dihydronopterin triphosphate 2'-epimerase, N-ethylmaleimide reductase, O-antigen ligase, O-antigen polymerase, UDP-2,3-diacylglucosamine hydrolase, arsenate reductase, carnitine racemase, cobalamin [5'-phosphate] synthase, cobinamide phosphate guanylyltransferase, enterobactin synthetase, enterochelin esterase, enterochelin synthetase, glycolate oxidase, integrase, lauroyl transferase, peptidoglycan synthetase, phosphopantetheinyltransferase, phosphoglucosamine mutase, phosphoheptose isomerase, quinolinate synthase, siroheme synthase, N-acylmannosamine-6-phosphate 2-epimerase, N-acetyl-anhydromuramoyl-L-alanine amidase, carbon-phosphorous lyase, heme-copper terminal oxidase, disulfide oxidoreductase, phthalate dioxygenase reductase, sphingosine-1-phosphate lyase, molybdopterin oxidoreductase,

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dehydrogenase, NADPH oxidase, naringenin-chalcone synthase, N-ethylammeline chlorohydrolase, polyketide synthase, aldolase, kinase, phosphatase, CoA-ligase, oxidoreductase, transferase, hydrolase, lyase, isomerase, ligase, ATPase, sulphydryl oxidase, lipoate-protein ligase, δ -1-pyrroline-5-carboxylate synthetase, lipoic acid synthase, and tRNA dihydrouridine synthase.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases which can be ameliorated by modulating the activity of various enzymes which are involved both in enzymatic processes inside cells as well as in cell signaling. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Cytoskeletal proteins:

The term "cytoskeletal proteins" refers to proteins involved in the structure formation of the cytoskeleton.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases which are caused or due to abnormalities in cytoskeleton, including cancerous cells, and diseased cells such as cells that do not propagate, grow or function normally. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, liver diseases such as cholestatic diseases [Lancet. 2003, 362(9390):1112-9], vascular diseases [J. Cell Biol. 2003, 162(6):1111-22], endocrinological diseases [Cancer Res. 2003, 63(16):4836-41], neuromuscular disorders such as muscular dystrophy [Neuromuscul. Disord. 2003, 13(7-8):579-88], or myopathy [Neuromuscul. Disord. 2003, 13(6):456-67] neurological disorders such as Alzheimer's disease [J. Alzheimers Dis. 2003, 5(3):209-28], cardiac disorders [J. Am. Coll. Cardiol. 2003, 42(2):319-27], skin disorders [J. Am. Coll. Cardiol. 2003, 42(2):319-27], and cancer [Proteomics. 2003, 3(6):979-90].

Structural proteins:

The term "structural proteins" refers to proteins involved in the structure formation of the cell, such as structural proteins of ribosome, cell wall structural

proteins, structural proteins of cytoskeleton, extracellular matrix structural proteins, extracellular matrix glycoproteins, amyloid proteins, plasma proteins, structural proteins of eye lens, structural protein of chorion (*sensu Insecta*), structural protein of cuticle (*sensu Insecta*), puparial glue protein (*sensu Diptera*), structural proteins of bone, yolk proteins, structural proteins of muscle, structural protein of vitelline membrane (*sensu Insecta*), structural proteins of peritrophic membrane (*sensu Insecta*), and structural proteins of nuclear pores.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases which are caused by abnormalities in cytoskeleton, including cancerous cells, and diseased cells such as cells that do not propagate, grow or function normally. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, blood vessels diseases such as aneurysms [Cardiovasc. Res. 2003, 60(1):205-13], joint diseases [Rheum. Dis. Clin. North Am. 2003, 29(3):631-45], muscular diseases such as muscular dystrophies [Curr. Opin. Clin. Nutr. Metab. Care. 2003, 6(4):435-9], neuronal diseases such as encephalitis [Neurovirol. 2003, 9(2):274-83], retinitis pigmentosa [Dev. Ophthalmol. 2003, 37:109-25], and infectious diseases [J. Virol. Methods. 2003, 109(1):75-83; FEMS Immunol. Med. Microbiol. 2003, 35(2):125-30; J. Exp. Med. 2003, 197(5):633-42].

Ligands:

The term "ligands" refers to proteins that bind to another chemical entity to form a larger complex, involved in various biological processes, such as signal transduction, metabolism, growth and differentiation, etc. This group of proteins includes opioid peptides, baboon receptor ligand, branchless receptor ligand, breathless receptor ligand, ephrin, frizzled receptor ligand, frizzled-2 receptor ligand, heartless receptor ligand, Notch receptor ligand, patched receptor ligand, punt receptor ligand, Ror receptor ligand, saxophone receptor ligand, SE20 receptor ligand, sevenless receptor ligand, smooth receptor ligand, thickveins receptor ligand, Toll receptor ligand, Torso receptor ligand, death receptor ligand, scavenger receptor ligand, neuroligin, integrin ligand, hormones, pheromones, growth factors, and sulfonylurea receptor ligand.

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Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases involved in impaired hormone function or diseases which involve abnormal secretion of proteins which may be due to abnormal presence, absence or impaired normal response to normal levels of secreted proteins. Those secreted proteins include hormones, neurotransmitters, and various other proteins secreted by cells to the extracellular environment. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, analgesia inhibited by orphanin FQ/nociceptin [Shane R., et al., (2001) Brain Res., 907(1-2):109-16], stroke protected by estrogen [Alkayed N. J., et al., (2001) J. Neurosci., 21(19):7543-50], atherosclerosis associated with growth hormone deficiency [Elhadd T. A., et al., (2001) J. Clin. Endocrinol. Metab., 86(9):4223-32], diabetes inhibited by α -galactosylceramide [Hong S., et al., (2001) Nat. Med., 7(9):1052-6], and Huntington's disease associated with huntingtin deficiency [Rao D. S., et al., (2001) Mol. Cell Biol., 21(22):7796-806].

Signal transducer:

The term "signal transducers" refers to proteins such as activin inhibitors, receptor-associated proteins, α -2 macroglobulin receptors, morphogens, quorum sensing signal generators, quorum sensing response regulators, receptor signaling proteins, ligands, receptors, two-component sensor molecules, and two-component response regulators.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases in which the signal-transduction is impaired, either as a cause, or as a result of the disease. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, altered sexual dimorphism associated with signal transducer and activator of transcription 5b [Udy G. B., et al., (1997) Proc. Natl. Acad. Sci. U S A, 94(14):7239-44], multiple sclerosis associated with sgp130 deficiency [Padberg F., et al., (1999) J. Neuroimmunol., 99(2):218-23], intestinal inflammation associated with elevated signal transducer and

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activator of transcription 3 activity [Suzuki A., et al., (2001) J Exp Med, 193(4):471-81], carcinoid tumor inhibited by increased signal transducer and activators of transcription 1 and 2 [Zhou Y., et al.; (2001) Oncology, 60(4):330-8], and esophageal cancer associated with loss of EGF-STAT1 pathway [Watanabe G., et al., (2001) Cancer J., 7(2):132-9].

RNA polymerase II transcription factors:

The phrase "RNA polymerase II transcription factors" refers to proteins such as specific and non-specific RNA polymerase II transcription factors, enhancer binding, ligand-regulated transcription factor, and general RNA polymerase II transcription factors.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases involving impaired function of RNA polymerase II transcription factors. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, cardiac diseases [Cell Cycle. 2003, 2(2):99-104], xeroderma pigmentosum [Bioessays. 2001, 23(8):671-3; Biochim. Biophys. Acta. 1997, 1354(3):241-51], muscular atrophy [J. Cell Biol. 2001, 152(1):75-85], neurological diseases such as Alzheimer's disease [Front Biosci. 2000, 5:D244-57], cancerous diseases such as breast cancer [Biol. Chem. 1999, 380(2):117-28], and autoimmune disorders [Clin. Exp. Immunol. 1997, 109(3):488-94].

RNA binding proteins:

The phrase "RNA binding proteins" refers to RNA binding proteins involved in splicing and translation regulation such as tRNA binding proteins, RNA helicases, double-stranded RNA and single-stranded RNA binding proteins, mRNA binding proteins, snRNA cap binding proteins, 5S RNA and 7S RNA binding proteins, poly-pyrimidine tract binding proteins, snRNA binding proteins, and AU-specific RNA binding proteins.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases involving transcription and translation factors such as helicases, isomerase, histones and nucleases, diseases where there is impaired transcription, splicing, post-transcriptional processing, translation

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or stability of the RNA. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, cancerous diseases such as lymphomas [Tumori. 2003, 89(3):278-84], prostate cancer [Prostate. 2003, 57(1):80-92] or lung cancer [J. Pathol. 2003, 200(5):640-6], blood diseases, such as fanconi anemia [Curr. Hematol. Rep. 2003, 2(4):335-40], cardiovascular diseases such as atherosclerosis [J. Thromb. Haemost. 2003, 1(7):1381-90] muscle diseases [Trends Cardiovasc. Med. 2003, 13(5):188-95] and brain and neuronal diseases [Trends Cardiovasc. Med. 2003, 13(5):188-95; Neurosci. Lett. 2003, 342(1-2):41-4].

Nucleic acid binding proteins:

The phrase "nucleic acid binding proteins" refers to proteins involved in RNA and DNA synthesis and expression regulation such as transcription factors, RNA and DNA binding proteins, zinc fingers, helicase, isomerase, histones, nucleases, ribonucleoproteins, and transcription and translation factors.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases involving DNA or RNA binding proteins such as: helicases, isomerases, histones and nucleases, for example diseases where there is abnormal replication or transcription of DNA and RNA respectively. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such diseases include, but are not limited to, neurological diseases such as reinitis pigmentoas [Am. J. Ophthalmol. 2003, 136(4):678-87] parkinsonism [Proc. Natl. Acad. Sci. U.S.A. 2003, 100(18):10347-52], Alzheimer [J. Neurosci. 2003, 23(17):6914-27] and canavan diseases [Brain Res Bull. 2003, 61(4):427-35], cancerous diseases such as leukemia [Anticancer Res. 2003, 23(4):3419-26] or lung cancer [J. Pathol. 2003, 200(5):640-6], miopathy [Neuromuscul Disord. 2003, 13(7-8):559-67] and liver diseases [J. Pathol. 2003, 200(5):553-60].

Proteins involved in Metabolism:

The phrase "proteins involved in metabolism" refers to proteins involved in the totality of the chemical reactions and physical changes that occur in living organisms,

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comprising anabolism and catabolism; may be qualified to mean the chemical reactions and physical processes undergone by a particular substance, or class of substances, in a living organism. This group includes proteins involved in the reactions of cell growth and maintenance such as: metabolism resulting in cell growth, carbohydrate metabolism, energy pathways, electron transport, nucleobase, nucleoside, nucleotide and nucleic acid metabolism, protein metabolism and modification, amino acid and derivative metabolism, protein targeting, lipid metabolism, aromatic compound metabolism, one-carbon compound metabolism, coenzymes and prosthetic group metabolism, sulfur metabolism, phosphorus metabolism, phosphate metabolism, oxygen and radical metabolism, xenobiotic metabolism, nitrogen metabolism, fat body metabolism (*sensu Insecta*), protein localization, catabolism, biosynthesis, toxin metabolism, methylglyoxal metabolism, cyanate metabolism, glycolate metabolism, carbon utilization and antibiotic metabolism.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat diseases involving cell metabolism. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases.

Examples of such metabolism-related diseases include, but are not limited to, multisystem mitochondrial disorder caused by mitochondrial DNA cytochrome C oxidase II deficiency [Campos Y., et al., (2001) Ann. Neurol. 50(3):409-13], conduction defects and ventricular dysfunction in the heart associated with heterogeneous connexin43 expression [Gutstein D. E., et al., (2001) Circulation, 104(10):1194-9], atherosclerosis associated with growth suppressor p27 deficiency [Diez-Juan A., and Andres V. (2001) FASEB J., 15(11):1989-95], colitis associated with glutathione peroxidase deficiency [Esworthy R. S., et al., (2001) Am. J. Physiol. Gastrointest. Liver Physiol., 281(3):G848-55], systemic lupus erythematosus associated with deoxyribonuclease I deficiency [Yasutomo K., et al., (2001) Nat. Genet., 28(4):313-4], alcoholic pancreatitis [Pancreas. 2003, 27(4):281-5], amyloidosis and diseases that are related to amyloid metabolism, such as FMF, atherosclerosis, diabetes, and especially diabetes long term consequences, neurological

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diseases such as Creutzfeldt-Jakob disease, and Parkinson or Rasmussen's encephalitis.

Cell growth and/or maintenance proteins:

The phrase "Cell growth and/or maintenance proteins" refers to proteins involved in any biological process required for cell survival, growth and maintenance, including proteins involved in biological processes such as cell organization and biogenesis, cell growth, cell proliferation, metabolism, cell cycle, budding, cell shape and cell size control, sporulation (*sensu Saccharomyces*), transport, ion homeostasis, autophagy, cell motility, chemi-mechanical coupling, membrane fusion, cell-cell fusion, and stress response.

Pharmaceutical compositions including such proteins or protein encoding sequences, antibodies directed against such proteins or polynucleotides capable of altering expression of such proteins, may be used to treat or prevent diseases such as cancer, degenerative diseases, for example neurodegenerative diseases or conditions associated with aging, or alternatively, diseases wherein apoptosis which should have taken place, does not take place. Antibodies and polynucleotides such as PCR primers and molecular probes designed to identify such proteins or protein encoding sequences may be used for diagnosis of such diseases, detection of pre-disposition to a disease, and determination of the stage of a disease.

Examples of such diseases include, but are not limited to, ataxia-telangiectasia associated with ataxia-telangiectasia mutated deficiency [Hande et al., (2001) Hum. Mol. Genet., 10(5):519-28], osteoporosis associated with osteonectin deficiency [Delany et al., (2000) J. Clin. Invest., 105(7):915-23], arthritis caused by membrane-bound matrix metalloproteinase deficiency [Holmbeck et al., (1999) Cell, 99(1):81-92], defective stratum corneum and early neonatal death associated with transglutaminase 1 deficiency [Matsuki et al., (1998) Proc. Natl. Acad. Sci. U S A, 95(3):1044-9], and Alzheimer's disease associated with estrogen [Simpkins et al., (1997) Am. J. Med., 103(3A):19S-25S].

Chaperones

Information derived from proteins such as ribosomal chaperone, peptidylprolyl isomerase, lectin-binding chaperone, nucleosome assembly chaperone, chaperonin ATPase, cochaperone, heat shock protein, HSP70/HSP90 organizing protein, fimbrial chaperone, metallochaperone, tubulin folding, HSC70-interacting protein can be used

to diagnose/treat diseases involving pathological conditions, which are associated with non-normal protein activity or structure. Binding of the products of the proteins of this family, or antibodies reactive therewith, can modulate a plurality of protein activities as well as change protein structure. Alternatively, diseases in which there is abnormal degradation of other proteins, which may cause non-normal accumulation of various proteinaceous products in cells, caused non- normal (prolonged or shortened) activity of proteins, etc.

Example of diseases that involve chaperones are cancerous diseases, such as prostate cancer (Semin Oncol. 2003 Oct;30(5):709-16.); infectious diseases, such as prion infection (EMBO J. 2003 Oct 15;22(20):5435-5445.); neurological syndromes (J Neuropathol Exp Neurol. 2003 Jul;62(7):751-64.; Antioxid Redox Signal. 2003 Jun;5(3):337-48.; J Neurochem. 2003 Jul;86(2):394-404.)

Variants of proteins which accumulate an element/compound

Variant proteins which their wild type version naturally binds a certain compound or element inside the cell for storage or accumulation may have therapeutic effect as secreted variants. Ferritin, accumulates iron inside the cells. A secreted variant of this protein is expected to bind plasma iron, reduce its levels and therefore have a desired therapeutic effect in the syndrome of Hemosiderosis characterized by high levels of iron in the blood.

Diseases that may be treated/diagnosed using the biomolecular sequences of the present invention

Inflammatory diseases

Examples of inflammatory diseases include, but are not limited to, chronic inflammatory diseases and acute inflammatory diseases.

Inflammatory diseases associated with hypersensitivity

Examples of hypersensitivity include, but are not limited to, Types I-IV hypersensitivity, immediate hypersensitivity, antibody mediated hypersensitivity, immune complex mediated hypersensitivity, T lymphocyte mediated hypersensitivity and DTH. An example of type I or immediate hypersensitivity is asthma. Examples of type II hypersensitivity include, but are not limited to, rheumatoid diseases, rheumatoid autoimmune diseases, rheumatoid arthritis [Krenn V. et al., Histol Histopathol 2000 Jul;15 (3):791], spondylitis, ankylosing spondylitis [Jan Voswinkel et al., Arthritis Res 2001; 3 (3): 189], systemic diseases, systemic autoimmune

diseases, systemic lupus erythematosus [Erikson J. *et al.*, Immunol Res 1998;17 (1-2):49], sclerosis, systemic sclerosis [Renaudineau Y. *et al.*, Clin Diagn Lab Immunol. 1999 Mar;6 (2):156; Chan OT. *et al.*, Immunol Rev 1999 Jun;169:107], glandular diseases, glandular autoimmune diseases, pancreatic autoimmune diseases, diabetes, Type I diabetes [Zimmet P. Diabetes Res Clin Pract 1996 Oct;34 Suppl:S125], thyroid diseases, autoimmune thyroid diseases, Graves' disease [Orgiazzi J. Endocrinol Metab Clin North Am 2000 Jun;29 (2):339], thyroiditis, spontaneous autoimmune thyroiditis [Braley-Mullen H. and Yu S, J Immunol 2000 Dec 15;165 (12):7262], Hashimoto's thyroiditis [Toyoda N. *et al.*, Nippon Rinsho 1999 Aug;57 (8):1810], myxedema, idiopathic myxedema [Mitsuma T. Nippon Rinsho. 1999 Aug;57 (8):1759], autoimmune reproductive diseases, ovarian diseases, ovarian autoimmunity [Garza KM. *et al.*, J Reprod Immunol 1998 Feb;37 (2):87], autoimmune anti-sperm infertility [Diekman AB. *et al.*, Am J Reprod Immunol. 2000 Mar;43 (3):134], repeated fetal loss [Tincani A. *et al.*, Lupus 1998;7 Suppl 2:S107-9], neurodegenerative diseases, neurological diseases, neurological autoimmune diseases, multiple sclerosis [Cross AH. *et al.*, J Neuroimmunol 2001 Jan 1;112 (1-2):1], Alzheimer's disease [Oron L. *et al.*, J Neural Transm Suppl. 1997;49:77], myasthenia gravis [Infante AJ. and Kraig E, Int Rev Immunol 1999;18 (1-2):83], motor neuropathies [Kornberg AJ. J Clin Neurosci. 2000 May;7 (3):191], Guillain-Barre syndrome, neuropathies and autoimmune neuropathies [Kusunoki S. Am J Med Sci. 2000 Apr;319 (4):234], myasthenic diseases, Lambert-Eaton myasthenic syndrome [Takamori M. Am J Med Sci. 2000 Apr;319 (4):204], paraneoplastic neurological diseases, cerebellar atrophy, paraneoplastic cerebellar atrophy, non-paraneoplastic stiff man syndrome, cerebellar atrophies, progressive cerebellar atrophies, encephalitis, Rasmussen's encephalitis, amyotrophic lateral sclerosis, Sydenham chorea, Gilles de la Tourette syndrome, polyendocrinopathies, autoimmune polyendocrinopathies [Antoine JC. and Honnorat J. Rev Neurol (Paris) 2000 Jan;156 (1):23], neuropathies, dysimmune neuropathies [Nobile-Orazio E. *et al.*, Electroencephalogr Clin Neurophysiol Suppl 1999;50:419], neuromyotonia, acquired neuromyotonia, arthrogryposis multiplex congenita [Vincent A. *et al.*, Ann N Y Acad Sci. 1998 May 13;841:482], cardiovascular diseases, cardiovascular autoimmune diseases, atherosclerosis [Matsuura E. *et al.*, Lupus. 1998;7 Suppl 2:S135], myocardial infarction [Vaarala O. Lupus. 1998;7 Suppl 2:S132], thrombosis [Tincani

A. *et al.*, Lupus 1998;7 Suppl 2:S107-9], granulomatosis, Wegener's granulomatosis, arteritis, Takayasu's arteritis and Kawasaki syndrome [Praprotnik S. *et al.*, Wien Klin Wochenschr 2000 Aug 25;112 (15-16):660], anti-factor VIII autoimmune disease [Lacroix-Desmazes S. *et al.*, Semin Thromb Hemost 2000;26 (2):157], vasculitises, necrotizing small vessel vasculitises, microscopic polyangiitis, Churg and Strauss syndrome, glomerulonephritis, pauci-immune focal necrotizing glomerulonephritis, crescentic glomerulonephritis [Noel LH. Ann Med Interne (Paris). 2000 May;151 (3):178], antiphospholipid syndrome [Flamholz R. *et al.*, J Clin Apheresis 1999;14 (4):171], heart failure, agonist-like β -adrenoceptor antibodies in heart failure [Wallukat G. *et al.*, Am J Cardiol. 1999 Jun 17;83 (12A):75H], thrombocytopenic purpura [Moccia F. Ann Ital Med Int. 1999 Apr-Jun;14 (2):114], hemolytic anemia, autoimmune hemolytic anemia [Efremov DG. *et al.*, Leuk Lymphoma 1998 Jan;28 (3-4):285], gastrointestinal diseases, autoimmune diseases of the gastrointestinal tract, intestinal diseases, chronic inflammatory intestinal disease [Garcia Herola A. *et al.*, Gastroenterol Hepatol. 2000 Jan;23 (1):16], celiac disease [Landau YE. and Shoenfeld Y. Harefuah 2000 Jan 16;138 (2):122], autoimmune diseases of the musculature, myositis, autoimmune myositis, Sjogren's syndrome [Feist E. *et al.*, Int Arch Allergy Immunol 2000 Sep;123 (1):92], smooth muscle autoimmune disease [Zauli D. *et al.*, Biomed Pharmacother 1999 Jun;53 (5-6):234], hepatic diseases, hepatic autoimmune diseases, autoimmune hepatitis [Manns MP. J Hepatol 2000 Aug;33 (2):326] and primary biliary cirrhosis [Strassburg CP. *et al.*, Eur J Gastroenterol Hepatol. 1999 Jun;11 (6):595].

Examples of type IV or T cell mediated hypersensitivity, include, but are not limited to, rheumatoid diseases, rheumatoid arthritis [Tisch R, McDevitt HO. Proc Natl Acad Sci U S A 1994 Jan 18;91 (2):437], systemic diseases, systemic autoimmune diseases, systemic lupus erythematosus [Datta SK., Lupus 1998;7 (9):591], glandular diseases, glandular autoimmune diseases, pancreatic diseases, pancreatic autoimmune diseases, Type 1 diabetes [Castano L. and Eisenbarth GS. Ann. Rev. Immunol. 8:647], thyroid diseases, autoimmune thyroid diseases, Graves' disease [Sakata S. *et al.*, Mol Cell Endocrinol 1993 Mar;92 (1):77], ovarian diseases [Garza KM. *et al.*, J Reprod Immunol 1998 Feb;37 (2):87], prostatitis, autoimmune prostatitis [Alexander RB. *et al.*, Urology 1997 Dec;50 (6):893], polyglandular syndrome, autoimmune polyglandular syndrome, Type I autoimmune polyglandular

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syndrome [Hara T. *et al.*, Blood. 1991 Mar 1;77 (5):1127], neurological diseases, autoimmune neurological diseases, multiple sclerosis, neuritis, optic neuritis [Soderstrom M. *et al.*, J Neurol Neurosurg Psychiatry 1994 May;57 (5):544], myasthenia gravis [Oshima M. *et al.*, Eur J Immunol 1990 Dec;20 (12):2563], stiff-man syndrome [Hiemstra HS. *et al.*, Proc Natl Acad Sci U S A 2001 Mar 27;98 (7):3988], cardiovascular diseases, cardiac autoimmunity in Chagas' disease [Cunha-Neto E. *et al.*, J Clin Invest 1996 Oct 15;98 (8):1709], autoimmune thrombocytopenic purpura [Semple JW. *et al.*, Blood 1996 May 15;87 (10):4245], anti-helper T lymphocyte autoimmunity [Caporossi AP. *et al.*, Viral Immunol 1998;11 (1):9], hemolytic anemia [Sallah S. *et al.*, Ann Hematol 1997 Mar;74 (3):139], hepatic diseases, hepatic autoimmune diseases, hepatitis, chronic active hepatitis [Franco A. *et al.*, Clin Immunol Immunopathol 1990 Mar;54 (3):382], biliary cirrhosis, primary biliary cirrhosis [Jones DE. Clin Sci (Colch) 1996 Nov;91 (5):551], nephric diseases, nephric autoimmune diseases, nephritis, interstitial nephritis [Kelly CJ. J Am Soc Nephrol 1990 Aug;1 (2):140], connective tissue diseases, ear diseases, autoimmune connective tissue diseases, autoimmune ear disease [Yoo TJ. *et al.*, Cell Immunol 1994 Aug;157 (1):249], disease of the inner ear [Gloddek B. *et al.*, Ann N Y Acad Sci 1997 Dec 29;830:266], skin diseases, cutaneous diseases, dermal diseases, bullous skin diseases, pemphigus vulgaris, bullous pemphigoid and pemphigus foliaceus.

Examples of delayed type hypersensitivity include, but are not limited to, contact dermatitis and drug eruption.

Autoimmune diseases

Examples of autoimmune diseases include, but are not limited to, cardiovascular diseases, rheumatoid diseases, glandular diseases, gastrointestinal diseases, cutaneous diseases, hepatic diseases, neurological diseases, muscular diseases, nephric diseases, diseases related to reproduction, connective tissue diseases and systemic diseases.

Examples of autoimmune cardiovascular and blood diseases include, but are not limited to, atherosclerosis [Matsuura E. *et al.*, Lupus. 1998;7 Suppl 2:S135], myocardial infarction [Vaarala O. Lupus. 1998;7 Suppl 2:S132], thrombosis [Tincani A. *et al.*, Lupus 1998;7 Suppl 2:S107-9], Wegener's granulomatosis, Takayasu's arteritis, Kawasaki syndrome [Praprotnik S. *et al.*, Wien Klin Wochenschr 2000 Aug 25;112 (15-16):660], anti-factor VIII autoimmune disease [Lacroix-Desmazes S. *et*

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al., Semin Thromb Hemost 2000;26 (2):157], necrotizing small vessel vasculitis, microscopic polyangiitis, Churg and Strauss syndrome, pauci-immune focal necrotizing and crescentic glomerulonephritis [Noel LH. Ann Med Interne (Paris). 2000 May;151 (3):178], antiphospholipid syndrome [Flamholz R. et al., J Clin Apheresis 1999;14 (4):171], antibody-induced heart failure [Wallukat G. et al., Am J Cardiol. 1999 Jun 17;83 (12A):75H], thrombocytopenic purpura [Moccia F. Ann Ital Med Int. 1999 Apr-Jun;14 (2):114; Semple JW. et al., Blood 1996 May 15;87 (10):4245], autoimmune hemolytic anemia [Efremov DG. et al., Leuk Lymphoma 1998 Jan;28 (3-4):285; Sallah S. et al., Ann Hematol 1997 Mar;74 (3):139], cardiac autoimmunity in Chagas' disease [Cunha-Neto E. et al.; J Clin Invest 1996 Oct 15;98 (8):1709] and anti-helper T lymphocyte autoimmunity [Caporossi AP. et al., Viral Immunol 1998;11 (1):9].

Examples of autoimmune rheumatoid diseases include, but are not limited to rheumatoid arthritis [Krenn V. et al., Histol Histopathol 2000 Jul;15 (3):791; Tisch R, McDevitt HO. Proc Natl Acad Sci units S A 1994 Jan 18;91 (2):437) and ankylosing spondylitis [Jan Voswinkel et al., Arthritis Res 2001; 3 (3): 189].

Examples of autoimmune glandular diseases include, but are not limited to, pancreatic disease, Type I diabetes, Type II diabetes, thyroid disease, Graves' disease, thyroiditis, spontaneous autoimmune thyroiditis, Hashimoto's thyroiditis, idiopathic myxedema, ovarian autoimmunity, autoimmune anti-sperm infertility, autoimmune prostatitis and Type I autoimmune polyglandular syndrome. diseases include, but are not limited to autoimmune diseases of the pancreas, Type 1 diabetes [Castano L. and Eisenbarth GS. Ann. Rev. Immunol. 8:647; Zimmet P. Diabetes Res Clin Pract 1996 Oct;34 Suppl:S125], autoimmune thyroid diseases, Graves' disease [Orgiazzi J. Endocrinol Metab Clin North Am 2000 Jun;29 (2):339; Sakata S. et al., Mol Cell Endocrinol 1993 Mar;92 (1):77], spontaneous autoimmune thyroiditis [Braley-Mullen H. and Yu S, J Immunol 2000 Dec 15;165 (12):7262], Hashimoto's thyroiditis [Toyoda N. et al., Nippon Rinsho 1999 Aug;57 (8):1810], idiopathic myxedema [Mitsuma T. Nippon Rinsho. 1999 Aug;57 (8):1759], ovarian autoimmunity [Garza KM. et al., J Reprod Immunol 1998 Feb;37 (2):87], autoimmune anti-sperm infertility [Diekman AB. et al., Am J Reprod Immunol. 2000 Mar;43 (3):134], autoimmune prostatitis [Alexander RB. et al., Urology 1997 Dec;50 (6):893] and Type I autoimmune polyglandular syndrome [Hara T. et al., Blood. 1991 Mar 1;77 (5):1127].

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Examples of autoimmune gastrointestinal diseases include, but are not limited to, chronic inflammatory intestinal diseases [Garcia Herola A. *et al.*, Gastroenterol Hepatol. 2000 Jan;23 (1):16], celiac disease [Landau YE. and Shoenfeld Y. Harefuah 2000 Jan 16;138 (2):122], colitis, ileitis and Crohn's disease and ulcerative colitis.

Examples of autoimmune cutaneous diseases include, but are not limited to, autoimmune bullous skin diseases, such as, but are not limited to, pemphigus vulgaris, bullous pemphigoid and pemphigus foliaceus.

Examples of autoimmune hepatic diseases include, but are not limited to, hepatitis, autoimmune chronic active hepatitis [Franco A. *et al.*, Clin Immunol Immunopathol 1990 Mar;54 (3):382], primary biliary cirrhosis [Jones DE. Clin Sci (Colch) 1996 Nov;91 (5):551; Strassburg CP. *et al.*, Eur J Gastroenterol Hepatol. 1999 Jun;11 (6):595] and autoimmune hepatitis [Manns MP. J Hepatol 2000 Aug;33 (2):326].

Examples of autoimmune neurological diseases include, but are not limited to, multiple sclerosis [Cross AH. *et al.*, J Neuroimmunol 2001 Jan 1;112 (1-2):1], Alzheimer's disease [Oron L. *et al.*, J Neural Transm Suppl. 1997;49:77], myasthenia gravis [Infante AJ. and Kraig E, Int Rev Immunol 1999;18 (1-2):83; Oshima M. *et al.*, Eur J Immunol 1990 Dec;20 (12):2563], neuropathies, motor neuropathies [Kornberg AJ. J Clin Neurosci. 2000 May;7 (3):191], Guillain-Barre syndrome and autoimmune neuropathies [Kusunoki S. Am J Med Sci. 2000 Apr;319 (4):234], myasthenia, Lambert-Eaton myasthenic syndrome [Takamori M. Am J Med Sci. 2000 Apr;319 (4):204], paraneoplastic neurological diseases, cerebellar atrophy, paraneoplastic cerebellar atrophy and stiff-man syndrome [Hiemstra HS. *et al.*, Proc Natl Acad Sci units S A 2001 Mar 27;98 (7):3988], non-paraneoplastic stiff man syndrome, progressive cerebellar atrophies, encephalitis, Rasmussen's encephalitis, amyotrophic lateral sclerosis, Sydenham chorea, Gilles de la Tourette syndrome and autoimmune polyendocrinopathies [Antoine JC. and Honnorat J. Rev Neurol (Paris) 2000 Jan;156 (1):23], dysimmune neuropathies [Nobile-Orazio E. *et al.*, Electroencephalogr Clin Neurophysiol Suppl 1999;50:419], acquired neuromyotonia, arthrogryposis multiplex congenita [Vincent A. *et al.*, Ann N Y Acad Sci. 1998 May 13;841:482], neuritis, optic neuritis [Soderstrom M. *et al.*, J Neurol Neurosurg Psychiatry 1994 May;57 (5):544] multiple sclerosis and neurodegenerative diseases.

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Examples of autoimmune muscular diseases include, but are not limited to, myositis, autoimmune myositis and primary Sjogren's syndrome [Feist E. *et al.*, Int Arch Allergy Immunol 2000 Sep;123 (1):92] and smooth muscle autoimmune disease [Zauli D. *et al.*, Biomed Pharmacother 1999 Jun;53 (5-6):234].

Examples of autoimmune nephric diseases include, but are not limited to, nephritis and autoimmune interstitial nephritis [Kelly CJ. J Am Soc Nephrol 1990 Aug;1 (2):140], glomerular nephritis.

Examples of autoimmune diseases related to reproduction include, but are not limited to, repeated fetal loss [Tincani A. *et al.*, Lupus 1998;7 Suppl 2:S107-9].

Examples of autoimmune connective tissue diseases include, but are not limited to, ear diseases, autoimmune ear diseases [Yoo TJ. *et al.*, Cell Immunol 1994 Aug;157 (1):249] and autoimmune diseases of the inner ear [Gloddek B. *et al.*, Ann N Y Acad Sci 1997 Dec 29;830:266].

Examples of autoimmune systemic diseases include, but are not limited to, systemic lupus erythematosus [Erikson J. *et al.*, Immunol Res 1998;17 (1-2):49] and systemic sclerosis [Renaudineau Y. *et al.*, Clin Diagn Lab Immunol. 1999 Mar;6 (2):156; Chan OT. *et al.*, Immunol Rev 1999 Jun;169:107].

Infectious diseases

Examples of infectious diseases include, but are not limited to, chronic infectious diseases, subacute infectious diseases, acute infectious diseases, viral diseases, bacterial diseases, protozoan diseases, parasitic diseases, fungal diseases, mycoplasma diseases, and prion diseases.

Graft rejection diseases

Examples of diseases associated with transplantation of a graft include, but are not limited to, graft rejection, chronic graft rejection, subacute graft rejection, hyperacute graft rejection, acute graft rejection, and graft versus host disease.

Allergic diseases

Examples of allergic diseases include, but are not limited to, asthma, hives, urticaria, pollen allergy, dust mite allergy, venom allergy, cosmetics allergy, latex allergy, chemical allergy, drug allergy, insect bite allergy, animal dander allergy, stinging plant allergy, poison ivy allergy and food allergy.

Cancerous diseases

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Examples of cancer include but are not limited to carcinoma, lymphoma, blastoma, sarcoma, and leukemia. Particular examples of cancerous diseases but are not limited to: Myeloid leukemia such as Chronic myelogenous leukemia. Acute myelogenous leukemia with maturation. Acute promyelocytic leukemia, Acute nonlymphocytic leukemia with increased basophils, Acute monocytic leukemia. Acute myelomonocytic leukemia with eosinophilia; malignant lymphoma, such as Birkitt's Non-Hodgkin's; Lymphocytic leukemia, such as acute lymphoblastic leukemia. Chronic lymphocytic leukemia; Myeloproliferative diseases, such as Solid tumors Benign Meningioma, Mixed tumors of salivary gland, Colonic adenomas; Adenocarcinomas, such as Small cell lung cancer, Kidney, Uterus, Prostate, Bladder, Ovary, Colon, Sarcomas, Liposarcoma, myxoid, Synovial sarcoma, Rhabdomyosarcoma (alveolar), Extraskeletal myxoid chondrosarcoma, Ewing's tumor; other include Testicular and ovarian dysgerminoma, Retinoblastoma, Wilms' tumor, Neuroblastoma, Malignant melanoma, Mesothelioma, breast, skin, prostate, and ovarian.

EXAMPLE 8

Data files supporting designation of alternative exons

File DataOnExons.txt - contains the summary of all details according to which the exon was declared as alternative. Each line in this file begins with the name of the exon, and thereafter contains the following fields:

1. #MOUSE_EXON – the name of the orthologous matching mouse exon. File mouse_exons.fasta contains the sequences of the mouse exons that correspond to the human exons (matching to the #MOUSE_EXON field in file DataOnExons.txt file).
 - #ST strand of this exon on the DNA
 - #EXON_LEN length of exon
 - #EXON_DIVIDABLE_BY_3 – is the exon divisible by 3 (1=yes, 0=no)
 - #EXON_ALN_LEN – length of human/mouse local exon alignment
 - #EXON_ALN_IDN – identity level in human/mouse local exon alignment

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- #UPSTREAM_ALN_LEN – length of human/mouse local alignment of upstream intronic sequences
- #UPSTREAM_ALN_IDN – identity level of human/mouse local alignment of upstream intronic sequences
- #DOWNSTREAM_ALN_LEN – length of human/mouse local alignment of downstream intronic sequences
- #DOWNSTREAM_ALN_IDN – identity level of human/mouse local alignment of downstream intronic sequences
- #EXON_GLOBAL_ALN_LEN – length of human/mouse global exon alignment
- #EXON_GLOBAL_ALN_IDN – identity level in human/mouse global exon alignment
- #PERC_CONST – percent of constitutive exons in training set that correspond to these combination of features
- #PERC_ALT – percent of alternative exons in training set that correspond to these combination of features
- #SCORE – alternativeness score, calculated as described in the text

EXAMPLE 9

Description of CD-ROM3

Enclosed CD-ROM3 contains the following files:

1. “CROG_localization_1”, containing protein cellular localization information.
2. “crog_proteins_ipr_report_1_dos”, containing information related to Interpro analysis of domains.
3. “CROG_expression_x”, wherein “x” may be 1 or 2, containing information related to expression of transcripts according to oligonucleotide data.
4. “oligo probs abbreviations for patent”, containing the information about abbreviations of tissue names for oligonucleotide probe binding.

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5. "crog_report_x_1", wherein "x" may be from 1 to 45, containing comparison reports between known protein sequences and variant protein sequences according to the present invention, including identifying unique regions therein.

6. "variants_report.txt", containing the information about the different variants of the known protein sequences (for example, due to known amino acid changes because of an SNP).

All tables are best viewed by using a text editor with the "word wrap" function disabled (to preserve line integrity) and in a fixed width font, such as Courier for example, preferably in font size 10. Table spacing is described for each table as a guide to assist in reading the tables.

With regard to protein cellular localization information, table structure is as follows: column 1 features the protein identifier as used throughout the application to identify this sequence; column 2 features the name of the protein; column 3 shows localization (which may be intracellular, membranal or secreted); and column 4 gives the reason for this localization in terms of results from particular software programs that were used to determine localization. Spacing for this table is as follows: column 1: characters 1-9; column 2: characters 10-45; column 3: 46-61; and column 4: characters 62-121.

Information given in the text with regard to cellular localization was determined according to four different software programs: (i) tmhmm (from Center for Biological Sequence Analysis, Technical University of Denmark DTU, <http://www.cbs.dtu.dk/services/TMHMM/TMHMM2.0b.guide.php>) or (ii) tmpred (from EMBnet, maintained by the ISREC Bioinformatics group and the LICR Information Technology Office, Ludwig Institute for Cancer Research, Swiss Institute of Bioinformatics, http://www.ch.embnet.org/software/TMPRED_form.html) for transmembrane region prediction; (iii) signalp_hmm or (iv) signalp_nn (both from Center for Biological Sequence Analysis, Technical University of Denmark DTU, <http://www.cbs.dtu.dk/services/SignalP/background/prediction.php>) for signal peptide prediction. The terms "signalp_hmm" and "signalp_nn" refer to two modes of operation for the program SignalP: hmm refers to Hidden Markov Model, while nn refers to neural networks. Localization was also determined through manual inspection of known protein localization and/or gene structure, and the use of

heuristics by the individual inventor. In some cases for the manual inspection of cellular localization prediction inventors used the ProLoc computational platform [Einat Hazkani-Covo, Erez Levanon, Galit Rotman, Dan Graur and Amit Novik; (2004) "Evolution of multicellularity in metazoa: comparative analysis of the subcellular localization of proteins in *Saccharomyces*, *Drosophila* and *Caenorhabditis*." Cell Biology International 2004;28(3):171-8.], which predicts protein localization based on various parameters including, protein domains (e.g., prediction of trans-membranous regions and localization thereof within the protein), pI, protein length, amino acid composition, homology to pre-annotated proteins, recognition of sequence patterns which direct the protein to a certain organelle (such as, nuclear localization signal, NLS, mitochondria localization signal), signal peptide and anchor modeling and using unique domains from Pfam that are specific to a single compartment.

With regard to Interpro analysis of domains, table structure is as follows: column 1 features the protein identifier as used throughout the application to identify this sequence; column 2 features the name of the protein; column 3 features the Intepro identifier; column 4 features the analysis type; column 5 features the domain description; and column 6 features the position(s) of the amino acid residues that are relevant to this domain on the protein (amino acid sequence). Spacing for this table is as follows: column 1: characters 1-8; column 2: characters 9-48; column 3: 49-72; column 4: characters 73-96; column 5: characters 97-136; and column 6: 137-168.

Interpro provides information with regard to the analysis of amino acid sequences to identify domains having certain functionality (see Mulder et al (2003), The InterPro Database, 2003 brings increased coverage and new features, Nucleic Acids Res. 31, 315-318 for a reference). It features a database of protein families, domains and functional sites in which identifiable features found in known proteins can be applied to unknown protein sequences. The analysis type relates to the type of software used to determine the domain: Pfam (see Bateman A, et al (2004) The Pfam protein families database. Nucleic Acids Res. 32, 138-41), SMART (see Letunic I, et al (2004) SMART 4.0: towards genomic data integration. Nucleic Acids Res. 32, 142-4), TIGRFAMs (see Haft DH, et al (2003) The TIGRFAMs database of protein families. Nucleic Acids Res. 31, 371-373), PIRSF (see Wu CH et al (2003) The Protein Information Resource. Nucleic Acids Res. 31, 345-347), and

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SUPERFAMILY (see Gough J et al (2001) Assignment of homology to genome sequences using a library of Hidden Markov Models that represent all proteins of known structure. Journal Molecular Biol. 313, 903-919) all use hidden Markov models (HMMs) to determine the location of domains on protein sequences.

With regard to transcript expression information, table structure is as follows: column 1 features the transcript identifier as used throughout the application to identify this sequence; column 2 features the name of the transcript; column 3 features the name of the probeset used in the chip experiment; and column 4 relates to the tissue and level of expression found. Spacing for this table is as follows: column 1: characters 1-9; column 2: characters 10-27; column 3: 28-41; and column 4: characters 42-121.

Information given in the text with regard to expression was determined according to oligonucleotide binding to arrays. Information is given with regard to overexpression of a cluster in cancer based on microarrays. As a microarray reference, in the specific segment paragraphs, the unabbreviated tissue name was used as the reference to the type of chip for which expression was measured.

Oligonucleotide microarray results were taken from Affymetrix data, available from Affymetrix Inc, Santa Clara, CA, USA (see for example data regarding the Human Genome U133 (HG-U133) Set at

www.affymetrix.com/products/arrays/specific/hgu133.affx; GeneChip Human Genome U133A 2.0 Array at

www.affymetrix.com/products/arrays/specific/hgu133av2.affx; and Human Genome U133 Plus 2.0 Array at

www.affymetrix.com/products/arrays/specific/hgu133plus.affx). The data is available from NCBI Gene Expression Omnibus (see www.ncbi.nlm.nih.gov/projects/geo/ and Edgar et al, Nucleic Acids Research, 2002, Vol. 30, No. 1 207-210). The dataset (including results) is available from

www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1133 for the Series GSE1133 database (published on March 2004); a reference to these results is as follows: Su et al (Proc Natl Acad Sci U S A. 2004 Apr 20;101(16):6062-7. Epub 2004 Apr 09).

With regard to comparison reports between variant protein according to the present invention and known protein, table structure is as follows: column 1 features the protein identifier as used throughout the application to identify this sequence;

column 2 features the name of the protein; column 3 reports on the differences between the variant protein sequence and the known protein sequence (including the name of the known protein); and column 4 shows the alignment between the variant protein sequence and the known protein sequence. Spacing for this table is as follows: characters 1-18: column 1; characters 19-32: column 2; characters 33-92: column 3; and characters 97-170: column 4.

Information given in the text with regard to the Homology to the known proteins was determined by Smith-Waterman version 5.1.2 using special (non default) parameters as follows:

```
-model=sw.model  
-GAPEXT=0  
-GAPOP=100.0  
-MATRIX=blosum100
```

In some cases, the known protein sequence was included with one or more known variations in order to assist in the above comparison. These sequences are given in variants_report.txt: column 1 features the name of the protein sequence as it appears in the comparison to the variant protein(s); column 2 features the altered protein sequence; column 3 features the type of variation (for example init_met refers to lack of methionine at the beginning of the original sequence); column 4 states the location of the variation in terms of the amino acid(s) that is/are changed; column 5 shows FROM; and column 6 shows TO (FROM and TO - start and end of the described feature on the protein sequence). Spacing for this table is as follows: column 1: characters 1-24; column 2: characters 25-96; column 3: characters 97-120; column 4: characters 121-144; and column 5: characters 145-169.

The comparison reports herein may optionally include such features as bridges, tails, heads and/or insertions (unique regions), and/or analogs, homologs and derivatives of such peptides (unique regions).

As used herein a "tail" refers to a peptide sequence at the end of an amino acid sequence that is unique to a splice variant according to the present invention. Therefore, a splice variant having such a tail may optionally be considered as a chimera, in that at least a first portion of the splice variant is typically highly homologous (often 100% identical) to a portion of the corresponding known protein, while at least a second portion of the variant comprises the tail.

As used herein a "head" refers to a peptide sequence at the beginning of an amino acid sequence that is unique to a splice variant according to the present invention. Therefore, a splice variant having such a head may optionally be considered as a chimera, in that at least a first portion of the splice variant comprises the head, while at least a second portion is typically highly homologous (often 100% identical) to a portion of the corresponding known protein.

As used herein "an edge portion" refers to a connection between two portions of a splice variant according to the present invention that were not joined in the wild type or known protein. An edge may optionally arise due to a join between the above "known protein" portion of a variant and the tail, for example, and/or may occur if an internal portion of the wild type sequence is no longer present, such that two portions of the sequence are now contiguous in the splice variant that were not contiguous in the known protein. A "bridge" may optionally be an edge portion as described above, but may also include a join between a head and a "known protein" portion of a variant, or a join between a tail and a "known protein" portion of a variant, or a join between an insertion and a "known protein" portion of a variant.

Optionally and preferably, a bridge between a tail or a head or a unique insertion, and a "known protein" portion of a variant, comprises at least about 10 amino acids, more preferably at least about 20 amino acids, most preferably at least about 30 amino acids, and even more preferably at least about 40 amino acids, in which at least one amino acid is from the tail/head/insertion and at least one amino acid is from the "known protein" portion of a variant. Also optionally, the bridge may comprise any number of amino acids from about 10 to about 40 amino acids (for example, 10, 11, 12, 13...37, 38, 39, 40 amino acids in length, or any number in between).

It should be noted that a bridge cannot be extended beyond the length of the sequence in either direction, and it should be assumed that every bridge description is to be read in such manner that the bridge length does not extend beyond the sequence itself.

Furthermore, bridges are described with regard to a sliding window in certain contexts below. For example, certain descriptions of the bridges feature the following format: a bridge between two edges (in which a portion of the known protein is not present in the variant) may optionally be described as follows: a bridge portion of

CONTIG-NAME_P1 (representing the name of the protein), comprising a polypeptide having a length "n", wherein n is at least about 10 amino acids in length, optionally at least about 20 amino acids in length, preferably at least about 30 amino acids in length, more preferably at least about 40 amino acids in length and most preferably at least about 50 amino acids in length, wherein at least two amino acids comprise XX (2 amino acids in the center of the bridge, one from each end of the edge), having a structure as follows (numbering according to the sequence of CONTIG-NAME_P1): a sequence starting from any of amino acid numbers 49-x to 49 (for example); and ending at any of amino acid numbers 50 + ((n-2) - x) (for example), in which x varies from 0 to n-2. In this example, it should also be read as including bridges in which n is any number of amino acids between 10-50 amino acids in length. Furthermore, the bridge polypeptide cannot extend beyond the sequence, so it should be read such that 49-x (for example) is not less than 1, nor 50 + ((n-2) - x) (for example) greater than the total sequence length.

In another embodiment, this invention provides antibodies specifically recognizing the splice variants and polypeptide fragments thereof of this invention. Preferably such antibodies differentially recognize splice variants of the present invention but do not recognize a corresponding known protein, optionally and more preferably through recognition of a unique region as described herein.

All nucleic acid sequences and/or amino acid sequences shown herein as embodiments of the present invention relate to their isolated form, as isolated polynucleotides (including for all transcripts), oligonucleotides (including for all segments, amplicons and primers), peptides (including for all tails, bridges, insertions or heads, optionally including other antibody epitopes as described herein) and/or polypeptides (including for all proteins). It should be noted that oligonucleotide and polynucleotide, or peptide and polypeptide, may optionally be used interchangeably.

It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable subcombination.

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Although the invention has been described in conjunction with specific embodiments thereof, it is evident that many alternatives, modifications and variations will be apparent to those skilled in the art. Accordingly, it is intended to embrace all such alternatives, modifications and variations that fall within the spirit and broad scope of the appended claims. All publications, patents and patent applications mentioned in this specification are herein incorporated in their entirety by reference into the specification, to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference. In addition, citation or identification of any reference in this application shall not be construed as an admission that such reference is available as prior art to the present invention.

CD-ROM Content

The following CD-ROMs are attached herewith:

Information provided as: File name/ date of creation/ byte size/ operating system/machine format (all files are text files – operation program is therefore any text editor, including MS_word).

CD-ROM1 (7 files)

1. transcripts.fasta/January 11, 2004/ 525,662 KB/ text file/PC
2. proteins.fasta/ January 11, 2004/ 88,638 KB/ text file/PC
3. AnnotationForPatent.txt/ January 15, 2004/ 68,448 KB/ text file/PC
4. DataOnExons.txt/ January 11, 2004/ 2,242 KB/ text file/PC
5. human_exons.fasta/ January 11, 2004/ 847 KB/ text file/PC
6. mouse_exons.fasta/ January 11, 2004/ 796 KB/ text file/PC
7. NAS_CROG.txt/ January 24, 2005/ 1 KB/ text file/PC

CD-ROM2 (3 files)

1. annotations/ January 13, 2004/ 6,997 KB/ text file/ PC
2. proteins/ January 13, 2004/ 8,313 KB/ text file/ PC
3. transcripts/ January 13, 2004/ 48,429 KB/ text file/ PC

CD-ROM3 (51 files)

1. CROG_localization_1/ January 21, 2005/ 453 KB/text file/PC
2. crog_proteins_ipr_report_1_dos/ January 22, 2005/ 5, 683 KB/text file/PC
3. CROG_expression_1.txt/ January 21, 2005/ 9, 248 KB/ text file/PC
4. CROG_expression_2.txt/January 21, 2005/ 1, 591 KB/ text file/PC
5. Oligos Probs Abbreviations for Patent.txt/January 24, 2005/2 KB/text file/PC.
6. crog_report_01_1.txt/January 21, 2005/3, 856 KB/text file/PC
7. crog_report_02_1.txt/ January 21, 2005/ 2,598 KB/text file/PC.
8. crog_report_03_1.txt/January 21, 2005/2,698 KB/text file/PC.
9. crog_report_04_1.txt/January 21, 2005/3,650 KB/text file/PC.
10. crog_report_05_1.txt/January 21, 2005/3,514 KB/text file/PC.
11. crog_report_06_1.txt/January 21, 2005/3,319 KB/text file/PC.
12. crog_report_07_1.txt/January 21, 2005/2,839 KB/text file/PC.

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13. crog_report_08_1.txt/January 21, 2005/2,905 KB/text file/PC.
14. crog_report_09_1.txt/January 21, 2005/2,619 KB/text file/PC.
15. crog_report_10_1.txt/January 21, 2005/2,476 KB/text file/PC.
16. crog_report_11_1.txt/January 21, 2005/2,147 KB/text file/PC.
17. crog_report_12_1.txt/January 21, 2005/3,171 KB/text file/PC.
18. crog_report_13_1.txt/January 21, 2005/3,630 KB/text file/PC.
19. crog_report_14_1.txt/January 21, 2005/5,194 KB/text file/PC.
20. crog_report_15_1.txt/January 21, 2005/3,956 KB/text file/PC.
21. crog_report_16_1.txt/January 21, 2005/3,771 KB/text file/PC.
22. crog_report_17_1.txt/January 21, 2005/4,180 KB/text file/PC.
23. crog_report_18_1.txt/January 21 2005/4,335 KB/text file/PC.
24. crog_report_19_1.txt/January 21, 2005/3,273 KB/text file/PC.
25. crog_report_20_1.txt/January 21, 2005/3,806 KB/text file/PC.
26. crog_report_21_1.txt/January 21, 2005/3,077 KB/text file/PC.
27. crog_report_22_1.txt/January 21, 2005/4,856 KB/text file/PC.
28. crog_report_23_1.txt/January 21, 2005/4,604 KB/text file/PC.
29. crog_report_24_1.txt/January 21, 2005/4,230 KB/text file/PC.
30. crog_report_25_1.txt/January 21, 2005/3,929 KB/text file/PC.
31. crog_report_26_1.txt/January 21, 2005/3,839 KB/text file/PC.
32. crog_report_27_1.txt/January 21, 2005/3,427 KB/text file/PC.
33. crog_report_28_1.txt/January 21, 2005/3,885 KB/text file/PC.
34. crog_report_29_1.txt/January 21, 2005/4,518 KB/text file/PC.
35. crog_report_30_1.txt/January 21, 2005/3,393 KB/text file/PC.
36. crog_report_31_1.txt/January 21, 2005/3,995 KB/text file/PC.
37. crog_report_32_1.txt/January 21, 2005/3,472 KB/text file/PC.
38. crog_report_33_1.txt/January 21, 2005/3,678 KB/text file/PC.
39. crog_report_34_1.txt/January 21, 2005/4,099 KB/text file/PC.
40. crog_report_35_1.txt/January 21, 2005/3,424 KB/text file/PC.
41. crog_report_36_1.txt/January 21, 2005/3,575 KB/text file/PC.
42. crog_report_37_1.txt/January 21, 2005/5,331 KB/text file/PC.
43. crog_report_38_1.txt/January 21, 2005/3,503 KB/text file/PC.
44. crog_report_39_1.txt/January 21, 2005/4,311 KB/text file/PC.
45. crog_report_40_1.txt/January 21, 2005/4,274 KB/text file/PC.

46. crog_report_41_1.txt/January 21, 2005/3,847 KB/text file/PC.
47. crog_report_42_1.txt/January 21, 2005/4,333 KB/text file/PC.
48. crog_report_43_1.txt/January 21, 2005/4,037 KB/text file/PC.
49. crog_report_44_1.txt/January 21, 2005/3,723 KB/text file/PC.
50. crog_report_45_1.txt/January 21, 2005/4,014 KB/text file/PC.
51. variants_report.txt/ January 22, 2005/ 2,801 KB/text file/PC

WHAT IS CLAIMED IS:

1. A method of identifying alternatively spliced exons, the method comprising, scoring each of a plurality of exon sequences derived from genes of a species according to at least one sequence parameter, wherein exon sequences of said plurality of exon sequences scoring above a predetermined threshold represent alternatively spliced exons, thereby identifying the alternatively spliced exons.
2. The method of claim 1, wherein said at least one sequence parameter is selected from the group consisting of:
 - (i) exon length;
 - (ii) division by 3;
 - (iii) conservation level between said plurality of exon sequences of genes of a species and corresponding exon sequences of genes of an orthologous species;
 - (iv) length of conserved intron sequences upstream of each of said plurality of exon sequences;
 - (v) length of conserved intron sequences downstream of each of said plurality of exon sequences ;
 - (vi) conservation level of said intron sequences upstream of each of said plurality of exon sequences ; and
 - (vii) conservation level of said intron sequences downstream of each of said plurality of exon sequences;
3. The method of claim 2, wherein said exon length does not exceed 1000 bp.
4. The method of claim 2, wherein said conservation level is at least 95 %.
5. The method of claim 2, wherein said length of conserved intron sequences upstream of each of said plurality of exon sequences is at least 12.

6. The method of claim 2, wherein said length of conserved intron sequences downstream of each of said plurality of exon sequences is at least 15.

7. The method of claim 2, wherein said conservation level of said intron sequences upstream of each of said plurality of exon sequences is at least 85 %.

8. The method of claim 2, wherein said conservation level of said intron sequences downstream of each of said plurality of exon sequences is at least 60 %.

9. A system for generating a database of alternatively spliced exons, the system comprising a processing unit, said processing unit executing a software application configured for:

- (a) scoring each of a plurality of exon sequences derived from genes of a species according to at least one sequence parameter, wherein exon sequences of said plurality of exon sequences scoring above a predetermined threshold represent alternatively spliced exons, to thereby identify the alternatively spliced exons; and
- (b) storing said identified alternatively spliced exons to thereby generate the database of alternatively spliced exons.

10. The system of claim 9, wherein said at least one sequence parameter is selected from the group consisting of:

- (i) exon length;
- (ii) division by 3;
- (iii) conservation level between said plurality of exon sequences of genes of a species and corresponding exon sequences of genes of an orthologous species;
- (iv) length of conserved intron sequences upstream of each of said plurality of exon sequences;
- (v) length of conserved intron sequences downstream of each of said plurality of exon sequences ;
- (vi) conservation level of said intron sequences upstream of each of said plurality of exon sequences ; and

(vii) conservation level of said intron sequences downstream of each of said plurality of exon sequences;

11. The system of claim 10, wherein said exon length does not exceed 1000 bp.

12. The system of claim 10, wherein said conservation level is at least 95 %.

13. The system of claim 10, wherein said length of conserved intron sequences upstream of each of said plurality of exon sequences is at least 12.

14. The system of claim 10, wherein said length of conserved intron sequences downstream of each of said plurality of exon sequences is at least 15.

15. The system of claim 10, wherein said conservation level of said intron sequences upstream of each of said plurality of exon sequences is at least 85 %.

16. The system of claim 10, wherein said conservation level of said intron sequences downstream of each of said plurality of exon sequences is at least 60 %.

17. A computer readable storage medium comprising data stored in a retrievable manner, said data including sequence information as set forth in the files "transcripts.fasta" and "proteins.fasta" of enclosed CD-ROM1 and in the files "transcripts" and "proteins" of enclosed CD-ROM2 and sequence annotations as set forth in the file "AnnotationForPatent.txt" of enclosed CD-ROM1.

18. A method of predicting expression products of a gene of interest, the method comprising:

(a) scoring exon sequences of the gene of interest according to at least one sequence parameter and identifying exon sequences scoring above a

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predetermined threshold as alternatively spliced exons of the gene of interest; and

- (b) analyzing chromosomal location of each of said alternatively spliced exons with respect to coding sequence of the gene of interest to thereby predict expression products of the gene of interest.

19. The method of claim 18, wherein said at least one sequence parameter is selected from the group consisting of:

- (i) exon length;
- (ii) division by 3;
- (iii) conservation level between said plurality of exon sequences of genes of a species and corresponding exon sequences of genes of an orthologous species;
- (iv) length of conserved intron sequences upstream of each of said plurality of exon sequences;
- (v) length of conserved intron sequences downstream of each of said plurality of exon sequences ;
- (vi) conservation level of said intron sequences upstream of each of said plurality of exon sequences ; and
- (vii) conservation level of said intron sequences downstream of each of said plurality of exon sequences;

20. The method of claim 19, wherein said exon length does not exceed 1000 bp.

21. The method of claim 19, wherein said conservation level is at least 95 %.

22. The method of claim 19, wherein said length of conserved intron sequences upstream of each of said plurality of exon sequences is at least 12.

23. The method of claim 19, wherein said length of conserved intron sequences downstream of each of said plurality of exon sequences is at least 15.

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24. The method of claim 19, wherein said conservation level of said intron sequences upstream of each of said plurality of exon sequences is at least 85 %.

25. The method of claim 19, wherein said conservation level of said intron sequences downstream of each of said plurality of exon sequences is at least 60 %.

26. A method of predicting expression products of a gene of interest in a given species, the method comprising:

- (a) providing a contig of exon sequences of the gene of interest of a first species;
- (b) identifying exon sequences of an orthologue of the gene of interest of said first species which align to a genome of said first species;
- (c) assembling said exon sequences of said orthologue of the gene of interest in said contig, thereby generating a hybrid contig;
- (d) identifying in said hybrid contig, exon sequences of said orthologue of the gene of interest, which do not align with said exon sequences of the gene of interest of said first species, thereby uncovering non-overlapping exon sequences of the gene of interest; and
- (e) analyzing chromosomal location of non-overlapping exon sequences of the gene of interest with respect to the chromosomal location of the gene of interest to thereby predict expression products of the gene of interest in a given species.

27. The method of claim 26, wherein at least a portion of said exon sequences are alternatively spliced sequences.

28. The method of claim 27, wherein said alternatively spliced sequences are identified by scoring exon sequences of the gene of interest according to at least one sequence parameter, wherein exon sequences scoring above a predetermined threshold represent said alternatively spliced exons of the gene of interest.

29. The method of claim 28, wherein said at least one sequence parameter is selected from the group consisting of:

- (i) exon length;
- (ii) division by 3;
- (iii) conservation level between said plurality of exon sequences of genes of a species and corresponding exon sequences of genes of an orthologous species;
- (iv) length of conserved intron sequences upstream of each of said plurality of exon sequences;
- (v) length of conserved intron sequences downstream of each of said plurality of exon sequences ;
- (vi) conservation level of said intron sequences upstream of each of said plurality of exon sequences ; and
- (vii) conservation level of said intron sequences downstream of each of said plurality of exon sequences;

30. The method of claim 29, wherein said exon length does not exceed 1000 bp.

31. The method of claim 29, wherein said conservation level is at least 95 %.

32. The method of claim 29, wherein said length of conserved intron sequences upstream of each of said plurality of exon sequences is at least 12.

33. The method of claim 29, wherein said length of conserved intron sequences downstream of each of said plurality of exon sequences is at least 15.

34. The method of claim 29, wherein said conservation level of said intron sequences upstream of each of said plurality of exon sequences is at least 85 %.

35. The method of claim 29, wherein said conservation level of said intron sequences downstream of each of said plurality of exon sequences is at least 60 %.

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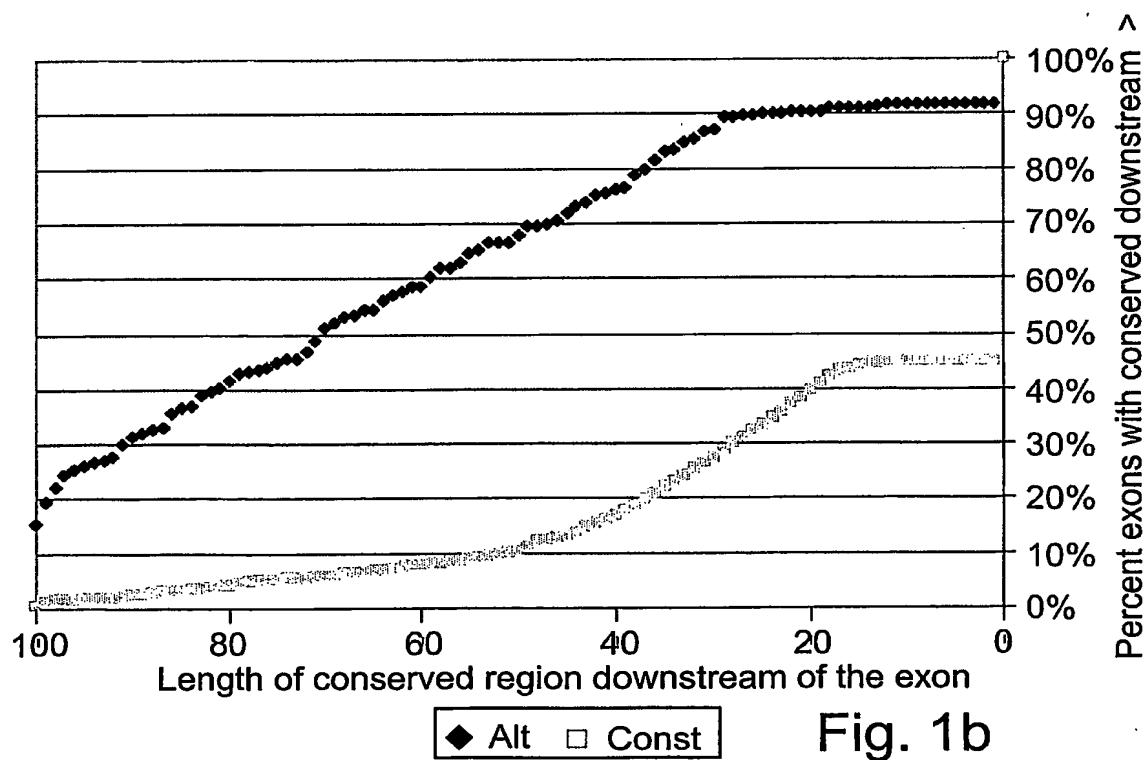
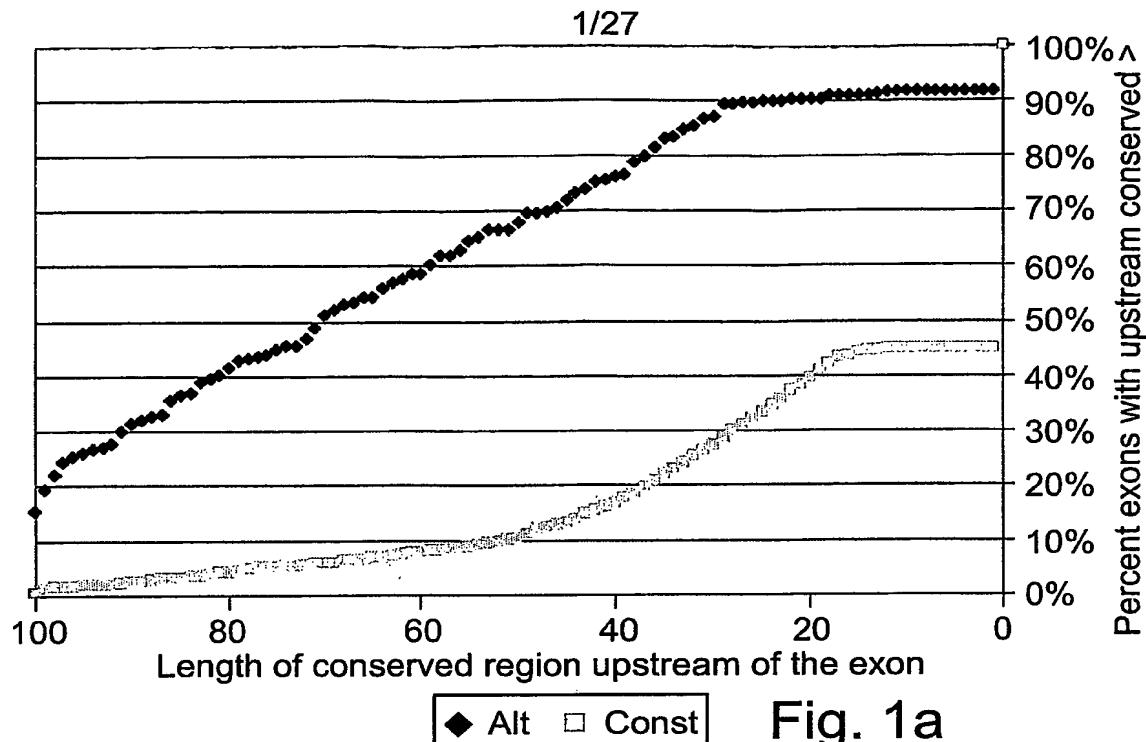
36. An isolated polynucleotide comprising a nucleic acid sequence being at least 70 % identical to a nucleic acid sequence of the sequences set forth in file "transcripts.fasta" of CD-ROM1 or in the file "transcripts" of CD-ROM2.

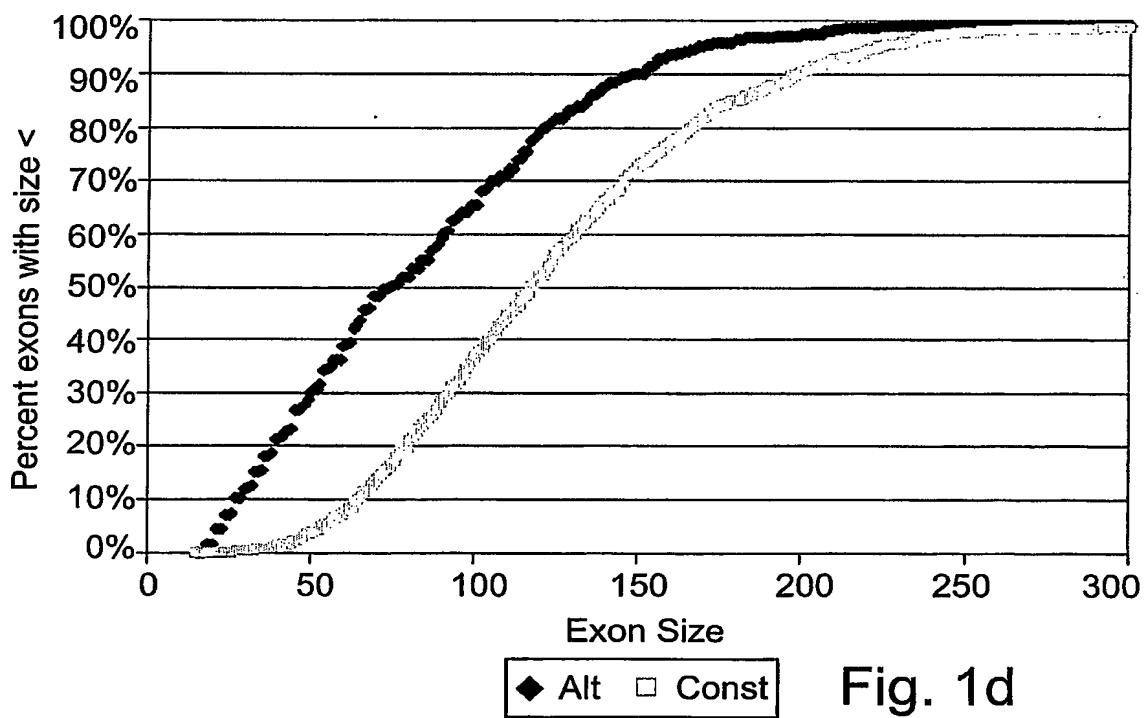
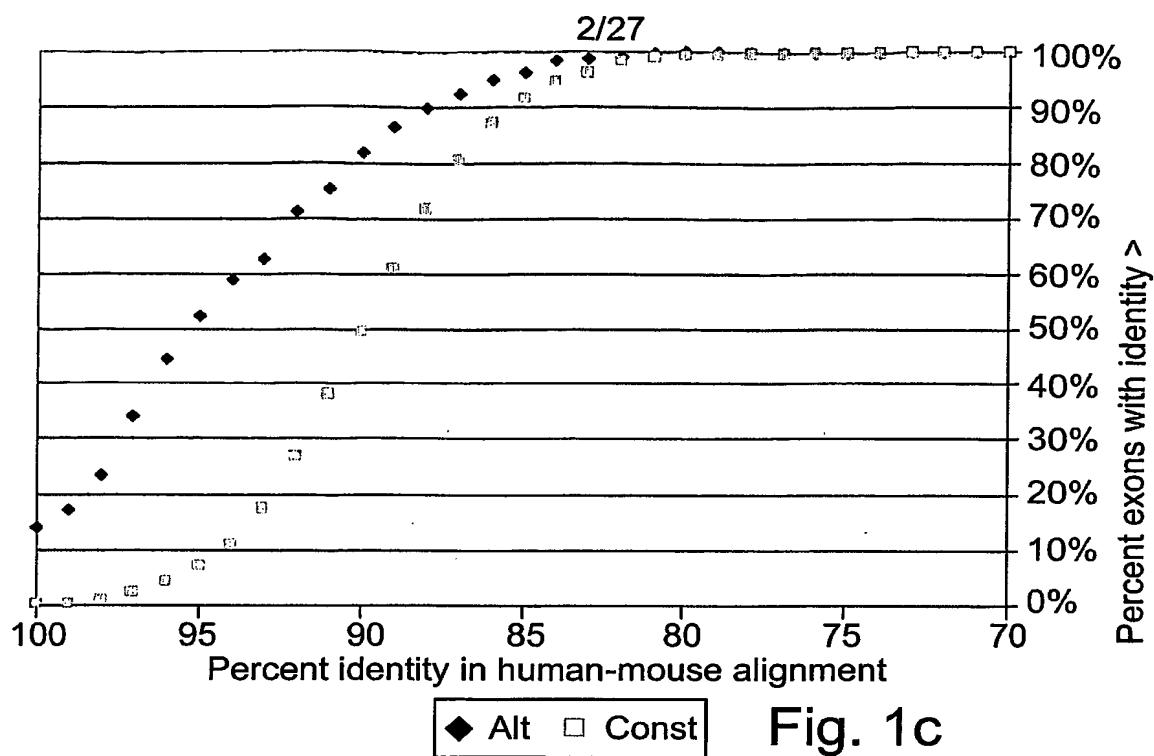
37. The isolated polynucleotide of claim 36, wherein said nucleic acid sequence is set forth in the file "transcripts.fasta" of enclosed CD-ROM1 or in the file "transcripts" of enclosed CD-ROM 2.

38. An isolated polynucleotide comprising a nucleic acid sequence encoding a polypeptide having an amino acid sequence at least 70 % homologous to a sequence set forth in the file "proteins.fasta" of enclosed CD-ROM1 or in the file "proteins" of enclosed CD-ROM2.

39. An isolated polypeptide having an amino acid sequence at least 80 % homologous to a sequence set forth in the file proteins.fasta" of enclosed CD-ROM1 or in the file "proteins" of enclosed CD-ROM2.

40. Use of a polynucleotide or polypeptide set forth in the file "transcripts.fasta" of CD-ROM1 or in the file "transcripts" of CD-ROM2 or in the file "proteins.fasta" of enclosed CD-ROM1 or in the file "proteins" of enclosed CD-ROM2 for the diagnosis and/or treatment of the diseases listed in Example 8.





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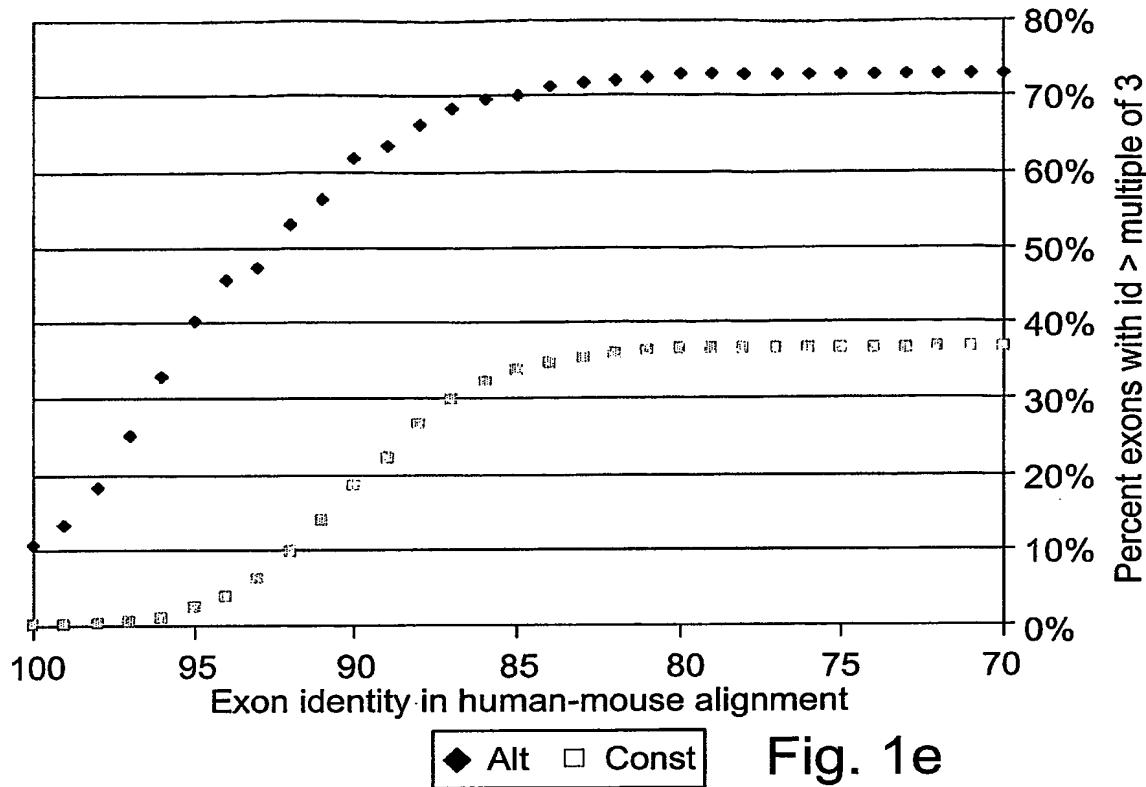
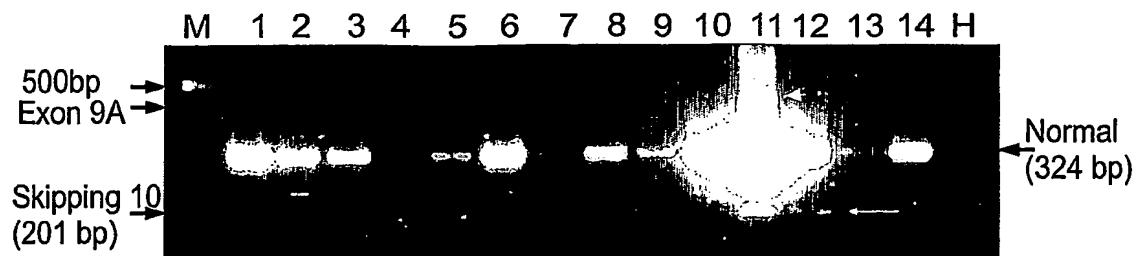


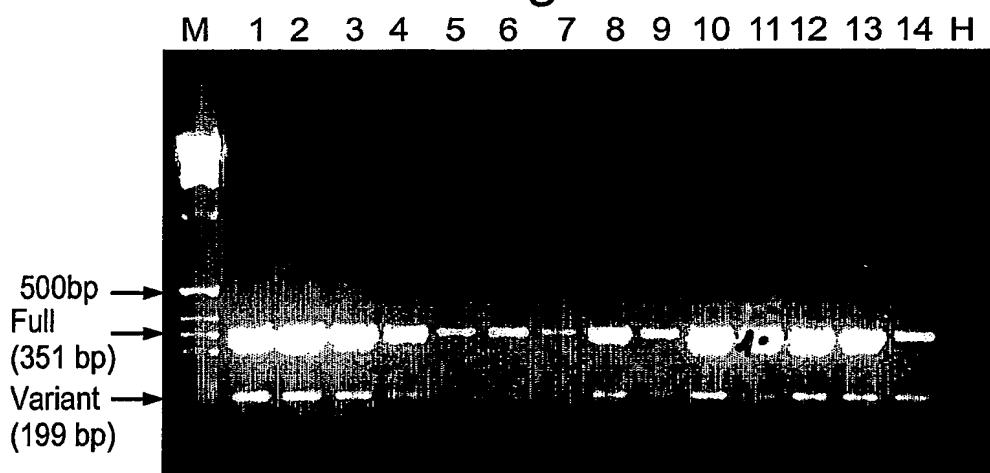
Fig. 1e

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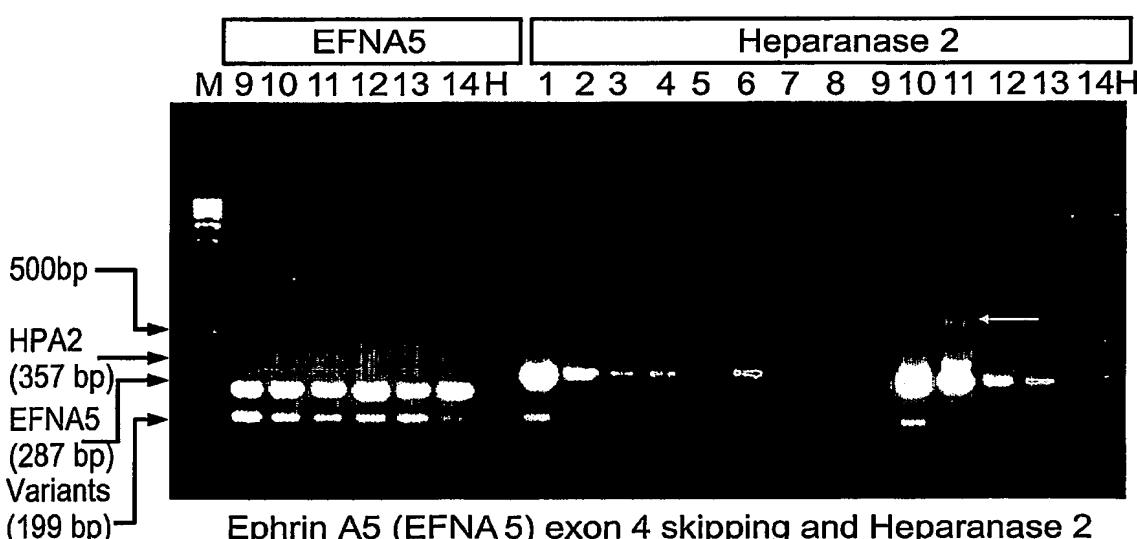
EPHB1 Skipping exon 10 and a new exon-9A

Fig. 2a



VEGFC exon 4 skipping

Fig. 2b



Ephrin A5 (EFNA 5) exon 4 skipping and Heparanase 2 exon 11 skipping

Fig. 2c

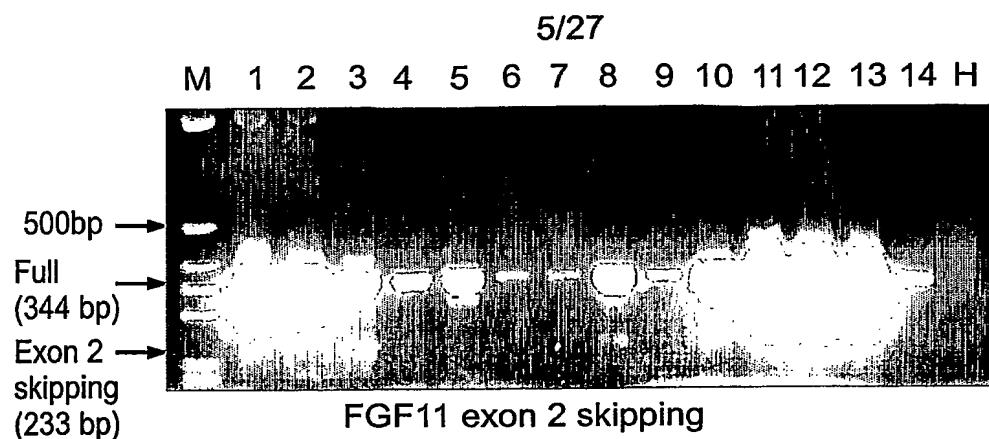


Fig. 2d

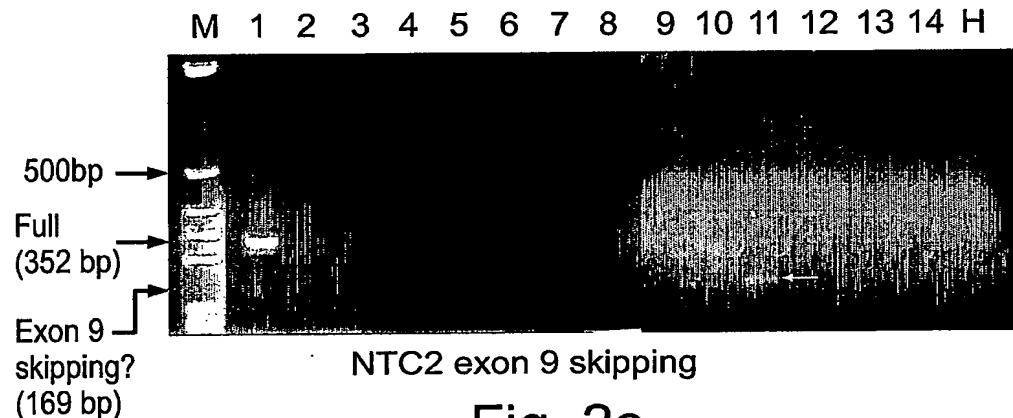


Fig. 2e

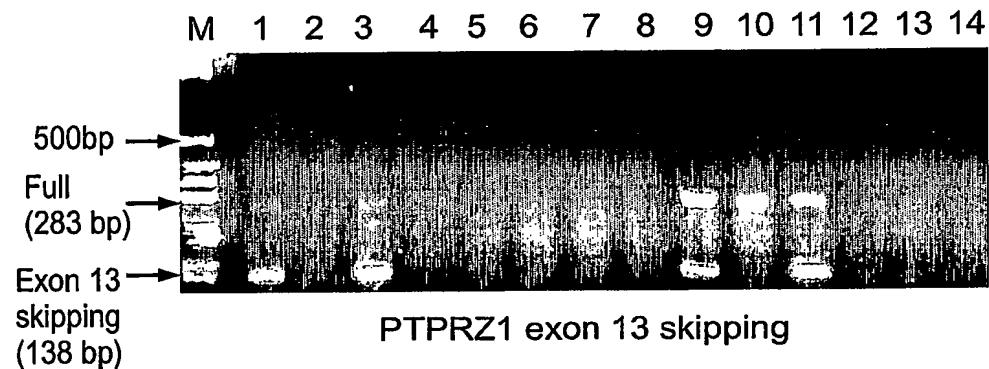
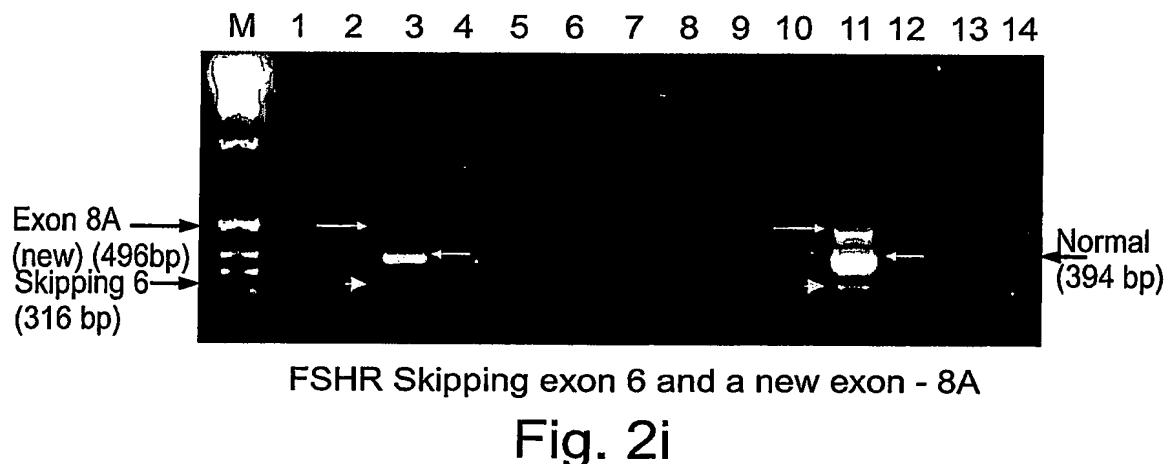
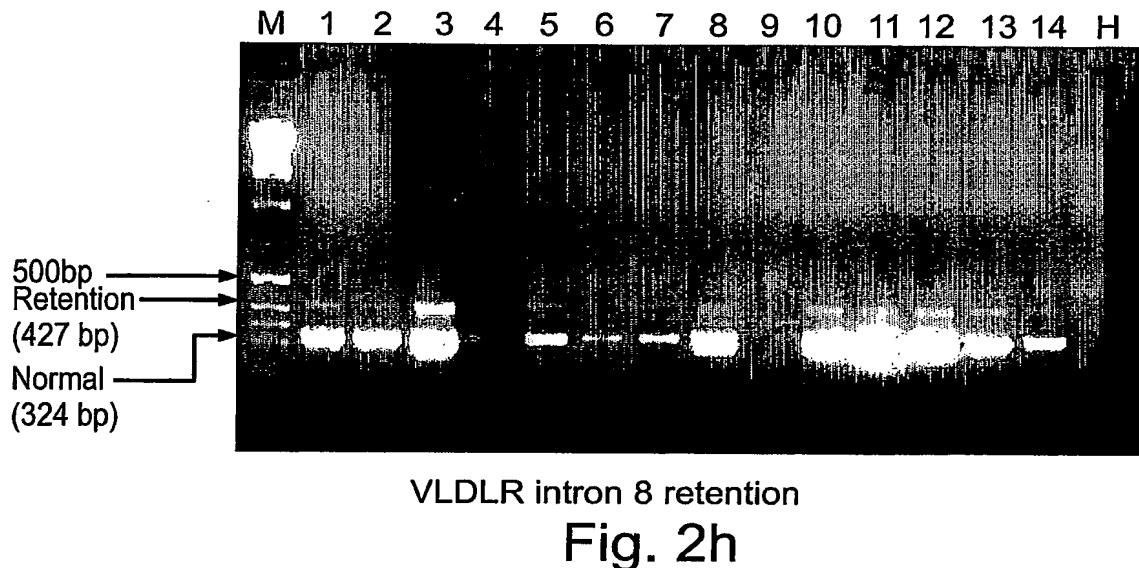
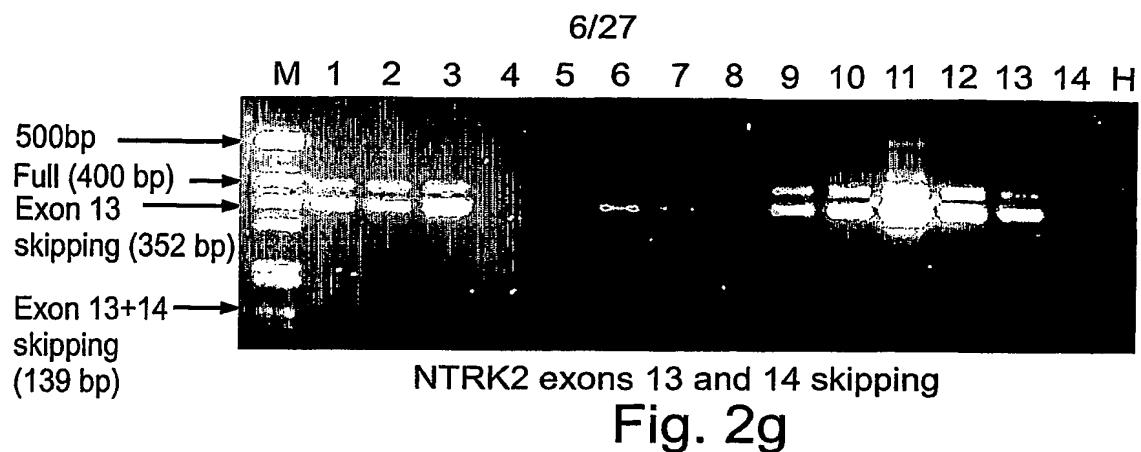


Fig. 2f



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Fig. 2j

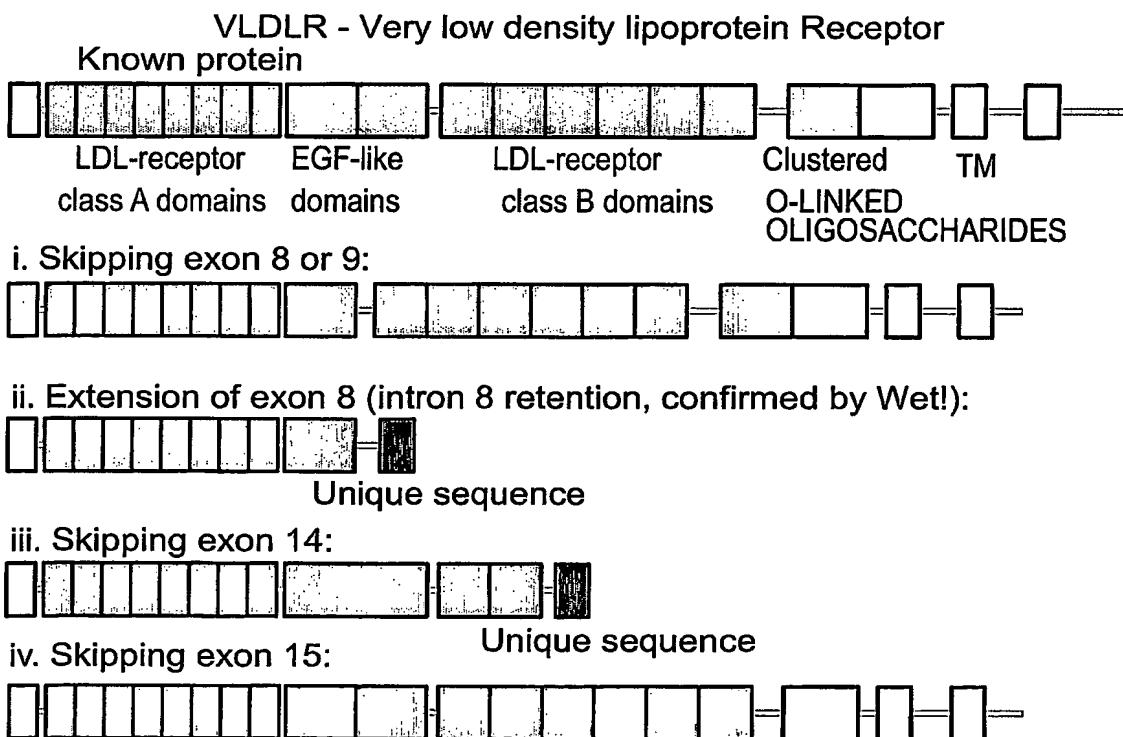
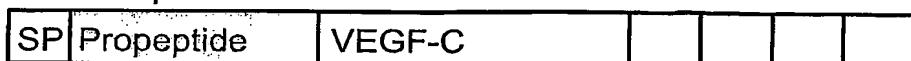


Fig. 3a

8/27

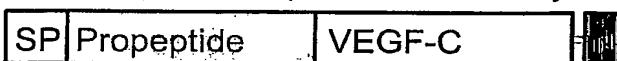
VEGFC - Vascular endothelial growth factor C

Known protein



16 AA REPEATS OF
C-X(10)-C-X-C-X(1,3)-C

Skipping exon 4 (was confirmed by wet validation):



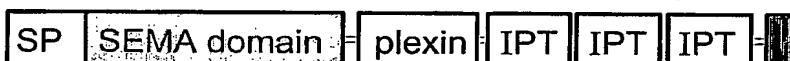
Unique sequence

Fig. 3b**MET protooncogen HGF receptor)**

Known protein



i. Extension of exon 12 (predicted by ESTs):



Unique sequence

ii. Skipping exon 14:



iii. Skipping exon 18:

**Fig. 3c**

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**ITGAV: integrin, alpha V
(vitronectin receptor, alpha polypeptide)**
ITGAV heavy chain incl. FG-GAP repeats
(4 last Ca⁺⁺binding)

Known protein



i. Skipping exon 11 (Truncated protein):



Unique sequence

ii. Skipping exon 20 (Truncated protein):



iii. Skipping exon 21 (in-frame deletion):



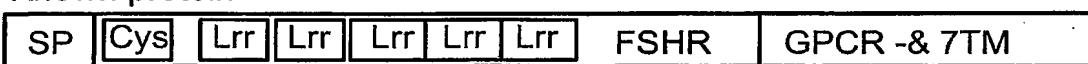
iv. Skipping exon 25 (in-frame deletion):



Fig. 3d

FSHR: follicle stimulating hormone receptor

Known protein

Cys rich N-ter flanking LRR
(LRRNT)

i. Skipping exon 7:



ii. Skipping exon 8:



iii. Intron 7 retention:



Fig. 3e

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LHCGR: luteinizing hormone/choriogonadotropin receptor

Full length:



i. Skipping either exon 2,3,5,6,7:



ii. Skipping exon 10:



iii. Intron 5 retention:

**Fig. 3f****Fibroblast growth factor-FGF11**

Full length:



Skipping exon 2 (in-frame deletion):

**Fig. 3g**

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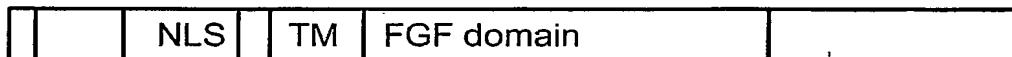
Fibroblast growth factors - FGF12/13

Full length has two isoforms, alternative promoter and 1st exon:

Isoform 1:



i. Skipping exon 2 in Isoform 1:



In Isoform 2:

	SP	FGF domain	
--	----	------------	--

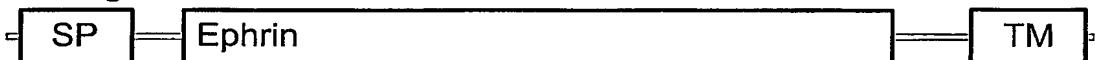
ii. Skipping exon 3 in Isoform 1:



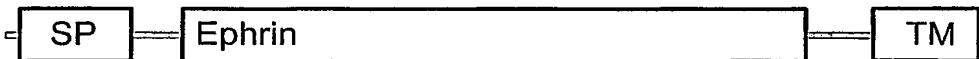
In Isoform 2: FGF domain

Fig. 3h

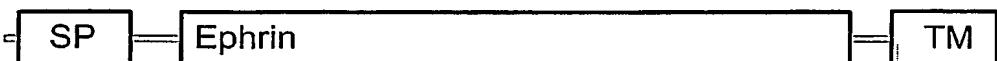
Full length: Ephrin ligand A family (EFNA 1,3&5)



i. Skipping exon 3 (EFNA1,3&5 - In-frame deletion):



ii. Skipping exon 4 (EFNA3&5 - In-frame deletion):



iii. Skipping both exons 3 & 4



Fig. 3i

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Ephrin ligand B family (EFNB2)

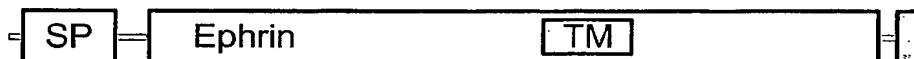
Full length:



i. Skipping exon 2 (truncated protein):



ii. Skipping exon 3 (In-frame deletion):



iii. Skipping exon 4 (In-frame deletion):



Fig. 3j

Ephrin type-A receptor 4 (EPHA4)

Full length

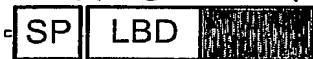


i. Skipping exon 2 (truncation):



Unique sequence

ii. Skipping exon 3 (truncation):



Unique sequence

iii. Skipping exon 4 (In-frame deletion):



iv. Skipping exon 12 (truncation):



Fig. 3k

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Ephrin type-A receptor 5 (EPHA5)

Full length:



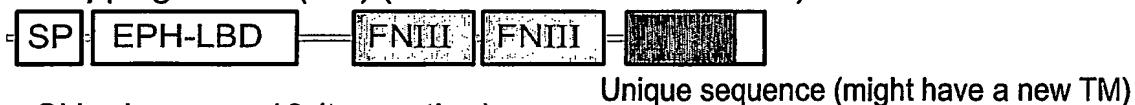
i. Skipping exon 4 (In-frame deletion):



ii. Skipping exon 5 (In-frame deletion):



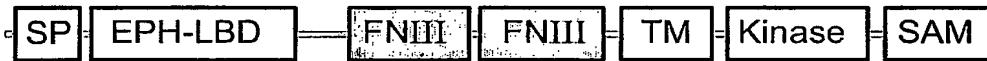
iii. Skipping exon 8 (TM) (Truncation-Soluble ECD?):



iv. Skipping exon 10 (truncation):



v. Skipping exon 14 (In-frame deletion):



vi. Skipping exon 16 (truncation):



vii. Skipping exon 17 (In-frame deletion):



Fig. 31

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Ephrin type-A receptor 7 (EPHA7)

Full length



i. Skipping exon 10 (In-frame deletion which creates a new "stop" between exons 9 and 11):



ii. Skipping exon 15 (truncation):



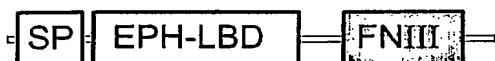
Fig. 3m

Full length

Ephrin type-B receptor 1 (EPHB1)



i. Skipping exon 6 (truncation):



ii. Skipping exon 8 (TM) (Truncation)-Soluble ECD:



iii. Skipping exon 10 (In-frame deletion):



Fig. 3n

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PTPRZ1-Protein-tyrosine phosphatase zeta 1

Full length

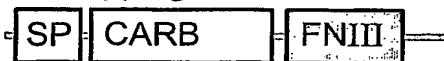


i. Skipping exon 7:



Unique sequence

ii. Skipping exon 11:



iii. Skipping exon 13 (Confirmed by PCR):



Unique sequence

iv. Skipping exon 15:



Unique sequence

v. Skipping exon 22:



Unique sequence

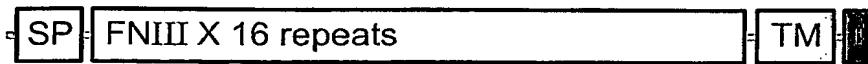
Fig. 3o

PTPRB1-Protein-tyrosine phosphatase beta 1

Full length



Skipping exon 26:



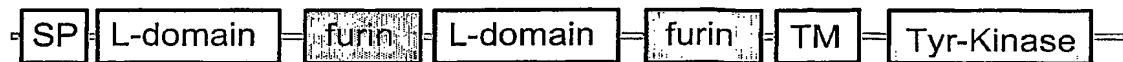
Unique sequence

Fig. 3p

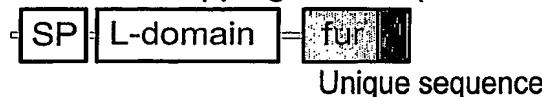
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ErbB2 and ErbB3 - Receptor Tyrosine Kinases

Full length:



i. ErbB2-Skipping exon 6 (truncation):



ii. ErbB3-Skipping exon 4 (In-frame deletion):



iii. ErbB3-Skipping exon 15 (Soluble ECD):



iv. ErbB3-Skipping exon 18 (In-frame deletion):

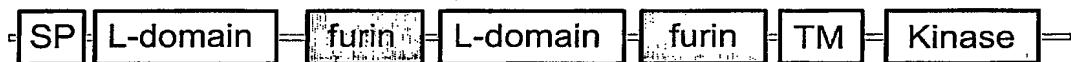


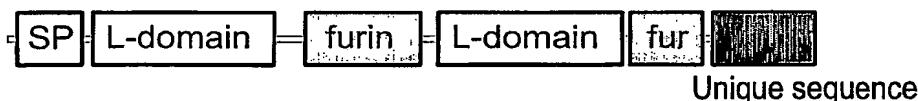
Fig. 3q

ErbB4 - Receptor Tyrosine Kinases

Full length



i. ErbB4-Skipping exon 14 (Soluble ECD):



ii. ErbB4-Skipping exon 16 (In-frame deletion):

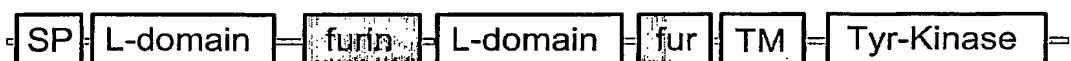


Fig. 3r

Full length

Heparanase



Skipping exon 10

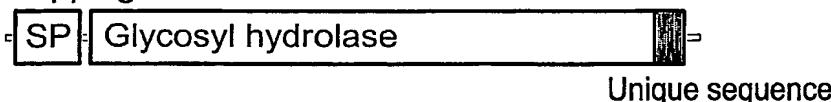


Fig. 3s

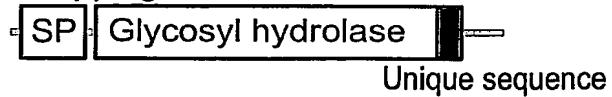
17/27

Heparanase 2

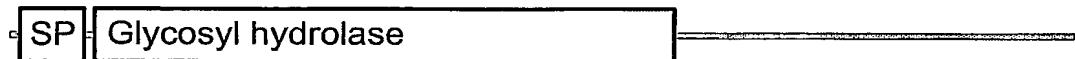
Full length



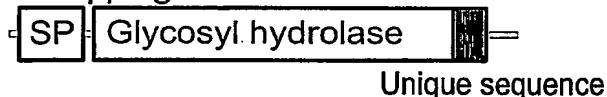
i. Skipping exon 5



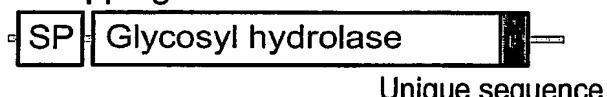
ii. Skipping exon 6 (In-frame deletion):



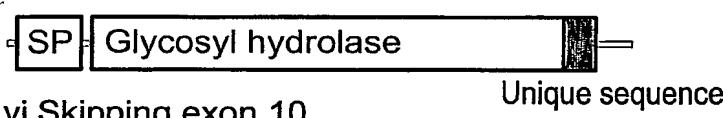
iii. Skipping exon 7



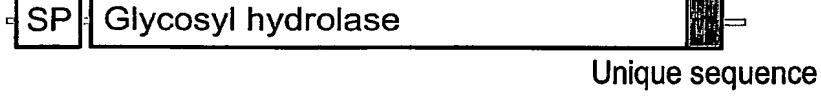
iv. Skipping exon 8



v. Skipping exon 9



vi. Skipping exon 10



vii. Skipping exon 11 (In-frame deletion-validated by PCR):

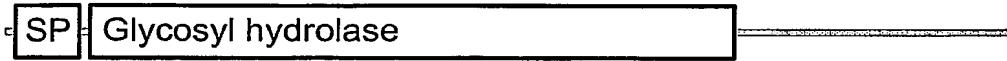
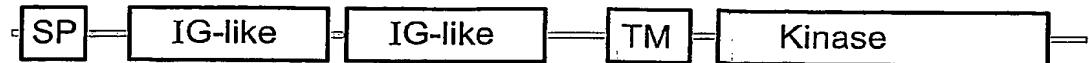


Fig. 3t

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Full length KIT oncogene (Tyrosine kinase receptor)



i. Skipping exon 8 (TM):



Unique sequence

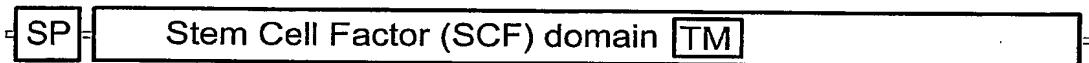
ii. Skipping exon 14:



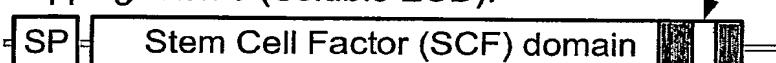
Unique sequence

Fig. 3u

Full length KIT - Ligand



Skipping exon 8 (Soluble ECD):

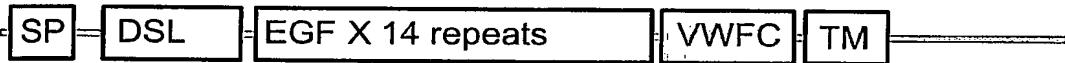


Unique sequence

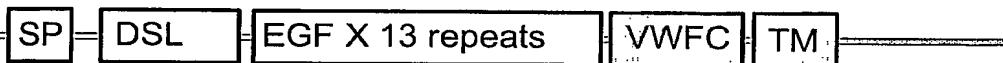
Fig. 3v

JAG1: Jagged-regulator of Angiogenesis

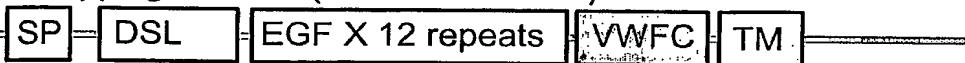
Full length



i. Skipping exon 10 or 18 (In-frame deletion):



ii. Skipping exon 12 (In-frame deletion):



iii. Skipping exon 22 (Soluble ECD):

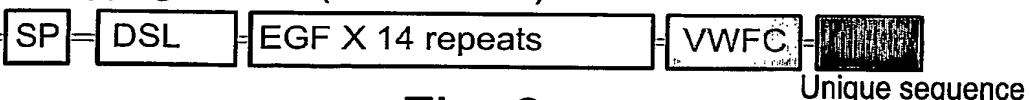


Fig. 3w

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Notch homologs NTC2, NTC3 & NTC4

Full length (Number of repeats varies between genes):



i. NTC2-Skipping exon 9 or 12 (In-frame deletion):



ii. NTC3-Skipping exon 2 (A new protein-same SP):



iii. NTC4-Skipping exon 8 (In-frame deletion):

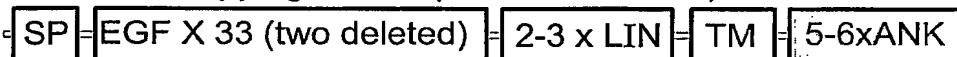


Fig. 3x

BDNF/NT-3 growth factors receptors (NTRK2/NTRK3)

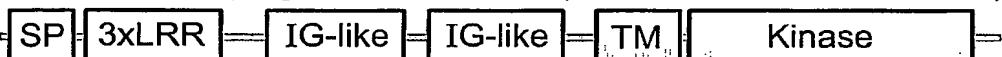
Full length



i. NTRK2-Skipping exon 14 (In-frame deletion):



ii. NTRK2-Skipping exon 13 and 14 (In-frame deletion-Validated):



iii. NTRK3-Skipping exon 5 (In-frame deletion):



iv. NTRK3-Skipping exon 16 (truncation):

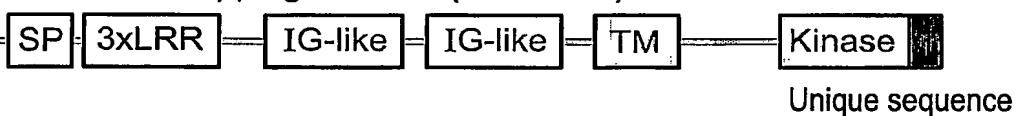
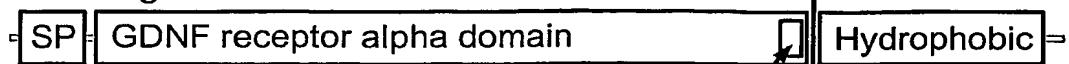


Fig. 3y

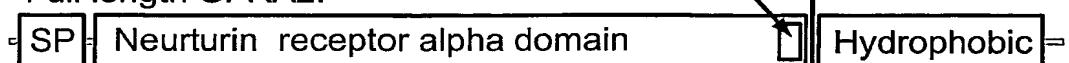
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GDNF receptor alpha (GFRA1) and Neurturin receptor alpha (GFRA2)-RET ligands

Full length GFRA1:

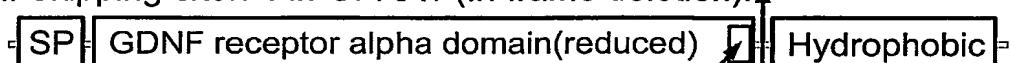


Full length GFRA2:



Cleavage

i. Skipping exon 4 in GFRA1 (In-frame deletion):



ii. Skipping exon 4 in GFRA2
(In-frame deletion):



Cleavage

Fig. 3z

Interleukin 16 -IL16 long and short isoforms:

Full length



i. Skipping exon 5 (truncation):



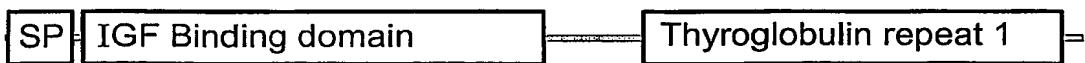
ii. Skipping exon 18:



Fig. 4a

Insulin growth factor binding protein 4-IGFBP4

Full length



Skipping exon 3 (In-frame deletion):

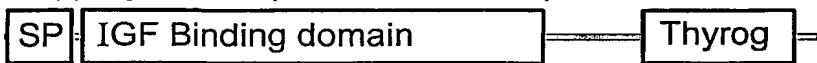


Fig. 4b

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ANGPT1-Angiopoietin-1

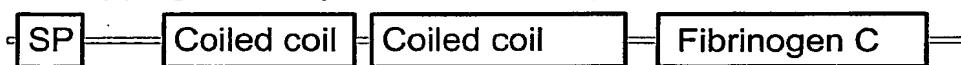
Full length (long isoform):



i. Skipping exon 5 (Truncation):



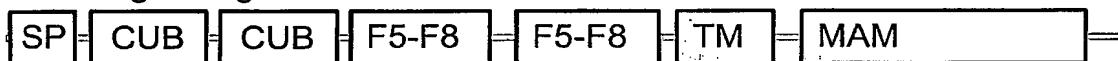
ii. Skipping exon 6 (In-frame deletion):



iii. Skipping exon 8 (Truncation):

**Fig. 4c****NRP1-Neuropilin-1**

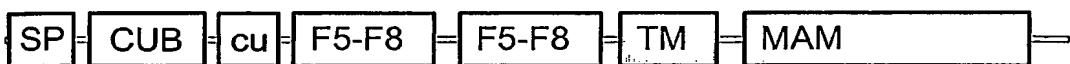
Full length long isoform:



Full length short isoform (soluble):



i. Skipping exon 5 long isoform:



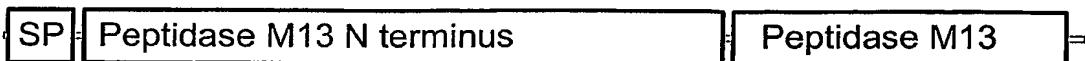
ii. Skipping exon 5 short isoform (soluble):

**Fig. 4d**

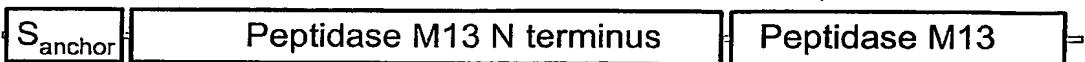
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ECE1-Endothelin converting Enzyme 1

Full length:



Skipping exon 2 (in-frame deletion, known for ECE2):

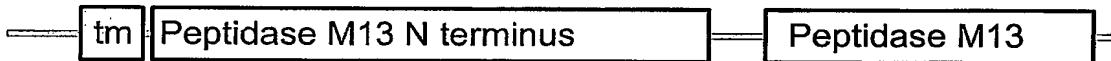


The variant converts the SP into a signal anchor.

Fig. 4e

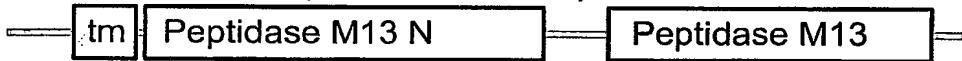
ECE2-Endothelin converting Enzyme 2

Full length:



(SignalP claims that there is no SP, TM pred predicts a TM)

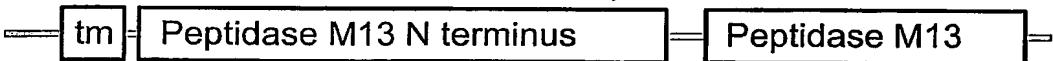
i. Skipping exon 8 (In-frame deletion):



ii. Skipping exon 12 (In-frame deletion):



iii. Skipping exon 13 (In-frame deletion):



iv. Skipping exon 15 (In-frame deletion):

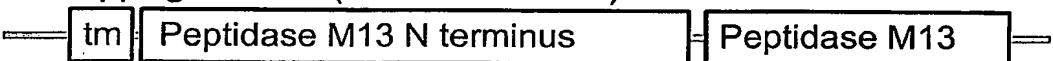
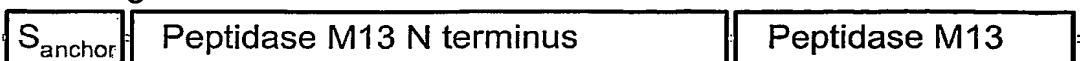
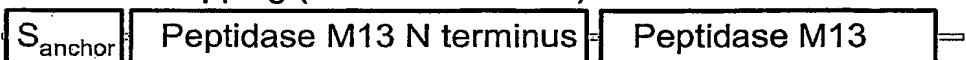
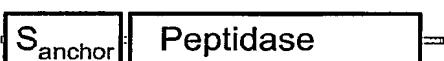
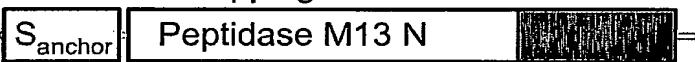
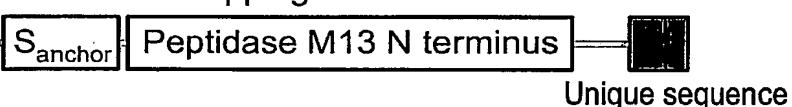
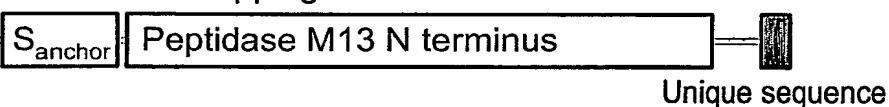


Fig. 4f

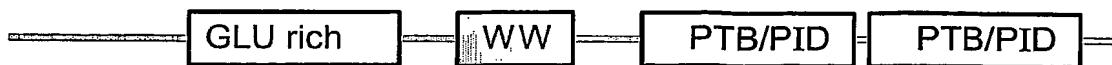
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MME-Neutral endopeptidase (Enkephalinase)**Full length:****i. Exon 4 skipping (In-frame deletion):****ii. Exon 7 skipping:****iii. Exon 9 skipping (In-frame deletion):****iv. Exon 11 skipping:****v. Exon 12 skipping:****vi. Exon 16 skipping:****Fig. 4g**

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APBB1-Alzheimer's disease amyloid A4 Binding protein

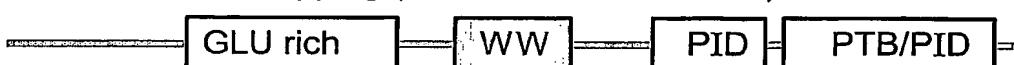
Full length:



i. Exon 3 skipping:



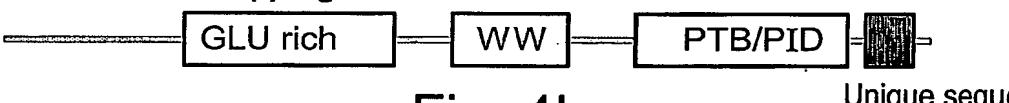
ii. Exon 7 or 9 skipping (both in-frame deletions):



iii. Exon 10 skipping:



iv. Exon 12 skipping:

**Fig. 4h****TGFB2-Transforming growth factor beta 2**

Full length:



Exon 5 skipping:



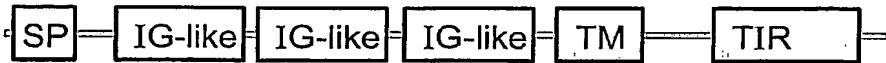
Unique sequence

Fig. 4i**IL1RAP - IL-1 receptor accessory protein**

Full length:



Exon 11 skipping (in-frame deletion):

**Fig. 4j**

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IL1RAPL1 & IL1RAPL2 - IL-1 receptor accessory protein like family

Full length



i. Exon 4 skipping (Truncation):

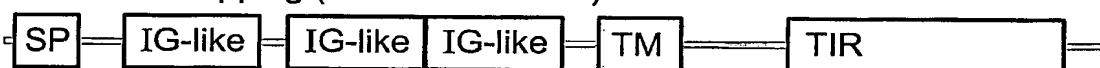


Unique sequence

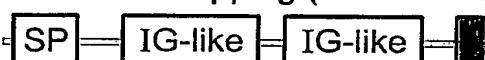
ii. Exon 5 skipping (Truncation):



iii. Exon 6 skipping (in-frame deletion):

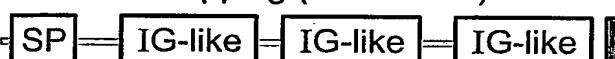


iv. Exon 7 skipping (Truncation):



Unique sequence

v. Exon 8 skipping (Truncation):



Unique sequence

Fig. 4k

PROS1-Vitamin K-dependent protein S precursor:

Full length



i. Exon 3 skipping:

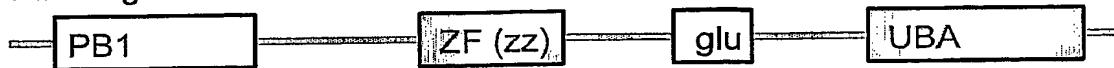


Fig. 4l

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M17S2-Ovarian carcinoma antigen CA125

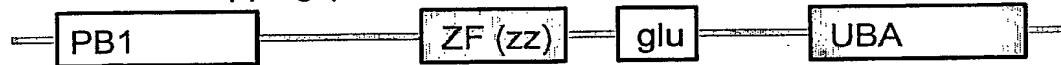
Full length



i. Exon 14 skipping:



ii. Exon 15 skipping (In-frame deletion):



iii. Exon 20 skipping (Truncation):



Fig. 4m

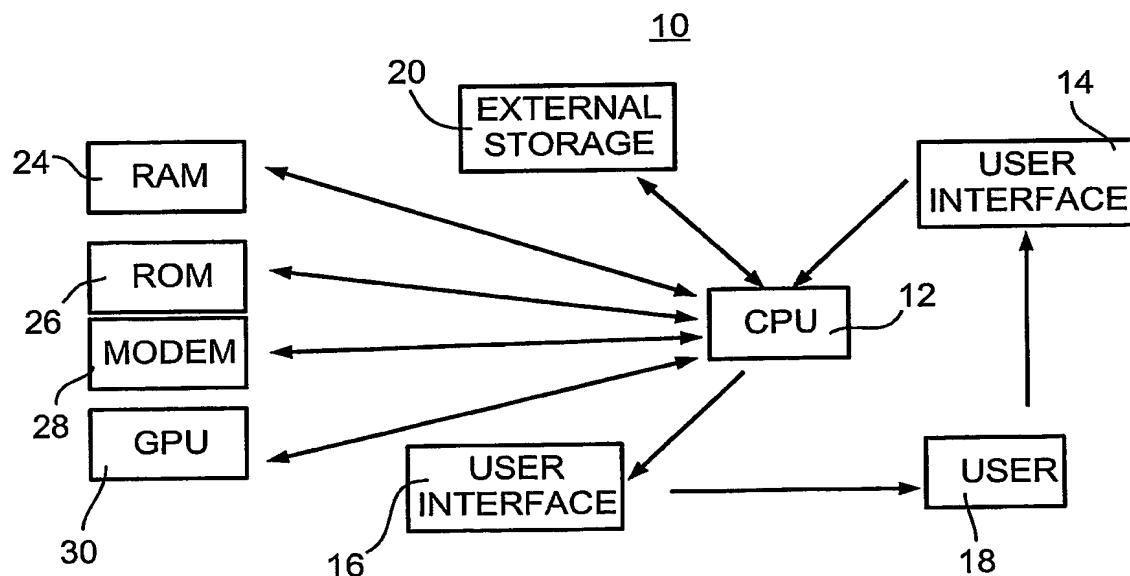


Fig. 5a

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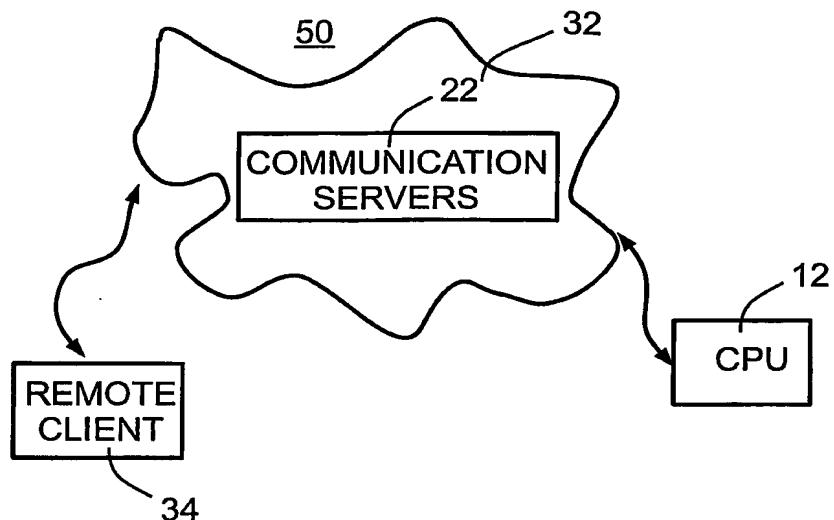


Fig. 5b

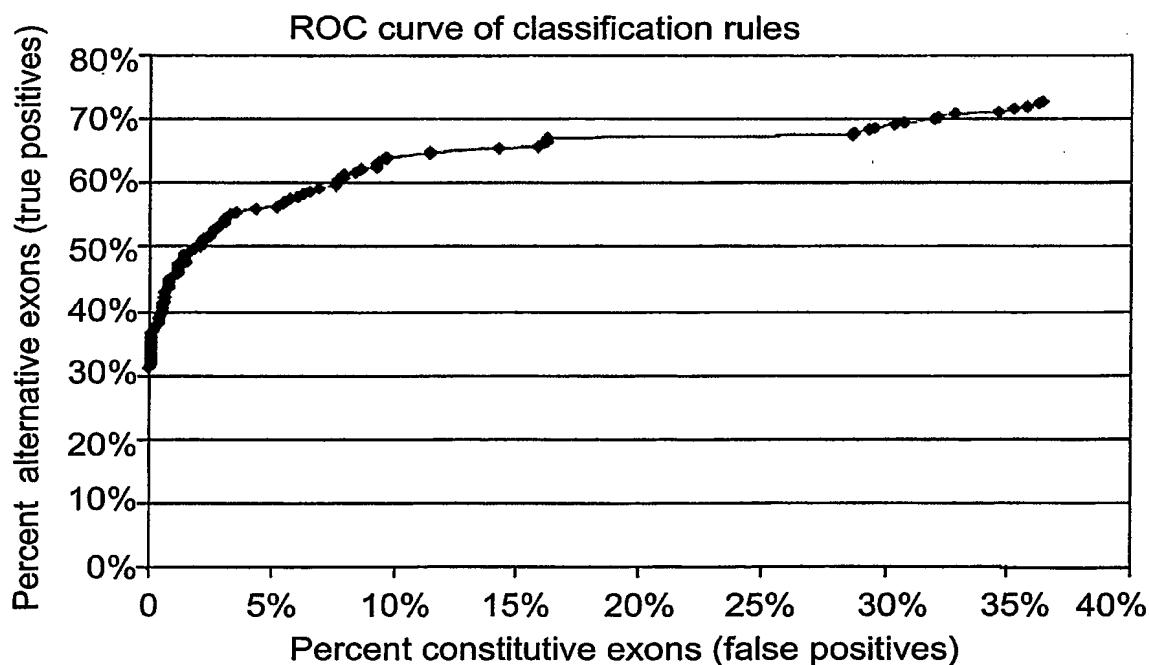


Fig. 6

SEQUENCE LISTING

<110> Sorek, Rotem
Pollock, Sarah
Diber, Alex
Levine, Zuri
Nemzer, Sergey
Kol, Guy
Wool, Assaf
Haviv, Ami
Cohen, Yuval
Cohen, Yossi
Shemeish, Ronen
Savitsky, Kinneret

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Leu Trp Lys Cys Asp Gly Asp Glu Asp Cys Val Asp Gly Ser Asp Glu
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Lys Asn Cys Val Lys Lys Thr Cys Ala Glu Ser Asp Phe Val Cys Asn
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Asn Gly Gln Cys Val Pro Ser Arg Trp Lys Cys Asp Gly Asp Pro Asp
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Cys Pro Ser Arg Thr Cys Arg Pro Asp Gln Phe Glu Cys Glu Asp Gly
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Pro Gly Gly Ile Asn Val Thr Thr Ala Val Ser Glu Val Ser Val Pro
740 745 750

Pro Lys Gly Thr Ser Ala Ala Trp Ala Ile Leu Pro Leu Leu Leu Leu
755 760 765

Val Met Ala Ala Val Gly Gly Tyr Leu Met Trp Arg Asn Trp Gln His
770 775 780

Lys Asn Met Lys Ser Met Asn Phe Asp Asn Pro Val Tyr Leu Lys Thr
785 790 795 800

Thr Glu Glu Asp Leu Ser Ile Asp Ile Gly Arg His Ser Ala Ser Val
805 810 815

Gly His Thr Tyr Pro Ala Ile Ser Val Val Ser Thr Asp Asp Asp Leu
820 825 830

Ala

<210> 24

<211> 831

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 24

Met Gly Thr Ser Ala Leu Trp Ala Leu Trp Leu Leu Ala Leu Cys
1 5 10 15

Trp Ala Pro Arg Glu Ser Gly Ala Thr Gly Thr Gly Arg Lys Ala Lys
20 25 30

Cys Glu Pro Ser Gln Phe Gln Cys Thr Asn Gly Arg Cys Ile Thr Leu
35 40 45

Leu Trp Lys Cys Asp Gly Asp Glu Asp Cys Val Asp Gly Ser Asp Glu
50 55 60

Lys Asn Cys Val Lys Lys Thr Cys Ala Glu Ser Asp Phe Val Cys Asn
65 70 75 80

Asn Gly Gln Cys Val Pro Ser Arg Trp Lys Cys Asp Gly Asp Pro Asp
85 90 95

Cys Glu Asp Gly Ser Asp Glu Ser Pro Glu Gln Cys His Met Arg Thr
100 105 110

Cys Arg Ile His Glu Ile Ser Cys Gly Ala His Ser Thr Gln Cys Ile
115 120 125

Pro Val Ser Trp Arg Cys Asp Gly Glu Asn Asp Cys Asp Ser Gly Glu
130 135 140

Asp Glu Glu Asn Cys Gly Asn Ile Thr Cys Ser Pro Asp Glu Phe Thr
145 150 155 160

Cys Ser Ser Gly Arg Cys Ile Ser Arg Asn Phe Val Cys Asn Gly Gln
165 170 175

Asp Asp Cys Ser Asp Gly Ser Asp Glu Leu Asp Cys Ala Pro Pro Thr
180 185 190

Cys Gly Ala His Glu Phe Gln Cys Ser Thr Ser Ser Cys Ile Pro Ile
195 200 205

Ser Trp Val Cys Asp Asp Ala Asp Cys Ser Asp Gln Ser Asp Glu
210 215 220

Ser Leu Glu Gln Cys Gly Arg Gln Pro Val Ile His Thr Lys Cys Pro
225 230 235 240

Ala Ser Glu Ile Gln Cys Gly Ser Gly Glu Cys Ile His Lys Lys Trp
245 250 255

Arg Cys Asp Gly Asp Pro Asp Cys Lys Asp Gly Ser Asp Glu Val Asn
260 265 270

Cys Pro Ser Arg Thr Cys Arg Pro Asp Gln Phe Glu Cys Glu Asp Gly
275 280 285

Ser Cys Ile His Gly Ser Arg Gln Cys Asn Gly Ile Arg Asp Cys Val
290 295 300

Asp Gly Ser Asp Glu Val Asn Cys Lys Asn Val Asn Gln Cys Leu Gly
305 310 315 320

Pro Gly Lys Phe Lys Cys Arg Ser Gly Glu Cys Ile Asp Ile Ser Lys
325 330 335

Val Cys Asn Gln Glu Gln Asp Cys Arg Asp Trp Ser Asp Glu Pro Leu
340 345 350

Lys Glu Cys His Ile Asn Glu Cys Leu Val Asn Asn Gly Gly Cys Ser
355 360 365

His Ile Cys Lys Asp Leu Val Ile Gly Tyr Glu Cys Asp Cys Ala Ala
370 375 380

Gly Phe Glu Leu Ile Asp Arg Lys Thr Cys Gly Gly Lys Glu Pro Ser
385 390 395 400

Leu Ile Phe Thr Asn Arg Arg Asp Ile Arg Lys Ile Gly Leu Glu Arg
405 410 415

Lys Glu Tyr Ile Gln Leu Val Glu Gln Leu Arg Asn Thr Val Ala Leu
420 425 430

Asp Ala Asp Ile Ala Ala Gln Lys Leu Phe Trp Ala Asp Leu Ser Gln
435 440 445

Lys Ala Ile Phe Ser Ala Ser Ile Asp Asp Lys Val Gly Arg His Val
450 455 460

Lys Met Ile Asp Asn Val Tyr Asn Pro Ala Ala Ile Ala Val Asp Trp
465 470 475 480

Val Tyr Lys Thr Ile Tyr Trp Thr Asp Ala Ala Ser Lys Thr Ile Ser
485 490 495

Val Ala Thr Leu Asp Gly Thr Lys Arg Lys Phe Leu Phe Asn Ser Asp
500 505 510

Leu Arg Glu Pro Ala Ser Ile Ala Val Asp Pro Leu Ser Gly Phe Val
515 520 525

Tyr Trp Ser Asp Trp Gly Glu Pro Ala Lys Ile Glu Lys Ala Gly Met
530 535 540

Asn Gly Phe Asp Arg Arg Pro Leu Val Thr Ala Asp Ile Gln Trp Pro
545 550 555 560

Asn Gly Ile Thr Leu Asp Leu Ile Lys Ser Arg Leu Tyr Trp Leu Asp
565 570 575

Ser Lys Leu His Met Leu Ser Ser Val Asp Leu Asn Gly Gln Asp Arg
580 585 590

Arg Ile Val Leu Lys Ser Leu Glu Phe Leu Ala His Pro Leu Ala Leu
595 600 605

Thr Ile Phe Glu Asp Arg Val Tyr Trp Ile Asp Gly Glu Asn Glu Ala
610 615 620

Val Tyr Gly Ala Asn Lys Phe Thr Gly Ser Glu Leu Ala Thr Leu Val
625 630 635 640

Asn Asn Leu Asn Asp Ala Gln Asp Ile Ile Val Tyr His Glu Leu Val
645 650 655

Gln Pro Ser Gly Lys Asn Trp Cys Glu Glu Asp Met Glu Asn Gly Gly
660 665 670

Cys Glu Tyr Leu Cys Leu Pro Ala Pro Gln Ile Asn Asp His Ser Pro
675 680 685

Lys Tyr Thr Cys Ser Cys Pro Ser Gly Tyr Asn Val Glu Glu Asn Gly

690	695	700
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Arg Asp Cys Gln Ser Thr Ala Thr Thr Val Thr Tyr Ser Glu Thr Lys
 705 710 715 720

Asp Thr Asn Thr Thr Glu Ile Ser Ala Thr Ser Gly Leu Val Pro Gly
 725 730 735

Gly Ile Asn Val Thr Thr Ala Val Ser Glu Val Ser Val Pro Pro Lys
 740 745 750

Gly Thr Ser Ala Ala Trp Ala Ile Leu Pro Leu Leu Leu Val Met
 755 760 765

Ala Ala Val Gly Gly Tyr Leu Met Trp Arg Asn Trp Gln His Lys Asn
 770 775 780

Met Lys Ser Met Asn Phe Asp Asn Pro Val Tyr Leu Lys Thr Thr Glu
 785 790 795 800

Glu Asp Leu Ser Ile Asp Ile Gly Arg His Ser Ala Ser Val Gly His
 805 810 815

Thr Tyr Pro Ala Ile Ser Val Val Ser Thr Asp Asp Asp Leu Ala
 820 825 830

<210> 25

<211> 577

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 25

Met Gly Thr Ser Ala Leu Trp Ala Leu Trp Leu Leu Leu Ala Leu Cys
 1 5 10 15

Trp Ala Pro Arg Glu Ser Gly Ala Thr Gly Thr Gly Arg Lys Ala Lys
 20 25 30

Cys Glu Pro Ser Gln Phe Gln Cys Thr Asn Gly Arg Cys Ile Thr Leu
 35 40 45

Leu Trp Lys Cys Asp Gly Asp Glu Asp Cys Val Asp Gly Ser Asp Glu
 50 55 60

Lys Asn Cys Val Lys Lys Thr Cys Ala Glu Ser Asp Phe Val Cys Asn
 65 70 75 80

Asn Gly Gln Cys Val Pro Ser Arg Trp Lys Cys Asp Gly Asp Pro Asp
 85 90 95

Cys Glu Asp Gly Ser Asp Glu Ser Pro Glu Gln Cys His Met Arg Thr
 100 105 110

Cys Arg Ile His Glu Ile Ser Cys Gly Ala His Ser Thr Gln Cys Ile
 115 120 125

Pro Val Ser Trp Arg Cys Asp Gly Glu Asn Asp Cys Asp Ser Gly Glu
 130 135 140

Asp Glu Glu Asn Cys Gly Asn Ile Thr Cys Ser Pro Asp Glu Phe Thr
 145 150 155 160

Cys Ser Ser Gly Arg Cys Ile Ser Arg Asn Phe Val Cys Asn Gly Gln
 165 170 175

Asp Asp Cys Ser Asp Gly Ser Asp Glu Leu Asp Cys Ala Pro Pro Thr
 180 185 190

Cys Gly Ala His Glu Phe Gln Cys Ser Thr Ser Ser Cys Ile Pro Ile
 195 200 205

Ser Trp Val Cys Asp Asp Asp Ala Asp Cys Ser Asp Gln Ser Asp Glu
 210 215 220

Ser Leu Glu Gln Cys Gly Arg Gln Pro Val Ile His Thr Lys Cys Pro
 225 230 235 240

Ala Ser Glu Ile Gln Cys Gly Ser Gly Glu Cys Ile His Lys Lys Trp
 245 250 255

Arg Cys Asp Gly Asp Pro Asp Cys Lys Asp Gly Ser Asp Glu Val Asn
 260 265 270

Cys Pro Ser Arg Thr Cys Arg Pro Asp Gln Phe Glu Cys Glu Asp Gly
 275 280 285

Ser Cys Ile His Gly Ser Arg Gln Cys Asn Gly Ile Arg Asp Cys Val
 290 295 300

Asp Gly Ser Asp Glu Val Asn Cys Lys Asn Val Asn Gln Cys Leu Gly
 305 310 315 320

Pro Gly Lys Phe Lys Cys Arg Ser Gly Glu Cys Ile Asp Ile Ser Lys
 325 330 335

Val Cys Asn Gln Glu Gln Asp Cys Arg Asp Trp Ser Asp Glu Pro Leu
 340 345 350

Lys Glu Cys His Ile Asn Glu Cys Leu Val Asn Asn Gly Gly Cys Ser
 355 360 365

His Ile Cys Lys Asp Leu Val Ile Gly Tyr Glu Cys Asp Cys Ala Ala
 370 375 380

Gly Phe Glu Leu Ile Asp Arg Lys Thr Cys Gly Asp Ile Asp Glu Cys
 385 390 395 400

Gln Asn Pro Gly Ile Cys Ser Gln Ile Cys Ile Asn Leu Lys Gly Gly
 405 410 415

Tyr Lys Cys Glu Cys Ser Arg Gly Tyr Gln Met Asp Leu Ala Thr Gly
 420 425 430

Val Cys Lys Ala Val Gly Lys Glu Pro Ser Leu Ile Phe Thr Asn Arg

435	440	445
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Arg Asp Ile Arg Lys Ile Gly Leu Glu Arg Lys Glu Tyr Ile Gln Leu
450 455 460

Val Glu Gln Leu Arg Asn Thr Val Ala Leu Asp Ala Asp Ile Ala Ala
465 470 475 480

Gln Lys Leu Phe Trp Ala Asp Ieu Ser Gln Lys Ala Ile Phe Ser Ala
485 490 495

Ser Ile Asp Asp Lys Val Gly Arg His Val Lys Met Ile Asp Asn Val
500 505 510

Tyr Asn Pro Ala Ala Ile Ala Val Asp Trp Val Tyr Lys Thr Ile Tyr
515 520 525

Trp Thr Asp Ala Ala Ser Lys Thr Ile Ser Val Ala Thr Leu Asp Gly
530 535 540

Thr Lys Arg Lys Phe Leu Phe Asn Ser Asp Leu Arg Glu Pro Ala Ser
545 550 555 560

Ile Ala Val Asp Pro Leu Ser Gly Pro Tyr Lys Lys Ser Pro Leu Leu
565 570 575

Ala:

<210> 26

<211> 694

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 26

Met Gly Thr Ser Ala Leu Trp Ala Leu Trp Leu Leu Leu Ala Leu Cys
1 5 10 15

Trp Ala Pro Arg Glu Ser Gly Ala Thr Gly Thr Gly Arg Lys Ala Lys
20 25 30

Cys Glu Pro Ser Gln Phe Gln Cys Thr Asn Gly Arg Cys Ile Thr Leu
35 40 45

Leu Trp Lys Cys Asp Gly Asp Glu Asp Cys Val Asp Gly Ser Asp Glu
50 55 60

Lys Asn Cys Val Lys Thr Cys Ala Glu Ser Asp Phe Val Cys Asn
65 70 75 80

Asn Gly Gln Cys Val Pro Ser Arg Trp Lys Cys Asp Gly Asp Pro Asp
85 90 95

Cys Glu Asp Gly Ser Asp Glu Ser Pro Glu Gln Cys His Met Arg Thr
100 105 110

Cys Arg Ile His Glu Ile Ser Cys Gly Ala His Ser Thr Gln Cys Ile
 115 120 125

Pro Val Ser Trp Arg Cys Asp Gly Glu Asn Asp Cys Asp Ser Gly Glu
 130 135 140

Asp Glu Glu Asn Cys Gly Asn Ile Thr Cys Ser Pro Asp Glu Phe Thr
 145 150 155 160

Cys Ser Ser Gly Arg Cys Ile Ser Arg Asn Phe Val Cys Asn Gly Gln
 165 170 175

Asp Asp Cys Ser Asp Gly Ser Asp Glu Leu Asp Cys Ala Pro Pro Thr
 180 185 190

Cys Gly Ala His Glu Phe Gln Cys Ser Thr Ser Ser Cys Ile Pro Ile
 195 200 205

Ser Trp Val Cys Asp Asp Asp Ala Asp Cys Ser Asp Gln Ser Asp Glu
 210 215 220

Ser Leu Glu Gln Cys Gly Arg Gln Pro Val Ile His Thr Lys Cys Pro
 225 230 235 240

Ala Ser Glu Ile Gln Cys Gly Ser Gly Glu Cys Ile His Lys Lys Trp
 245 250 255

Arg Cys Asp Gly Asp Pro Asp Cys Lys Asp Gly Ser Asp Glu Val Asn
 260 265 270

Cys Pro Ser Arg Thr Cys Arg Pro Asp Gln Phe Glu Cys Glu Asp Gly
 275 280 285

Ser Cys Ile His Gly Ser Arg Gln Cys Asn Gly Ile Arg Asp Cys Val
 290 295 300

Asp Gly Ser Asp Glu Val Asn Cys Lys Asn Val Asn Gln Cys Leu Gly
 305 310 315 320

Pro Gly Lys Phe Lys Cys Arg Ser Gly Glu Cys Ile Asp Ile Ser Lys
 325 330 335

Val Cys Asn Gln Glu Gln Asp Cys Arg Asp Trp Ser Asp Glu Pro Leu
 340 345 350

Lys Glu Cys His Ile Asn Glu Cys Leu Val Asn Asn Gly Gly Cys Ser
 355 360 365

His Ile Cys Lys Asp Leu Val Ile Gly Tyr Glu Cys Asp Cys Ala Ala
 370 375 380

Gly Phe Glu Leu Ile Asp Arg Lys Thr Cys Gly Asp Ile Asp Glu Cys
 385 390 395 400

Gln Asn Pro Gly Ile Cys Ser Gln Ile Cys Ile Asn Leu Lys Gly Gly
 405 410 415

Tyr Lys Cys Glu Cys Ser Arg Gly Tyr Gln Met Asp Leu Ala Thr Gly

420	425	430
Val Cys Lys Ala Val Gly Lys Glu Pro Ser Leu Ile Phe Thr Asn Arg		
435	440	445
Arg Asp Ile Arg Lys Ile Gly Leu Glu Arg Lys Glu Tyr Ile Gln Leu		
450	455	460
Val Glu Gln Leu Arg Asn Thr Val Ala Leu Asp Ala Asp Ile Ala Ala		
465	470	475
Gln Lys Leu Phe Trp Ala Asp Leu Ser Gln Lys Ala Ile Phe Ser Ala		
485	490	495
Ser Ile Asp Asp Lys Val Gly Arg His Val Lys Met Ile Asp Asn Val		
500	505	510
Tyr Asn Pro Ala Ala Ile Ala Val Asp Trp Val Tyr Lys Thr Ile Tyr		
515	520	525
Trp Thr Asp Ala Ala Ser Lys Thr Ile Ser Val Ala Thr Leu Asp Gly		
530	535	540
Thr Lys Arg Lys Phe Leu Phe Asn Ser Asp Leu Arg Glu Pro Ala Ser		
545	550	555
Ile Ala Val Asp Pro Leu Ser Gly Phe Val Tyr Trp Ser Asp Trp Gly		
565	570	575
Glu Pro Ala Lys Ile Glu Lys Ala Gly Met Asn Gly Phe Asp Arg Arg		
580	585	590
Pro Leu Val Thr Ala Asp Ile Gln Trp Pro Asn Gly Ile Thr Leu Asp		
595	600	605
Leu Ile Lys Ser Arg Leu Tyr Trp Leu Asp Ser Lys Leu His Met Leu		
610	615	620
Ser Ser Val Asp Leu Asn Gly Gln Asp Arg Arg Ile Val Leu Lys Ser		
625	630	635
640		
Leu Glu Phe Leu Ala His Pro Leu Ala Leu Thr Ile Phe Glu Val Lys		
645	650	655
Ile Gly Val Lys Lys Thr Trp Arg Met Glu Asp Val Asn Thr Tyr Ala		
660	665	670
Cys Gln His His Arg Leu Met Ile Thr Leu Gln Asn Ile Pro Val Pro		
675	680	685
Val Pro Val Gly Thr Met		
690		
<210> 27		
<211> 824		
<212> PRT		
<213> Artificial sequence		
<220>		

<223> A novel predicted alternative spliced variant protein product

<400> 27.

Met Gly Thr Ser Ala Leu Trp Ala Leu Trp Leu Leu Leu Ala Leu Cys
1 5 10 15

Trp Ala Pro Arg Glu Ser Gly Ala Thr Gly Thr Gly Arg Lys Ala Lys
20 25 30

Cys Glu Pro Ser Gln Phe Gln Cys Thr Asn Gly Arg Cys Ile Thr Leu
35 40 45

Leu Trp Lys Cys Asp Gly Asp Glu Asp Cys Val Asp Gly Ser Asp Glu
50 55 60

Lys Asn Cys Val Lys Lys Thr Cys Ala Glu Ser Asp Phe Val Cys Asn
65 70 75 80

Asn Gly Gln Cys Val Pro Ser Arg Trp Lys Cys Asp Gly Asp Pro Asp
85 90 95

Cys Glu Asp Gly Ser Asp Glu Ser Pro Glu Gln Cys His Met Arg Thr
100 105 110

Cys Arg Ile His Glu Ile Ser Cys Gly Ala His Ser Thr Gln Cys Ile
115 120 125

Pro Val Ser Trp Arg Cys Asp Gly Glu Asn Asp Cys Asp Ser Gly Glu
130 135 140

Asp Glu Glu Asn Cys Gly Asn Ile Thr Cys Ser Pro Asp Glu Phe Thr
145 150 155 160

Cys Ser Ser Gly Arg Cys Ile Ser Arg Asn Phe Val Cys Asn Gly Gln
165 170 175

Asp Asp Cys Ser Asp Gly Ser Asp Glu Leu Asp Cys Ala Pro Pro Thr
180 185 190

Cys Gly Ala His Glu Phe Gln Cys Ser Thr Ser Ser Cys Ile Pro Ile
195 200 205

Ser Trp Val Cys Asp Asp Ala Asp Cys Ser Asp Gln Ser Asp Glu
210 215 220

Ser Leu Glu Gln Cys Gly Arg Gln Pro Val Ile His Thr Lys Cys Pro
225 230 235 240

Ala Ser Glu Ile Gln Cys Gly Ser Gly Glu Cys Ile His Lys Lys Trp
245 250 255

Arg Cys Asp Gly Asp Pro Asp Cys Lys Asp Gly Ser Asp Glu Val Asn
260 265 270

Cys Pro Ser Arg Thr Cys Arg Pro Asp Gln Phe Glu Cys Glu Asp Gly
275 280 285

Ser Cys Ile His Gly Ser Arg Gln Cys Asn Gly Ile Arg Asp Cys Val

290	295	300
Asp Gly Ser Asp Glu Val Asn Cys Lys Asn Val Asn Gln Cys Leu Gly		
305	310	315
320		
Pro Gly Lys Phe Lys Cys Arg Ser Gly Glu Cys Ile Asp Ile Ser Lys		
325	330	335
Val Cys Asn Gln Glu Gln Asp Cys Arg Asp Trp Ser Asp Glu Pro Leu		
340	345	350
Lys Glu Cys His Ile Asn Glu Cys Leu Val Asn Asn Gly Gly Cys Ser		
355	360	365
His Ile Cys Lys Asp Ieu Val Ile Gly Tyr Glu Cys Asp Cys Ala Ala		
370	375	380
Gly Phe Glu Leu Ile Asp Arg Lys Thr Cys Gly Asp Ile Asp Glu Cys		
385	390	395
400		
Gln Asn Pro Gly Ile Cys Ser Gln Ile Cys Ile Asn Leu Lys Gly Gly		
405	410	415
Tyr Lys Cys Glu Cys Ser Arg Gly Tyr Gln Met Asp Leu Ala Thr Gly		
420	425	430
Val Cys Lys Ala Val Gly Lys Glu Pro Ser Leu Ile Phe Thr Asn Arg		
435	440	445
Arg Asp Ile Arg Lys Ile Gly Leu Glu Arg Lys Glu Tyr Ile Gln Leu		
450	455	460
Val Glu Gln Leu Arg Asn Thr Val Ala Leu Asp Ala Asp Ile Ala Ala		
465	470	475
480		
Gln Lys Leu Phe Trp Ala Asp Leu Ser Gln Lys Ala Ile Phe Ser Ala		
485	490	495
Ser Ile Asp Asp Lys Val Gly Arg His Val Lys Met Ile Asp Asn Val		
500	505	510
Tyr Asn Pro Ala Ala Ile Ala Val Asp Trp Val Tyr Lys Thr Ile Tyr		
515	520	525
Trp Thr Asp Ala Ala Ser Lys Thr Ile Ser Val Ala Thr Leu Asp Gly		
530	535	540
Thr Lys Arg Lys Phe Leu Phe Asn Ser Asp Leu Arg Glu Pro Ala Ser		
545	550	555
560		
Ile Ala Val Asp Pro Leu Ser Gly Phe Val Tyr Trp Ser Asp Trp Gly		
565	570	575
Glu Pro Ala Lys Ile Glu Lys Ala Gly Met Asn Gly Phe Asp Arg Arg		
580	585	590
Pro Leu Val Thr Ala Asp Ile Gln Trp Pro Asn Gly Ile Thr Leu Asp		
595	600	605

Leu Ile Lys Ser Arg Leu Tyr Trp Leu Asp Ser Lys Leu His Met Leu
 610 615 620

Ser Ser Val Asp Leu Asn Gly Gln Asp Arg Arg Ile Val Leu Lys Ser
 625 630 635 640

Leu Glu Phe Leu Ala His Pro Leu Ala Leu Thr Ile Phe Glu Asp Arg
 645. 650 655

Val Tyr Trp Ile Asp Gly Glu Asn Glu Ala Val Tyr Gly Ala Asn Lys
 660 665 670

Phe Thr Gly Ser Glu Leu Ala Thr Leu Val Asn Asn Leu Asn Asp Ala
 675 680 685

Gln Asp Ile Ile Val Tyr His Glu Leu Val Gln Pro Ser Gly Thr Ala
 690 695 700

Thr Thr Val Thr Tyr Ser Glu Thr Lys Asp Thr Asn Thr Thr Glu Ile
 705 710 715 720

Ser Ala Thr Ser Gly Leu Val Pro Gly Gly Ile Asn Val Thr Thr Ala
 725 730 735

Val Ser Glu Val Ser Val Pro Pro Lys Gly Thr Ser Ala Ala Trp Ala
 740 745 750

Ile Leu Pro Leu Leu Leu Val Met Ala Ala Val Gly Gly Tyr Leu
 755 760 765

Met Trp Arg Asn Trp Gln His Lys Asn Met Lys Ser Met Asn Phe Asp
 770 775 780

Asn Pro Val Tyr Leu Lys Thr Thr Glu Glu Asp Leu Ser Ile Asp Ile
 785 790 795 800

Gly Arg His Ser Ala Ser Val Gly His Thr Tyr Pro Ala Ile Ser Val
 805 810 815

Val Ser Thr Asp Asp Asp Leu Ala
 820

<210> 28

<211> 431

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 28

Met Gly Thr Ser Ala Leu Trp Ala Leu Trp Leu Leu Ala Leu Cys
 1 5 10 15

Trp Ala Pro Arg Glu Ser Gly Ala Thr Gly Thr Gly Arg Lys Ala Lys
 20 25 30

Cys Glu Pro Ser Gln Phe Gln Cys Thr Asn Gly Arg Cys Ile Thr Leu

35 40 45

Leu Trp Lys Cys Asp Gly Asp Glu Asp Cys Val Asp Gly Ser Asp Glu
 50 55 60

Lys Asn Cys Val Lys Lys Thr Cys Ala Glu Ser Asp Phe Val Cys Asn
 65 70 75 80

Asn Gly Gln Cys Val Pro Ser Arg Trp Lys Cys Asp Gly Asp Pro Asp
 85 90 95

Cys Glu Asp Gly Ser Asp Glu Ser Pro Glu Gln Cys His Met Arg Thr
 100 105 110

Cys Arg Ile His Glu Ile Ser Cys Gly Ala His Ser Thr Gln Cys Ile
 115 120 125

Pro Val Ser Trp Arg Cys Asp Gly Glu Asn Asp Cys Asp Ser Gly Glu
 130 135 140

Asp Glu Glu Asn Cys Gly Asn Ile Thr Cys Ser Pro Asp Glu Phe Thr
 145 150 155 160

Cys Ser Ser Gly Arg Cys Ile Ser Arg Asn Phe Val Cys Asn Gln
 165 170 175

Asp Asp Cys Ser Asp Gly Ser Asp Glu Leu Asp Cys Ala Pro Pro Thr
 180 185 190

Cys Gly Ala His Glu Phe Gln Cys Ser Thr Ser Ser Cys Ile Pro Ile
 195 200 205

Ser Trp Val Cys Asp Asp Ala Asp Cys Ser Asp Gln Ser Asp Glu
 210 215 220

Ser Leu Glu Gln Cys Gly Arg Gln Pro Val Ile His Thr Lys Cys Pro
 225 230 235 240

Ala Ser Glu Ile Gln Cys Gly Ser Gly Glu Cys Ile His Lys Lys Trp
 245 250 255

Arg Cys Asp Gly Asp Pro Asp Cys Lys Asp Gly Ser Asp Glu Val Asn
 260 265 270

Cys Pro Ser Arg Thr Cys Arg Pro Asp Gln Phe Glu Cys Glu Asp Gly
 275 280 285

Ser Cys Ile His Gly Ser Arg Gln Cys Asn Gly Ile Arg Asp Cys Val
 290 295 300

Asp Gly Ser Asp Glu Val Asn Cys Lys Asn Val Asn Gln Cys Leu Gly
 305 310 315 320

Pro Gly Lys Phe Lys Cys Arg Ser Gly Glu Cys Ile Asp Ile Ser Lys
 325 330 335

Val Cys Asn Gln Glu Gln Asp Cys Arg Asp Trp Ser Asp Glu Pro Leu
 340 345 350

Lys Glu Cys His Ile Asn Glu Cys Leu Val Asn Asn Gly Gly Cys Ser
 355 360 365

His Ile Cys Lys Asp Leu Val Ile Gly Tyr Glu Cys Asp Cys Ala Ala
 370 375 380

Gly Phe Glu Leu Ile Asp Arg Lys Thr Cys Gly Gly Glu Ser Lys Lys
 385 390 395 400

Lys Thr Trp Thr Leu Gln Val Met Gly Lys Asp Ser Met Tyr Leu Val
 405 410 415

Arg Tyr Arg Ser Ser Lys Thr Asn Ser Asp Phe Pro Pro Arg Tyr
 420 425 430

<210> 29

<211> 199

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 29

Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
 1 5 10 15

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe
 20 25 30

Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala.
 35 40 45

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
 50 55 60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
 65 70 75 80

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
 85 90 95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
 100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
 115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
 130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
 145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
 165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Val Ser Gly Ser Glu Gln Asp Leu

180 185 190

Pro His Gln Leu His Val Glu
195

<210> 30

<211> 1300

<212> PRT

<213> Artificial sequence.

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 30

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
20 25 30

Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
35 40 45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
50 55 60

Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
65 70 75 80

Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
85 90 95

Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
100 105 110

Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
115 120 125

Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
130 135 140

Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
145 150 155 160

Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
165 170 175

Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
180 185 190

Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
195 200 205

Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
210 215 220

Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
225 230 235 240

Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
 245 250 255

Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys
 260 265 270

Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His
 275 280 285

Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys
 290 295 300

Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys
 305 310 315 320

Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Phe Ile Thr Val
 325 330 335

Lys His Arg Lys Gln Gln Val Leu Glu Thr Val Ala Gly Lys Arg Ser
 340 345 350

Tyr Arg Leu Ser Met Lys Val Lys Ala Phe Pro Ser Pro Glu Val Val
 355 360 365

Trp Leu Lys Asp Gly Leu Pro Ala Thr Glu Lys Ser Ala Arg Tyr Leu
 370 375 380

Thr Arg Gly Tyr Ser Leu Ile Ile Lys Asp Val Thr Glu Glu Asp Ala
 385 390 395 400

Gly Asn Tyr Thr Ile Leu Leu Ser Ile Lys Gln Ser Asn Val Phe Lys
 405 410 415

Asn Leu Thr Ala Thr Leu Ile Val Asn Val Lys Pro Gln Ile Tyr Glu
 420 425 430

Lys Ala Val Ser Ser Phe Pro Asp Pro Ala Leu Tyr Pro Leu Gly Ser
 435 440 445

Arg Gln Ile Leu Thr Cys Thr Ala Tyr Gly Ile Pro Gln Pro Thr Ile
 450 455 460

Lys Trp Phe Trp His Pro Cys Asn His Asn His Ser Glu Ala Arg Cys
 465 470 475 480

Asp Phe Cys Ser Asn Asn Glu Glu Ser Phe Ile Leu Asp Ala Asp Ser
 485 490 495

Asn Met Gly Asn Arg Ile Glu Ser Ile Thr Gln Arg Met Ala Ile Ile
 500 505 510

Glu Gly Lys Asn Lys Met Ala Ser Thr Leu Val Val Ala Asp Ser Arg
 515 520 525

Ile Ser Gly Ile Tyr Ile Cys Ile Ala Ser Asn Lys Val Gly Thr Val
 530 535 540

Gly Arg Asn Ile Ser Phe Tyr Ile Thr Asp Val Pro Asn Gly Phe His

545	550	555	560
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Val Asn Leu Glu Lys Met Pro Thr Glu Gly Glu Asp Leu Lys Leu Ser
 565 570 575

Cys Thr Val Asn Lys Phe Leu Tyr Arg Asp Val Thr Trp Ile Leu Leu
 580 585 590

Arg Thr Val Asn Asn Arg Thr Met His Tyr Ser Ile Ser Lys Gln Lys
 595 600 605

Met Ala Ile Thr Lys Glu His Ser Ile Thr Leu Asn Leu Thr Ile Met
 610 615 620

Asn Val Ser Leu Gln Asp Ser Gly Thr Tyr Ala Cys Arg Ala Arg Asn
 625 630 635 640

Val Tyr Thr Gly Glu Glu Ile Leu Gln Lys Lys Glu Ile Thr Ile Arg
 645 650 655

Asp Gln Glu Ala Pro Tyr Leu Leu Arg Asn Leu Ser Asp His Thr Val
 660 665 670

Ala Ile Ser Ser Ser Thr Thr Leu Asp Cys His Ala Asn Gly Val Pro
 675 680 685

Glu Pro Gln Ile Thr Trp Phe Lys Asn Asn His Lys Ile Gln Gln Glu
 690 695 700

Pro Gly Ile Ile Leu Gly Pro Gly Ser Ser Thr Leu Phe Ile Glu Arg
 705 710 715 720

Val Thr Glu Glu Asp Glu Gly Val Tyr His Cys Lys Ala Thr Asn Gln
 725 730 735

Lys Gly Ser Val Glu Ser Ser Ala Tyr Leu Thr Val Gln Gly Thr Ser
 740 745 750

Asp Lys Ser Asn Leu Glu Leu Ile Thr Leu Thr Cys Thr Cys Val Ala
 755 760 765

Ala Thr Leu Phe Trp Leu Leu Leu Thr Leu Leu Ile Arg Lys Met Lys
 770 775 780

Arg Ser Ser Ser Glu Ile Lys Thr Asp Tyr Leu Ser Ile Ile Met Asp
 785 790 795 800

Pro Asp Glu Val Pro Leu Asp Glu Gln Cys Glu Arg Leu Pro Tyr Asp
 805 810 815

Ala Ser Lys Trp Glu Phe Ala Arg Glu Arg Leu Lys Leu Gly Lys Ser
 820 825 830

Leu Gly Arg Gly Ala Phe Gly Lys Val Val Gln Ala Ser Ala Phe Gly
 835 840 845

Ile Lys Lys Ser Pro Thr Cys Arg Thr Val Ala Val Lys Met Leu Lys
 850 855 860

Gly Pro Leu Met Val Ile Val Glu Tyr Cys Lys Tyr Gly Asn Leu Ser
 865 870 875 880

Asn Tyr Leu Lys Ser Lys Arg Asp Leu Phe Phe Leu Asn Lys Asp Ala
 885 890 895

Ala Leu His Met Glu Pro Lys Lys Glu Lys Met Glu Pro Gly Leu Glu
 900 905 910

Gln Gly Lys Lys Pro Arg Leu Asp Ser Val Thr Ser Ser Glu Ser Phe
 915 920 925

Ala Ser Ser Gly Phe Gln Glu Asp Lys Ser Leu Ser Asp Val Glu Glu
 930 935 940

Glu Glu Asp Ser Asp Gly Phe Tyr Lys Glu Pro Ile Thr Met Glu Asp
 945 950 955 960

Leu Ile Ser Tyr Ser Phe Gln Val Ala Arg Gly Met Glu Phe Leu Ser
 965 970 975

Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu
 980 985 990

Ser Glu Asn Asn Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp
 995 1000 1005

Ile Tyr Lys Asn Pro Asp Tyr Val Arg Lys Gly Asp Thr Arg Leu
 1010 1015 1020

Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asp Lys Ile Tyr
 1025 1030 1035

Ser Thr Lys Ser Asp Val Trp Ser Tyr Gly Val Leu Leu Trp Glu
 1040 1045 1050

Ile Phe Ser Leu Gly Gly Ser Pro Tyr Pro Gly Val Gln Met Asp
 1055 1060 1065

Glu Asp Phe Cys Ser Arg Leu Arg Glu Gly Met Arg Met Arg Ala
 1070 1075 1080

Pro Glu Tyr Ser Thr Pro Glu Ile Tyr Gln Ile Met Leu Asp Cys
 1085 1090 1095

Trp His Arg Asp Pro Lys Glu Arg Pro Arg Phe Ala Glu Leu Val
 1100 1105 1110

Glu Lys Leu Gly Asp Leu Leu Gln Ala Asn Val Gln Gln Asp Gly
 1115 1120 1125

Lys Asp Tyr Ile Pro Ile Asn Ala Ile Leu Thr Gly Asn Ser Gly
 1130 1135 1140

Phe Thr Tyr Ser Thr Pro Ala Phe Ser Glu Asp Phe Phe Lys Glu
 1145 1150 1155

Ser Ile Ser Ala Pro Lys Phe Asn Ser Gly Ser Ser Asp Asp Val
1160 1165 1170

Arg Tyr Val Asn Ala Phe Lys Phe Met Ser Leu Glu Arg Ile Lys
1175 1180 1185

Thr Phe Glu Glu Leu Leu Pro Asn Ala Thr Ser Met Phe Asp Asp
1190 1195 1200

Tyr Gln Gly Asp Ser Ser Thr Leu Leu Ala Ser Pro Met Leu Lys
1205 1210 1215

Arg Phe Thr Trp Thr Asp Ser Lys Pro Lys Ala Ser Leu Lys Ile
1220 1225 1230

Asp Leu Arg Val Thr Ser Lys Ser Lys Glu Ser Gly Leu Ser Asp
1235 1240 1245

Val Ser Arg Pro Ser Phe Cys His Ser Ser Cys Gly His Val Ser
1250 1255 1260

Glu Gly Lys Arg Arg Phe Thr Tyr Asp His Ala Glu Leu Glu Arg
1265 1270 1275

Lys Ile Ala Cys Cys Ser Pro Pro Pro Asp Tyr Asn Ser Val Val
1280 1285 1290

Leu Tyr Ser Thr Pro Pro Ile
1295 1300

<210> 31
<211> 773
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 31

Met Gln Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu
1 5 10 15

Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
20 25 30

Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
35 40 45

Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
50 55 60

Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
65 70 75 80

Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
85 90 95

Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
100 105 110

Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
 115 120 125

Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
 130 135 140

Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
 145 150 155 160

Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg
 165 170 175

Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile
 180 185 190

Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser
 195 200 205

Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr
 210 215 220

Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
 225 230 235 240

Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
 245 250 255

Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
 260 265 270

Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
 275 280 285

Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
 290 295 300

Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
 305 310 315 320

Phe Val Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met
 325 330 335

Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala
 340 345 350

Lys Tyr Leu Gly Tyr Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly
 355 360 365

Ile Pro Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr
 370 375 380

Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu
 385 390 395 400

Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val
 405 410 415

Val Tyr Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val
 420 425 430

Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr
 435 440 445

Ala Ile Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu
 450 455 460

Glu Cys Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr
 465 470 475 480

Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys
 485 490 495

Ile Glu Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys
 500 505 510

Thr Val Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr
 515 520 525

Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser
 530 535 540

Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln
 545 550 555 560

Pro Thr Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser
 565 570 575

Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro
 580 585 590

Ile His Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr
 595 600 605

Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile
 610 615 620

Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr
 625 630 635 640

Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val
 645 650 655

Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn
 660 665 670

Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys
 675 680 685

Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn
 690 695 700

Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg
 705 710 715 720

Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr
 725 730 735

Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe
 740 745 750

Ile Ile Glu Gly Gln Trp Arg Gly Thr Glu Asp Arg Leu Leu Val His
 755 760 765

Arg His Gly Ser Arg
 770

<210> 32

<211> 802

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 32

Met Gln Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu
 1 5 10 15

Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
 20 25 30

Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
 35 40 45

Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
 50 55 60

Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
 65 70 75 80

Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
 85 90 95

Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
 100 105 110

Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
 115 120 125

Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
 130 135 140

Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
 145 150 155 160

Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg
 165 170 175

Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile
 180 185 190

Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser
 195 200 205

Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr
 210 215 220

Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
 225 230 235 240

Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
 245 250 255

Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
 260 265 270

Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
 275 280 285

Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
 290 295 300

Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
 305 310 315 320

Phe Val Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met
 325 330 335

Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala
 340 345 350

Lys Tyr Leu Gly Tyr Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly
 355 360 365

Ile Pro Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr
 370 375 380

Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu
 385 390 395 400

Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val
 405 410 415

Val Tyr Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val
 420 425 430

Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr
 435 440 445

Ala Ile Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu
 450 455 460

Glu Cys Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr
 465 470 475 480

Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Asn Lys
 485 490 495

Ile Glu Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys
 500 505 510

Thr Val Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr
 515 520 525

Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser
 530 535 540

Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln
 545 550 555 560

Pro Thr Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser
 565 570 575

Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro
 580 585 590

Ile His Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr
 595 600 605

Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile
 610 615 620

Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr
 625 630 635 640

Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val
 645 650 655

Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn
 660 665 670

Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys
 675 680 685

Thr Ala Ser Gly Asn Pro Pro Gln Ile Met Trp Phe Lys Asp Asn
 690 695 700

Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg
 705 710 715 720

Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr
 725 730 735

Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe
 740 745 750

Ile Ile Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Leu
 755 760 765

Val Gly Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile
 770 775 780

Ile Leu Arg Thr Val Lys Arg Val Ser Leu Leu Ala Val Val Pro Leu
 785 790 795 800

Ala Lys

<211> 1176

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 33

Met	Gln	Ser	Lys	Val	Ieu	Leu	Ala	Val	Ala	Leu	Trp	Leu	Cys	Val	Glu
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Thr	Arg	Ala	Ala	Ser	Val	Gly	Leu	Pro	Ser	Val	Ser	Leu	Asp	Leu	Pro
	20				25					30					

Arg	Leu	Ser	Ile	Gln	Lys	Asp	Ile	Leu	Thr	Ile	Lys	Ala	Asn	Thr	Thr
	35				40					45					

Leu	Gln	Ile	Thr	Cys	Arg	Gly	Gln	Arg	Asp	Leu	Asp	Trp	Leu	Trp	Pro
	50				55				60						

Asn	Asn	Gln	Ser	Gly	Ser	Glu	Gln	Arg	Val	Glu	Val	Thr	Glu	Cys	Ser
	65				70				75			80			

Asp	Gly	Leu	Phe	Cys	Lys	Thr	Leu	Thr	Ile	Pro	Lys	Val	Ile	Gly	Asn
	85				90				95						

Asp	Thr	Gly	Ala	Tyr	Lys	Cys	Phe	Tyr	Arg	Glu	Thr	Asp	Leu	Ala	Ser
	100				105				110						

Val	Ile	Tyr	Val	Tyr	Val	Gln	Asp	Tyr	Arg	Ser	Pro	Phe	Ile	Ala	Ser
	115				120				125						

Val	Ser	Asp	Gln	His	Gly	Val	Val	Tyr	Ile	Thr	Glu	Asn	Lys	Asn	Lys
	130				135				140						

Thr	Val	Val	Ile	Pro	Cys	Leu	Gly	Ser	Ile	Ser	Asn	Leu	Asn	Val	Ser
	145				150				155			160			

Leu	Cys	Ala	Arg	Tyr	Pro	Glu	Lys	Arg	Phe	Val	Pro	Asp	Gly	Asn	Arg
	165				170				175						

Ile	Ser	Trp	Asp	Ser	Lys	Lys	Gly	Phe	Thr	Ile	Pro	Ser	Tyr	Met	Ile
	180				185				190						

Ser	Tyr	Ala	Gly	Met	Val	Phe	Cys	Glu	Ala	Lys	Ile	Asn	Asp	Glu	Ser
	195				200				205						

Tyr	Gln	Ser	Ile	Met	Tyr	Ile	Val	Val	Val	Val	Gly	Tyr	Arg	Ile	Tyr
	210				215				220						

Asp	Val	Val	Ieu	Ser	Pro	Ser	His	Gly	Ile	Glu	Leu	Ser	Val	Gly	Glu
	225				230				235			240			

Lys	Leu	Val	Leu	Asn	Cys	Thr	Ala	Arg	Thr	Glu	Leu	Asn	Val	Gly	Ile
	245				250				255						

Asp	Phe	Asn	Trp	Glu	Tyr	Pro	Ser	Ser	Lys	His	Gln	His	Lys	Lys	Leu
	260				265				270						

Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
275 280 285

Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
290 295 300

Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
 305 .310 315 320

Phe Val Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met
325 330 335

Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala
340 345 350

Lys Tyr Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly
355 360 365

Ile Pro Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr
370 375 380

Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu
385 390 395 400

Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val
..... 405 410 415

Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr
435 440 445

Ala Ile Pro Pro Pro-His His Ile His Trp Tyr Trp Gln Leu Glu Glu
450 455 460

Glu Cys Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr
 465 470 475 480

Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys
485 490 495

Ile Glu Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Lys Asn Lys
500 505 510

Thr Val Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr
 515 520 525

Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser
530 535 540

Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln
545 550 555 560

Pro Thr Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser
565. 570 575

Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro

580

585

590

Ile His Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr
 595 600 605

Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile
 610 615 620

Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr
 625 630 635 640

Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val
 645 650 655

Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn
 660 665 670

Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys
 675 680 685

Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn
 690 695 700

Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg
 705 710 715 720

Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr
 725 730 735

Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe
 740 745 750

Ile Ile Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu
 755 760 765

Val Gly Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile
 770 775 780

Ile Leu Arg Thr Val Lys Arg Ala Asn Gly Glu Leu Lys Thr Gly
 785 790 795 800

Tyr Leu Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His
 805 810 815

Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp
 820 825 830

Arg Leu Lys Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gin Val
 835 840 845

Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr
 850 855 860

Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg
 865 870 875 880

Ala Leu Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu
 885 890 895

Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu
 900 905 910

Met Val Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu
 915 920 925

Arg Ser Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg
 930 935 940

Phe Arg Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys
 945 950 955 960

Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly
 965 970 975

Phe Val Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Ala Pro
 980 985 990

Glu Asp Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr
 995 1000 1005

Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys
 1010 1015 1020

Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu
 1025 1030 1035

Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile
 1040 1045 1050

Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro
 1055 1060 1065

Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr
 1070 1075 1080

Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile
 1085 1090 1095

Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu
 1100 1105 1110

Glu Phe Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro
 1115 1120 1125

Asp Tyr Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp
 1130 1135 1140

His Gly Glu Pro Ser Gln Arg Pro Thr Phe Ser Glu Leu Val Glu
 1145 1150 1155

His Leu Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln Ser Val Ser
 1160 1165 1170

Ala Glu Gln
 1175

<210> 34
<211> 1235
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 34

Met Gln Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu
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Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
20 25 30

Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
35 40 45

Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
50 55 60

Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
65 70 75 80

Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
85 90 95

Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
100 105 110

Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
115 120 125

Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
130 135 140

Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
145 150 155 160

Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg
165 170 175

Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile
180 185 190

Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser
195 200 205

Tyr Gln Ser Ile Met Tyr Ile Val Val Val Gly Tyr Arg Ile Tyr
210 215 220

Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
225 230 235 240

Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
245 250 255

Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Leu
260 265 270

Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
275 280 285

Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
290 295 . . . 300

Phe Val Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met
325. 330 335

Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala
 340 345 350

Lys Tyr Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly
355 360 365

Ile Pro Leu Glu Ser Asn His Thr Ile Lys Ala GLy His Val Val Leu Thr
370 375 380

Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu
385 390 395 400

Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val
405 410 415

Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr
435 440 445

Ala Ile Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu
450 455 460

Glu Cys Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr
465 470 475 480

Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys
485 490 495

Ile Glu Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys
500 505 510

Thr Val Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr
515 520 525

Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser
530 535 540

Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln
545 550 555 560

Pro Thr Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser
 565 570 575

Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro
580 585 590

Ile His Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr
595 600 605

Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile
610 615 620

Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr
625 630 635 640

Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val
645 650 655

Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn
660 665 670

Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys
675 680 685

Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn
690 695 700

Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg
705 710 715 720

Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr
725 730 735

Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe
740 745 750

Ile Ile Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu
755 760 765

Val Gly Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile
770 775 780

Ile Leu Arg Thr Val Lys Arg Ala Asn Gly Gly Glu Leu Lys Thr Gly
785 790 795 800

Tyr Leu Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His
805 810 815

Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp
820 825 830

Arg Leu Lys Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Val
835 840 845

Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr
850 855 860

Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg
865 870 875 880

Ala Leu Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu
 885 890 895

Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu
 900 905 910

Met Val Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu
 915 920 925

Arg Ser Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg
 930 935 940

Phe Arg Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys
 945 950 955 960

Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly
 965 970 975

Phe Val Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Ala Pro
 980 985 990

Glu Asp Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr
 995 1000 1005

Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys
 1010 1015 1020

Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu
 1025 1030 1035

Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile
 1040 1045 1050

Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro
 1055 1060 1065

Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr
 1070 1075 1080

Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile
 1085 1090 1095

Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu
 1100 1105 1110

Glu Phe Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro
 1115 1120 1125

Asp Tyr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp
 1130 1135 1140

His Gly Glu Pro Ser Gln Arg Pro Thr Phe Ser Glu Leu Val Glu
 1145 1150 1155

His Leu Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys
 1160 1165 1170

Asp Tyr Ile Val Leu Pro Ile Ser Glu Thr Leu Ser Met Glu Glu

1175 1180 1185
Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met Glu
1190 1195 1200

Glu Glu Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala
1205 1210 1215

Gly Ile Arg Thr Thr Arg Arg Thr Val Val Trp Phe Leu Pro Gln
1220 1225 1230

Lys Ser
1235

<210> 35
<211> 1267
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 35

Met Gln Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu
1 5 10 15

Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
20 25 30

Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
35 40 45

Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
50 55 60

Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
65 70 75 80

Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
85 90 95

Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
100 105 110

Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
115 120 125

Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
130 135 140

Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
145 150 155 160

Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg
165 170 175

Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile
180 185 190

Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser
 195 200 205

Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr
 210 215 220

Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
 225 230 235 240

Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
 245 250 255

Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
 260 265 270

Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
 275 280 285

Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
 290 295 300

Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
 305 310 315 320

Phe Val Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met
 325 330 335

Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala
 340 345 350

Lys Tyr Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly
 355 360 365

Ile Pro Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr
 370 375 380

Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu
 385 390 395 400

Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val
 405 410 415

Val Tyr Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val
 420 425 430

Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr
 435 440 445

Ala Ile Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu
 450 455 460

Glu Cys Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr
 465 470 475 480

Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Asn Lys
 485 490 495

Ile Glu Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys

500

505

510

Thr Val Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr
515 520 525

Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser
530 535 540

Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln
545 550 555 560

Pro Thr Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser
565 570 575

Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro
580 585 590

Ile His Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr
595 600 605

Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile
610 615 620

Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr
625 630 635 640

Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val
645 650 655

Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn
660 665 670

Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys
675 680 685

Thr Ala Ser Gly Asn Pro Pro Gln Ile Met Trp Phe Lys Asp Asn
690 695 700

Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg
705 710 715 720

Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr
725 730 735

Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe
740 745 750

Ile Ile Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu
755 760 765

Val Gly Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile
770 775 780

Ile Leu Arg Thr Val Lys Arg Ala Asn Gly Gly Glu Leu Lys Thr Gly
785 790 795 800

Tyr Leu Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His
805 810 815

Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp
 820 825 830

Arg Leu Lys Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Val
 835 840 845

Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr
 850 855 860

Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg
 865 870 875 880

Ala Leu Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu
 885 890 895

Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu
 900 905 910

Met Val Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu
 915 920 925

Arg Ser Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg
 930 935 940

Phe Arg Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys
 945 950 955 960

Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly
 965 970 975

Phe Val Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Ala Pro
 980 985 990

Glu Asp Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr
 995 1000 1005

Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys
 1010 1015 1020

Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu
 1025 1030 1035

Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile
 1040 1045 1050

Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro
 1055 1060 1065

Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr
 1070 1075 1080

Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile
 1085 1090 1095

Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu
 1100 1105 1110

Glu Phe Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro
1115 1120 1125

Asp Tyr Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp
1130 1135 1140

His Gly Glu Pro Ser Gln Arg Pro Thr Phe Ser Glu Leu Val Glu
1145 1150 1155

His Leu Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys
1160 1165 1170

Asp Tyr Ile Val Leu Pro Ile Ser Glu Thr Leu Ser Met Glu Glu
1175 1180 1185

Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met Glu
1190 1195 1200

Glu Glu Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala
1205 1210 1215

Gly Ile Ser Gln Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg Pro
1220 1225 1230

Val Ser Val Lys Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu
1235 1240 1245

Val Lys Val Ile Pro Asp Trp Asn Gly Ala Gln Gln Lys Gln Gly
1250 1255 1260

Val Cys Gly Ile
1265

<210> 36

<211> 317

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 36

Met Ala Phe Pro Pro Arg Arg Leu Arg Leu Gly Pro Arg Gly Leu
1 5 10 15

Pro Leu Leu Leu Ser Gly Leu Leu Pro Leu Cys Arg Ala Phe Asn
20 25 30

Leu Asp Val Asp Ser Pro Ala Glu Tyr Ser Gly Pro Glu Gly Ser Tyr
35 40 45

Phe Gly Phe Ala Val Asp Phe Phe Val Pro Ser Ala Ser Ser Arg Met
50 55 60

Phe Leu Leu Val Gly Ala Pro Lys Ala Asn Thr Thr Gln Pro Gly Ile
65 70 75 80

Val Glu Gly Gly Gln Val Leu Lys Cys Asp Trp Ser Ser Thr Arg Arg
85 90 95

Cys Gln Pro Ile Glu Phe Asp Ala Thr Gly Asn Arg Asp Tyr Ala Lys
 100 105 110

Asp Asp Pro Leu Glu Phe Lys Ser His Gln Trp Phe Gly Ala Ser Val
 115 120 125

Arg Ser Lys Gln Asp Lys Ile Leu Ala Cys Ala Pro Leu Tyr His Trp
 130 135 140

Arg Thr Glu Met Lys Gln Glu Arg Glu Pro Val Gly Thr Cys Phe Leu
 145 150 155 160

Gln Asp Gly Thr Lys Thr Val Glu Tyr Ala Pro Cys Arg Ser Gln Asp
 165 170 175

Ile Asp Ala Asp Gly Gln Gly Phe Cys Gln Gly Phe Ser Ile Asp
 180 185 190

Phe Thr Lys Ala Asp Arg Val Leu Leu Gly Gly Pro Gly Ser Phe Tyr
 195 200 205

Trp Gln Gly Gln Leu Ile Ser Asp Gln Val Ala Glu Ile Val Ser Lys
 210 215 220

Tyr Asp Pro Asn Val Tyr Ser Ile Lys Tyr Asn Asn Gln Leu Ala Thr
 225 230 235 240

Arg Thr Ala Gln Ala Ile Phe Asp Asp Ser Tyr Leu Gly Tyr Ser Val
 245 250 255

Ala Val Gly Asp Phe Asn Gly Asp Gly Ile Asp Asp Phe Val Ser Gly
 260 265 270

Val Pro Arg Ala Ala Arg Thr Leu Gly Met Val Tyr Ile Tyr Asp Gly
 275 280 285

Lys Asn Met Ser Ser Leu Tyr Asn Phe Thr Gly Glu Gln Leu Cys Arg
 290 295 300

Cys Val Tyr Trp Ser Thr Ser Leu His Gly Ser Trp Leu
 305 310 315

<210> 37

<211> 643

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 37

Met Ala Phe Pro Pro Arg Arg Leu Arg Leu Gly Pro Arg Gly Leu
 1 5 10 15

Pro Leu Leu Leu Ser Gly Leu Leu Pro Leu Cys Arg Ala Phe Asn
 20 25 30

Leu Asp Val Asp Ser Pro Ala Glu Tyr Ser Gly Pro Glu Gly Ser Tyr

35. 40 45

Phe Gly Phe Ala Val Asp Phe Phe Val Pro Ser Ala Ser Ser Arg Met
50 55 60

Phe Leu Leu Val Gly Ala Pro Lys Ala Asn Thr Thr Gln Pro Gly Ile
65 70 75 80

Val Glu Gly Gly Gln Val Leu Lys Cys Asp Trp Ser Ser Thr Arg Arg
85 90 95

Cys Gln Pro Ile Glu Phe Asp Ala Thr Gly Asn Arg Asp Tyr Ala Lys
100 105 110

Asp Asp Pro Leu Glu Phe Lys Ser His Gln Trp Phe Gly Ala Ser Val
115 120

Arg Ser Lys Gln Asp Lys Ile Leu Ala Cys Ala Pro Leu Tyr His Trp
130 135 140

Arg Thr Glu Met Lys Gln Glu Arg Glu Pro Val Gly Thr Cys Phe Leu
145 150 155 160

Gln Asp Gly Thr Lys Thr Val Glu Tyr Ala Pro Cys Arg Ser Gln Asp
165 170 175

Ile Asp Ala Asp Gly Gln Gly Phe Cys Gln Gly Phe Ser Ile Asp
180 185 190

Phe Thr Lys Ala Asp Arg Val Leu Leu Gly Gly Pro Gly Ser Phe Tyr
195 200 205

Trp Gln Gly Gln Leu Ile Ser Asp Gln Val Ala Glu Ile Val Ser Lys
210 215 220

Tyr Asp Pro Asn Val Tyr Ser Ile Lys Tyr Asn Asn Gln Leu Ala Thr
225 230 235 240

Arg Thr Ala Gln Ala Ile Phe Asp Asp Ser Tyr Leu Gly Tyr Ser Val
245 250 255

Ala Val Gly Asp Phe Asn Gly Asp Gly Ile Asp Asp Phe Val Ser Gly
260 265 270

Val Pro Arg Ala Ala Arg Thr Leu Gly Met Val Tyr Ile Tyr Asp Gly
275 280 285

Lys Asn Met Ser Ser Leu Tyr Asn Phe Thr Gly Glu Gln Met Ala Ala
290 295 300

Tyr Phe Gly Phe Ser Val Ala Ala Thr Asp Ile Asn Gly Asp Asp Tyr
305 310 315 320

Ala Asp Val Phe Ile Gly Ala Pro Leu Phe Met Asp Arg Gly Ser Asp
325 330 335

Gly Lys Leu Gln Glu Val Gly Gln Val Ser Val Ser Leu Gln Arg Ala
340 345 350

Ser Gly Asp Phe Gln Thr Thr Lys Leu Asn Gly Phe Glu Val Phe Ala
355 360 365

Arg Phe Gly Ser Ala Ile Ala Pro Leu Gly Asp Leu Asp Gln Asp Gly
370 375 380

Phe Asn Asp Ile Ala Ile Ala Ala Pro Tyr Gly Gly Glu Asp Lys Lys
385 390 395 400

Gly Ile Val Tyr Ile Phe Asn Gly Arg Ser Thr Gly Leu Asn Ala Val
405 410 415

Pro Ser Gln Ile Leu Glu Gly Gln Trp Ala Ala Arg Ser Met Pro Pro
420 425 430

Ser Phe Gly Tyr Ser Met Lys Gly Ala Thr Asp Ile Asp Lys Asn Gly
435 440 445

Tyr Pro Asp Leu Ile Val Gly Ala Phe Gly Val Asp Arg Ala Ile Leu
450 455 460

Tyr Arg Ala Arg Pro Val Ile Thr Val Asn Ala Gly Leu Glu Val Tyr
465 470 475 480

Pro Ser Ile Leu Asn Gln Asp Asn Lys Thr Cys Ser Leu Pro Gly Thr
485 490 495

Ala Leu Lys Val Ser Cys Phe Asn Val Arg Phe Cys Leu Lys Ala Asp
500 505 510

Gly Lys Gly Val Leu Pro Arg Lys Leu Asn Phe Gln Val Glu Leu Leu
515 520 525

Leu Asp Lys Leu Lys Gln Lys Gly Ala Ile Arg Arg Ala Leu Phe Leu
530 535 540

Tyr Ser Arg Ser Pro Ser His Ser Lys Asn Met Thr Ile Ser Arg Gly
545 550 555 560

Gly Leu Met Gln Cys Glu Glu Leu Ile Ala Tyr Leu Arg Asp Glu Ser
565 570 575

Glu Phe Arg Asp Lys Leu Thr Pro Ile Thr Ile Phe Met Glu Tyr Arg
580 585 590

Leu Asp Tyr Arg Thr Ala Ala Asp Thr Thr Gly Leu Gln Pro Ile Leu
595 600 605

Asn Gln Phe Thr Pro Ala Asn Ile Ser Arg Gln Ala His Ile Leu Leu
610 615 620

Asp Cys Gly Glu Asp Asn Val Cys Lys Pro Lys Leu Glu Val Ser Val
625 630 635 640

Asp Arg Pro

<210> 38
<211> 1017
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 38

Met Ala Phe Pro Pro Arg Arg Arg Leu Arg Leu Gly Pro Arg Gly Leu
1 5 10 15

Pro Leu Leu Leu Ser Gly Leu Leu Pro Leu Cys Arg Ala Phe Asn
20 25 30

Leu Asp Val Asp Ser Pro Ala Glu Tyr Ser Gly Pro Glu Gly Ser Tyr
35 40 45

Phe Gly Phe Ala Val Asp Phe Phe Val Pro Ser Ala Ser Ser Arg Met
50 55 60

Phe Leu Leu Val Gly Ala Pro Lys Ala Asn Thr Thr Gln Pro Gly Ile
65 70 75 80

Val Glu Gly Gly Gln Val Leu Lys Cys Asp Trp Ser Ser Thr Arg Arg
85 90 95

Cys Gln Pro Ile Glu Phe Asp Ala Thr Gly Asn Arg Asp Tyr Ala Lys
100 105 110

Asp Asp Pro Leu Glu Phe Lys Ser His Gln Trp Phe Gly Ala Ser Val
115 120 125

Arg Ser Lys Gln Asp Lys Ile Leu Ala Cys Ala Pro Leu Tyr His Trp
130 135 140

Arg Thr Glu Met Lys Gln Glu Arg Glu Pro Val Gly Thr Cys Phe Leu
145 150 155 160

Gln Asp Gly Thr Lys Thr Val Glu Tyr Ala Pro Cys Arg Ser Gln Asp
165 170 175

Ile Asp Ala Asp Gly Gln Gly Phe Cys Gln Gly Phe Ser Ile Asp
180 185 190

Phe Thr Lys Ala Asp Arg Val Leu Leu Gly Gly Pro Gly Ser Phe Tyr
195 200 205

Trp Gln Gly Gln Leu Ile Ser Asp Gln Val Ala Glu Ile Val Ser Lys
210 215 220

Tyr Asp Pro Asp Val Tyr Ser Ile Lys Tyr Asn Asn Gln Leu Ala Thr
225 230 235 240

Arg Thr Ala Gln Ala Ile Phe Asp Asp Ser Tyr Leu Gly Tyr Ser Val
245 250 255

Ala Val Gly Asp Phe Asp Gly Asp Gly Ile Asp Asp Phe Val Ser Gly
260 265 270

Val Pro Arg Ala Ala Arg Thr Leu Gly Met Val Tyr Ile Tyr Asp Gly
275 280 285

Lys Asn Met Ser Ser Leu Tyr Asn Phe Thr Gly Glu Gln Met Ala Ala
290 295 300

Tyr Phe Gly Phe Ser Val Ala Ala Thr Asp Ile Asn Gly Asp Asp Tyr
305 310 315 320

Ala Asp Val Phe Ile Gly Ala Pro Leu Phe Met Asp Arg Gly Ser Asp
325 330 335

Gly Lys Leu Gln Glu Val Gly Gln Val Ser Val Ser Leu Gln Arg Ala
340 345 350

Ser Gly Asp Phe Gln Thr Thr Lys Leu Asn Gly Phe Glu Val Phe Ala
355 360 365

Arg Phe Gly Ser Ala Ile Ala Pro Leu Gly Asp Leu Asp Gln Asp Gly
370 375 380

Phe Asn Asp Ile Ala Ile Ala Ala Pro Tyr Gly Glu Asp Lys Lys
385 390 395 400

Gly Ile Val Tyr Ile Phe Asn Gly Arg Ser Thr Gly Leu Asn Ala Val
405 410 415

Pro Ser Gln Ile Leu Glu Gly Gln Trp Ala Ala Arg Ser Met Pro Pro
420 425 430

Ser Phe Gly Tyr Ser Met Lys Gly Ala Thr Asp Ile Asp Lys Asn Gly
435 440 445

Tyr Pro Asp Leu Ile Val Gly Ala Phe Gly Val Asp Arg Ala Ile Leu
450 455 460

Tyr Arg Ala Arg Pro Val Ile Thr Val Asn Ala Gly Leu Glu Val Tyr
465 470 475 480

Pro Ser Ile Leu Asn Gln Asp Asn Lys Thr Cys Ser Leu Pro Gly Thr
485 490 495

Ala Leu Lys Val Ser Cys Phe Asn Val Arg Phe Cys Leu Lys Ala Asp
500 505 510

Gly Lys Gly Val Leu Pro Arg Lys Leu Asn Phe Gln Val Glu Leu Leu
515 520 525

Leu Asp Lys Leu Lys Gln Lys Gly Ala Ile Arg Arg Ala Leu Phe Leu
530 535 540

Tyr Ser Arg Ser Pro Ser His Ser Lys Asn Met Thr Ile Ser Arg Gly
545 550 555 560

Gly Leu Met Gln Cys Glu Glu Leu Ile Ala Tyr Leu Arg Asp Glu Ser
565 570 575

Glu Phe Arg Asp Lys Leu Thr Pro Ile Thr Ile Phe Met Glu Tyr Arg
580 585 590

Leu Asp Tyr Arg Thr Ala Ala Asp Thr Thr Gly Leu Gln Pro Ile Leu
595 600 605

Asn Gln Phe Thr Pro Ala Asn Ile Ser Arg Gln Ala His Ile Leu Leu
610 615 620

Asp Cys Gly Glu Asp Asn Val Cys Lys Pro Lys Leu Glu Val Ser Val
625 630 635 640

Asp Ser Asp Gln Lys Lys Ile Tyr Ile Gly Asp Asp Asn Pro Leu Thr
645 650 655

Leu Ile Val Lys Ala Gln Asn Gln Gly Glu Gly Ala Tyr Glu Ala Glu
660 665 670

Leu Ile Val Ser Ile Pro Leu Gln Ala Asp Phe Ile Gly Val Val Arg
675 680 685

Asn Asn Glu Leu Leu Ala Gly Leu Arg Phe Ser Val His Gln Gln Ser
690 695 700

Glu Met Asp Thr Ser Val Lys Phe Asp Leu Gln Ile Gln Ser Ser Asn
705 710 715 720

Leu Phe Asp Lys Val Ser Pro Val Val Ser His Lys Val Asp Leu Ala
725 730 735

Val Leu Ala Ala Val Glu Ile Arg Gly Val Ser Ser Pro Asp His Ile
740 745 750

Phe Leu Pro Ile Pro Asn Trp Glu His Lys Glu Asn Pro Glu Thr Glu
755 760 765

Glu Asp Val Gly Pro Val Val Gln His Ile Tyr Glu Leu Arg Asn Asn
770 775 780

Gly Pro Ser Ser Phe Ser Lys Ala Met Leu His Leu Gln Trp Pro Tyr
785 790 795 800

Lys Tyr Asn Asn Asn Thr Leu Leu Tyr Ile Leu His Tyr Asp Ile Asp
805 810 815

Gly Pro Met Asn Cys Thr Ser Asp Met Glu Ile Asn Pro Leu Arg Ile
820 825 830

Lys Ile Ser Ser Leu Gln Thr Thr Glu Lys Asn Asp Thr Val Ala Gly
835 840 845

Gln Gly Glu Arg Asp His Leu Ile Thr Lys Arg Asp Leu Ala Leu Ser
850 855 860

Glu Gly Asp Ile His Thr Leu Gly Cys Gly Val Ala Gln Cys Leu Lys
865 870 875 880

Ile Val Cys Gln Val Gly Arg Leu Asp Arg Gly Lys Ser Ala Ile Leu
885 890 895

Tyr Val Lys Ser Leu Leu Trp Thr Glu Thr Phe Met Asn Lys Glu Asn
900 905 910

Gln Asn His Ser Tyr Ser Leu Lys Ser Ser Ala Ser Phe Asn Val Ile
915 920 925

Glu Phe Pro Tyr Lys Asn Leu Pro Ile Glu Asp Ile Thr Asn Ser Thr
930 935 940

Leu Val Thr Thr Asn Val Thr Trp Gly Ile Gln Pro Ala Pro Met Pro
945 950 955 960

Val Pro Val Trp Val Ile Leu Ala Val Leu Ala Gly Leu Leu Leu
965 970 975

Leu Ala Val Leu Val Phe Val Met Tyr Arg Met Gly Phe Phe Lys Arg
980 985 990

Val Arg Pro Pro Gln Glu Glu Gln Glu Arg Glu Gln Leu Gln Pro His
995 1000 1005

Glu Asn Gly Glu Gly Asn Ser Glu Thr
1010 1015

<210> 39

<211> 995

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 39

Met Ala Phe Pro Pro Arg Arg Arg Leu Arg Leu Gly Pro Arg Gly Leu
1 5 10 15

Pro Leu Leu Leu Ser Gly Leu Leu Leu Pro Leu Cys Arg Ala Phe Asn
20 25 30

Leu Asp Val Asp Ser Pro Ala Glu Tyr Ser Gly Pro Glu Gly Ser Tyr
35 40 45

Phe Gly Phe Ala Val Asp Phe Phe Val Pro Ser Ala Ser Ser Arg Met
50 55 60

Phe Leu Leu Val Gly Ala Pro Lys Ala Asn Thr Thr Gln Pro Gly Ile
65 70 75 80

Val Glu Gly Gly Gln Val Leu Lys Cys Asp Trp Ser Ser Thr Arg Arg
85 90 95

Cys Gln Pro Ile Glu Phe Asp Ala Thr Gly Asn Arg Asp Tyr Ala Lys
100 105 110

Asp Asp Pro Leu Glu Phe Lys Ser His Gln Trp Phe Gly Ala Ser Val
115 120 125

Arg Ser Lys Gln Asp Lys Ile Leu Ala Cys Ala Pro Leu Tyr His Trp
130 135 140

Arg Thr Glu Met Lys Gln Glu Arg Glu Pro Val Gly Thr Cys Phe Leu
145 150 155 160

Gln Asp Gly Thr Lys Thr Val Glu Tyr Ala Pro Cys Arg Ser Gln Asp
165 170 175

Ile Asp Ala Asp Gly Gln Gly Phe Cys Gln Gly Gly Phe Ser Ile Asp
180 185 190

Phe Thr Lys Ala Asp Arg Val Leu Leu Gly Gly Pro Gly Ser Phe Tyr
195 200 205

Trp Gln Gly Gln Leu Ile Ser Asp Gln Val Ala Glu Ile Val Ser Lys
210 215 220

Tyr Asp Pro Asn Val Tyr Ser Ile Lys Tyr Asn Asn Gln Leu Ala Thr
225 230 235 240

Arg Thr Ala Gln Ala Ile Phe Asp Asp Ser Tyr Leu Gly Tyr Ser Val
245 250 255

Ala Val Gly Asp Phe Asn Gly Asp Gly Ile Asp Asp Phe Val Ser Gly
260 265 270

Val Pro Arg Ala Ala Arg Thr Leu Gly Met Val Tyr Ile Tyr Asp Gly
275 280 285

Lys Asn Met Ser Ser Leu Tyr Asn Phe Thr Gly Glu Gln Met Ala Ala
290 295 300

Tyr Phe Gly Phe Ser Val Ala Ala Thr Asp Ile Asn Gly Asp Asp Tyr
305 310 315 320

Ala Asp Val Phe Ile Gly Ala Pro Leu Phe Met Asp Arg Gly Ser Asp
325 330 335

Gly Lys Leu Gln Glu Val Gly Gln Val Ser Val Ser Leu Gln Arg Ala
340 345 350

Ser Gly Asp Phe Gln Thr Thr Lys Leu Asn Gly Phe Glu Val Phe Ala
355 360 365

Arg Phe Gly Ser Ala Ile Ala Pro Leu Gly Asp Leu Asp Gln Asp Gly
370 375 380

Phe Asn Asp Ile Ala Ile Ala Ala Pro Tyr Gly Gly Glu Asp Lys Lys
385 390 395 400

Gly Ile Val Tyr Ile Phe Asn Gly Arg Ser Thr Gly Leu Asn Ala Val
405 410 415

Pro Ser Gln Ile Leu Glu Gly Gln Trp Ala Ala Arg Ser Met Pro Pro
420 425 430

Ser Phe Gly Tyr Ser Met Lys Gly Ala Thr Asp Ile Asp Lys Asn Gly
435 440 445

Tyr Pro Asp Leu Ile Val Gly Ala Phe Gly Val Asp Arg Ala Ile Leu
450 455 460

Tyr Arg Ala Arg Pro Val Ile Thr Val Asn Ala Gly Leu Glu Val Tyr
465 470 475 480

Pro Ser Ile Leu Asn Gln Asp Asn Lys Thr Cys Ser Leu Pro Gly Thr
485 490 495

Ala Leu Lys Val Ser Cys Phe Asn Val Arg Phe Cys Leu Lys Ala Asp
500 505 510

Gly Lys Gly Val Leu Pro Arg Lys Leu Asn Phe Gln Val Glu Leu Leu
515 520 525

Leu Asp Lys Leu Lys Gln Lys Gly Ala Ile Arg Arg Ala Leu Phe Leu
530 535 540

Tyr Ser Arg Ser Pro Ser His Ser Lys Asn Met Thr Ile Ser Arg Gly
545 550 555 560

Gly Leu Met Gln Cys Glu Glu Leu Ile Ala Tyr Leu Arg Asp Glu Ser
565 570 575

Glu Phe Arg Asp Lys Leu Thr Pro Ile Thr Ile Phe Met Glu Tyr Arg
580 585 590

Leu Asp Tyr Arg Thr Ala Ala Asp Thr Thr Gly Leu Gln Pro Ile Leu
595 600 605

Asn Gln Phe Thr Pro Ala Asn Ile Ser Arg Gln Ala His Ile Leu Leu
610 615 620

Asp Cys Gly Glu Asp Asn Val Cys Lys Pro Lys Leu Glu Val Ser Val
625 630 635 640

Asp Ser Asp Gln Lys Ile Tyr Ile Gly Asp Asp Asn Pro Leu Thr
645 650 655

Leu Ile Val Lys Ala Gln Asn Gln Gly Glu Gly Ala Tyr Glu Ala Glu
660 665 670

Leu Ile Val Ser Ile Pro Leu Gln Ala Asp Phe Ile Gly Val Val Arg
675 680 685

Asn Asn Glu Ala Leu Ala Arg Leu Ser Cys Ala Phe Lys Thr Glu Asn
690 695 700

Gln Thr Arg Gln Val Val Cys Asp Leu Gly Asn Pro Met Lys Ala Gly
705 710 715 720

Thr Gln Leu Leu Ala Gly Leu Arg Phe Ser Val His Gln Gln Ser Glu
725 730 735

Met Asp Thr Ser Val Lys Phe Asp Leu Gln Ile Gln Ser Ser Asn Leu

740 745 750

Phe Asp Lys Val Ser Pro Val Val Ser His Lys Val Asp Leu Ala Val
755 760 765

Leu Ala Ala Val Glu Ile Arg Gly Val Ser Ser Pro Asp His Ile Phe
770 775 780

Leu Pro Ile Pro Asn Trp Glu His Lys Glu Asn Pro Glu Thr Glu Glu
785 790 795 800

Asp Val Gly Pro Val Val Gln His Ile Tyr Glu Ile Ser Ser Leu Gln
805 810 815

Thr Thr Glu Lys Asn Asp Thr Val Ala Gly Gln Gly Glu Arg Asp His
820 825 830

Leu Ile Thr Lys Arg Asp Leu Ala Leu Ser Glu Gly Asp Ile His Thr
835 840 845

Leu Gly Cys Gly Val Ala Gln Cys Leu Lys Ile Val Cys Gln Val Gly
850 855 860

Arg Leu Asp Arg Gly Lys Ser Ala Ile Leu Tyr Val Lys Ser Leu Leu
865 870 875 880

Trp Thr Glu Thr Phe Met Asn Lys Glu Asn Gln Asn His Ser Tyr Ser
885 890 895

Leu Lys Ser Ser Ala Ser Phe Asn Val Ile Glu Phe Pro Tyr Lys Asn
900 905 910

Leu Pro Ile Glu Asp Ile Thr Asn Ser Thr Leu Val Thr Thr Asn Val
915 920 925

Thr Trp Gly Ile Gln Pro Ala Pro Met Pro Val Pro Val Trp Val Ile
930 935 940

Ile Leu Ala Val Leu Ala Gly Leu Leu Leu Ala Val Leu Val Phe
945 950 955 960

Val Met Tyr Arg Met Gly Phe Phe Lys Arg Val Arg Pro Pro Gln Glu
965 970 975

Glu Gln Glu Arg Glu Gln Leu Gln Pro His Glu Asn Gly Glu Gly Asn
980 985 990

Ser Glu Thr
995

<210> 40

<211> 1341

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 40

Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu Val Leu Leu Phe
 1 5 10 15

Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys
 20 25 30

Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn Phe Thr Ala
 35 40 45

Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu
 50 55 60

Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu Asp Leu Gln Lys
 65 70 75 80

Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His Pro Asp Cys Phe
 85 90 95

Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Gly Val Trp
 100 105 110

Lys Asp Asn Ile Asn Met Ala Leu Val Val Asp Thr Tyr Tyr Asp Asp
 115 120 125

Gln Leu Ile Ser Cys Gly Ser Val Asn Arg Gly Thr Cys Gln Arg His
 130 135 140

Val Phe Pro His Asn His Thr Ala Asp Ile Gln Ser Glu Val His Cys
 145 150 155 160

Ile Phe Ser Pro Gln Ile Glu Glu Pro Ser Gln Cys Pro Asp Cys Val
 165 170 175

Val Ser Ala Leu Gly Ala Lys Val Leu Ser Ser Val Lys Asp Arg Phe
 180 185 190

Ile Asn Phe Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp
 195 200 205

His Pro Leu His Ser Ile Ser Val Arg Arg Leu Lys Glu Thr Lys Asp
 210 215 220

Gly Phe Met Phe Leu Thr Asp Gln Ser Tyr Ile Asp Val Leu Pro Glu
 225 230 235 240

Phe Arg Asp Ser Tyr Pro Ile Lys Tyr Val His Ala Phe Glu Ser Asn
 245 250 255

Asn Phe Ile Tyr Phe Leu Thr Val Gln Arg Glu Thr Leu Asp Ala Gln
 260 265 270

Thr Phe His Thr Arg Ile Ile Arg Phe Cys Ser Ile Asn Ser Gly Leu
 275 280 285

His Ser Tyr Met Glu Met Pro Leu Glu Cys Ile Leu Thr Glu Lys Arg
 290 295 300

Lys Lys Arg Ser Thr Lys Lys Glu Val Phe Asn Ile Leu Gln Ala Ala

305	310	315	320
-----	-----	-----	-----

Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser
 325 330 335

Leu Asn Asp Asp Ile Leu Phe Gly Val Phe Ala Gln Ser Lys Pro Asp
 340 345 350

Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys
 355 360 365

Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg
 370 375 380

Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His Cys Phe Asn Arg
 385 390 395 400

Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg Arg Asp Glu Tyr
 405 410 415

Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
 420 425 430

Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr Phe Ile Lys Gly
 435 440 445

Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
 450 455 460

Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
 465 470 475 480

Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
 485 490 495

Asn Gln Asn Gly Tyr Thr Leu Val Ile Thr Gly Lys Lys Ile Thr Lys
 500 505 510

Ile Pro Leu Asn Gly Leu Gly Cys Arg His Phe Gln Ser Cys Ser Gln
 515 520 525

Cys Leu Ser Ala Pro Pro Phe Val Gln Cys Gly Trp Cys His Asp Lys
 530 535 540

Cys Val Arg Ser Glu Glu Cys Leu Ser Gly Thr Trp Thr Gln Gln Ile
 545 550 555 560

Cys Leu Pro Ala Ile Tyr Lys Val Phe Pro Asn Ser Ala Pro Leu Glu
 565 570 575

Gly Gly Thr Arg Leu Thr Ile Cys Gly Trp Asp Phe Gly Phe Arg Arg
 580 585 590

Asn Asn Lys Phe Asp Leu Lys Lys Thr Arg Val Leu Gly Asn Glu
 595 600 605

Ser Cys Thr Leu Thr Leu Ser Glu Ser Thr Met Asn Thr Leu Lys Cys
 610 615 620

Thr Val Gly Pro Ala Met Asn Lys His Phe Asn Met Ser Ile Ile Ile
625 630 635 640

Ser Asn Gly His Gly Thr Thr Gln Tyr Ser Thr Phe Ser Tyr Val Asp
645 650 655

Pro Val Ile Thr Ser Ile Ser Pro Lys Tyr Gly Pro Met Ala Gly Gly
660 665 670

Thr Leu Leu Thr Leu Thr Gly Asn Tyr Leu Asn Ser Gly Asn Ser Arg
675 680 685

His Ile Ser Ile Gly Gly Lys Thr Cys Thr Leu Lys Ser Val Ser Asn
690 695 700

Ser Ile Leu Glu Cys Tyr Thr Pro Ala Gln Thr Ile Ser Thr Glu Phe
705 710 715 720

Ala Val Lys Leu Lys Ile Asp Leu Ala Asn Arg Glu Thr Ser Ile Phe
725 730 735

Ser Tyr Arg Glu Asp Pro Ile Val Tyr Glu Ile His Pro Thr Lys Ser
740 745 750

Phe Ile Ser Gly Gly Ser Thr Ile Thr Gly Val Gly Lys Asn Leu Asn
755 760 765

Ser Val Ser Val Pro Arg Met Val Ile Asn Val His Glu Ala Gly Arg
770 775 780

Asn Phe Thr Val Ala Cys Gln His Arg Ser Asn Ser Glu Ile Ile Cys
785 790 795 800

Cys Thr Thr Pro Ser Leu Gln Gln Leu Asn Leu Gln Leu Pro Leu Lys
805 810 815

Thr Lys Ala Phe Phe Met Leu Asp Gly Ile Leu Ser Lys Tyr Phe Asp
820 825 830

Leu Ile Tyr Val His Asn Pro Val Phe Lys Pro Phe Glu Lys Pro Val
835 840 845

Met Ile Ser Met Gly Asn Glu Asn Val Leu Glu Ile Lys Trp Lys Gln
850 855 860

Ala Ile Ser Ser Thr Val Leu Gly Lys Val Ile Val Gln Pro Asp Gln
865 870 875 880

Asn Phe Thr Gly Leu Ile Ala Gly Val Val Ser Ile Ser Thr Ala Leu
885 890 895

Leu Leu Leu Leu Gly Phe Phe Leu Trp Leu Lys Lys Arg Lys Gln Ile
900 905 910

Lys Asp Leu Gly Ser Glu Leu Val Arg Tyr Asp Ala Arg Val His Thr
915 920 925

Pro His Leu Asp Arg Leu Val Ser Ala Arg Ser Val Ser Pro Thr Thr
 930 935 940

Glu Met Val Ser Asn Glu Ser Val Asp Tyr Arg Ala Thr Phe Pro Glu
 945 950 955 960

Asp Gln Phe Pro Asn Ser Ser Gln Asn Gly Ser Cys Arg Gln Val Gln
 965 970 975

Tyr Pro Leu Thr Asp Met Ser Pro Ile Leu Thr Ser Gly Asp Ser Asp
 980 985 990

Ile Ser Ser Pro Leu Leu Gln Asn Thr Val His Ile Asp Leu Ser Ala
 995 1000 1005

Leu Asn Pro Glu Leu Val Gln Ala Val Gln His Val Val Ile Gly
 1010 1015 1020

Pro Ser Ser Leu Ile Val His Phe Asn Glu Val Ile Gly Arg Gly
 1025 1030 1035

His Phe Gly Cys Val Tyr His Gly Thr Leu Leu Asp Asn Asp Gly
 1040 1045 1050

Lys Lys Ile His Cys Ala Val Lys Ser Leu Asn Arg Ile Thr Asp
 1055 1060 1065

Ile Gly Glu Val Ser Gln Phe Leu Thr Glu Gly Ile Ile Met Lys
 1070 1075 1080

Asp Phe Ser His Pro Asn Val Leu Ser Leu Leu Gly Ile Cys Leu
 1085 1090 1095

Arg Ser Glu Gly Ser Pro Leu Val Val Leu Pro Tyr Met Lys His
 1100 1105 1110

Gly Asp Leu Arg Asn Phe Ile Arg Asn Glu Thr His Asn Pro Thr
 1115 1120 1125

Val Lys Asp Leu Ile Gly Phe Gly Leu Gln Val Ala Lys Gly Met
 1130 1135 1140

Lys Tyr Leu Ala Ser Lys Lys Phe Val His Arg Asp Leu Ala Ala
 1145 1150 1155

Arg Asn Cys Met Leu Asp Glu Lys Phe Thr Val Lys Val Ala Asp
 1160 1165 1170

Phe Gly Leu Ala Arg Asp Met Tyr Asp Lys Glu Tyr Tyr Ser Val
 1175 1180 1185

His Asn Lys Thr Gly Ala Lys Leu Pro Val Lys Trp Met Ala Leu
 1190 1195 1200

Glu Ser Leu Gln Thr Gln Lys Phe Thr Thr Lys Ser Asp Val Trp
 1205 1210 1215

Ser Phe Gly Val Val Leu Trp Glu Leu Met Thr Arg Gly Ala Pro
 1220 1225 1230

Pro Tyr Pro Asp Val Asn Thr Phe Asp Ile Thr Val Tyr Leu Leu
 1235 1240 1245

Gln Gly Arg Arg Leu Leu Gln Pro Glu Tyr Cys Pro Asp Pro Leu
 1250 1255 1260

Tyr Glu Val Met Leu Lys Cys Trp His Pro Lys Ala Glu Met Arg
 1265 1270 1275

Pro Ser Phe Ser Glu Leu Val Ser Arg Ile Ser Ala Ile Phe Ser
 1280 1285 1290

Thr Phe Ile Gly Glu His Tyr Val His Val Asn Ala Thr Tyr Val
 1295 1300 1305

Asn Val Lys Cys Val Ala Pro Tyr Pro Ser Leu Leu Ser Ser Glu
 1310 1315 1320

Asp Asn Ala Asp Asp Glu Val Asp Thr Arg Pro Ala Ser Phe Trp
 1325 1330 1335

Glu Thr Ser
 1340

<210> 41

<211> 1343

<212> PRT

<213> Artificial sequence.

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 41

Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu Val Leu Phe
 1 5' 10 15

Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys
 20 25 30

Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn Phe Thr Ala
 35 40 45

Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu
 50 55 60

Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu Asp Leu Gln Lys
 65 70 75 80

Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His Pro Asp Cys Phe
 85 90 95

Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Val Trp
 100 105 110

Lys Asp Asn Ile Asn Met Ala Leu Val Val Asp Thr Tyr Tyr Asp Asp
 115 120 125

Gln Leu Ile Ser Cys Gly Ser Val Asn Arg Gly Thr Cys Gln Arg His
 130 135 140

Val Phe Pro His Asn His Thr Ala Asp Ile Gln Ser Glu Val His Cys
 145 150 155 160

Ile Phe Ser Pro Gln Ile Glu Glu Pro Ser Gln Cys Pro Asp Cys Val
 165 170 175

Val Ser Ala Leu Gly Ala Lys Val Leu Ser Ser Val Lys Asp Arg Phe
 180 185 190

Ile Asn Phe Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp
 195 200 205

His Pro Leu His Ser Ile Ser Val Arg Arg Leu Lys Glu Thr Lys Asp
 210 215 220

Gly Phe Met Phe Leu Thr Asp Gln Ser Tyr Ile Asp Val Leu Pro Glu
 225 230 235 240

Phe Arg Asp Ser Tyr Pro Ile Lys Tyr Val His Ala Phe Glu Ser Asn
 245 250 255

Asn Phe Ile Tyr Phe Leu Thr Val Gln Arg Glu Thr Leu Asp Ala Gln
 260 265 270

Thr Phe His Thr Arg Ile Ile Arg Phe Cys Ser Ile Asn Ser Gly Leu
 275 280 285

His Ser Tyr Met Glu Met Pro Leu Glu Cys Ile Leu Thr Glu Lys Arg
 290 295 300

Lys Lys Arg Ser Thr Lys Lys Glu Val Phe Asn Ile Leu Gln Ala Ala
 305 310 315 320

Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser
 325 330 335

Leu Asn Asp Asp Ile Leu Phe Gly Val Phe Ala Gln Ser Lys Pro Asp
 340 345 350

Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys
 355 360 365

Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg
 370 375 380

Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His Cys Phe Asn Arg
 385 390 395 400

Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg Arg Asp Glu Tyr
 405 410 415

Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
 420 425 430

Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr Phe Ile Lys Gly
 435 440 445

Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
 450 455 460

Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
 465 470 475 480

Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
 485 490 495

Asn Gln Asn Gly Tyr Thr Leu Val Ile Thr Gly Lys Lys Ile Thr Lys
 500 505 510

Ile Pro Leu Asn Gly Ile Gly Cys Arg His Phe Gln Ser Cys Ser Gln
 515 520 525

Cys Leu Ser Ala Pro Pro Phe Val Gln Cys Gly Trp Cys His Asp Lys
 530 535 540

Cys Val Arg Ser Glu Glu Cys Leu Ser Gly Thr Trp Thr Gln Gln Ile
 545 550 555 560

Cys Leu Pro Ala Ile Tyr Lys Val Phe Pro Asn Ser Ala Pro Leu Glu
 565 570 575

Gly Gly Thr Arg Leu Thr Ile Cys Gly Trp Asp Phe Gly Phe Arg Arg
 580 585 590

Asn Asn Lys Phe Asp Leu Lys Lys Thr Arg Val Leu Leu Gly Asn Glu
 595 600 605

Ser Cys Thr Leu Thr Leu Ser Glu Ser Thr Met Asn Thr Leu Lys Cys
 610 615 620

Thr Val Gly Pro Ala Met Asn Lys His Phe Asn Met Ser Ile Ile Ile
 625 630 635 640

Ser Asn Gly His Gly Thr Thr Gln Tyr Ser Thr Phe Ser Tyr Val Asp
 645 650 655

Pro Val Ile Thr Ser Ile Ser Pro Lys Tyr Gly Pro Met Ala Gly Gly
 660 665 670

Thr Leu Leu Thr Leu Thr Gly Asn Tyr Leu Asn Ser Gly Asn Ser Arg
 675 680 685

His Ile Ser Ile Gly Gly Lys Thr Cys Thr Leu Lys Ser Val Ser Asn
 690 695 700

Ser Ile Leu Glu Cys Tyr Thr Pro Ala Gln Thr Ile Ser Thr Glu Phe
 705 710 715 720

Ala Val Lys Leu Lys Ile Asp Leu Ala Asn Arg Glu Thr Ser Ile Phe
 725 730 735

Ser Tyr Arg Glu Asp Pro Ile Val Tyr Glu Ile His Pro Thr Lys Ser

740

745

750

Phe Ile Ser Gly Gly Ser Thr Ile Thr Gly Val Gly Lys Asn Leu Asn
755 760 765

Ser Val Ser Val Pro Arg Met Val Ile Asn Val His Glu Ala Gly Arg
770 775 780

Asn Phe Thr Val Ala Cys Gln His Arg Ser Asn Ser Glu Ile Ile Cys
785 790 795 800

Cys Thr Thr Pro Ser Leu Gln Gln Leu Asn Leu Gln Leu Pro Leu Lys
805 810 815

Thr Lys Ala Phe Phe Met Leu Asp Gly Ile Leu Ser Lys Tyr Phe Asp
820 825 830

Leu Ile Tyr Val His Asn Pro Val Phe Lys Pro Phe Glu Lys Pro Val
835 840 845

Met Ile Ser Met Gly Asn Glu Asn Val Leu Glu Ile Lys Gly Asn Asp
850 855 860

Ile Asp Pro Glu Ala Val Lys Gly Glu Val Leu Lys Val Gly Asn Lys
865 870 875 880

Ser Cys Glu Asn Ile His Leu His Ser Glu Ala Val Leu Cys Thr Val
885 890 895

Pro Asn Asp Leu Leu Lys Leu Asn Ser Glu Leu Asn Ile Glu Trp Lys
900 905 910

Gln Ala Ile Ser Ser Thr Val Leu Gly Lys Val Ile Val Gln Pro Asp
915 920 925

Gln Asn Phe Thr Gly Ile Ala Gly Val Val Ser Ile Ser Thr Ala
930 935 940

Leu Leu Leu Leu Leu Gly Phe Phe Leu Trp Leu Lys Lys Arg Lys Gln
945 950 955 960

Ile Lys Asp Gln Phe Pro Asn Ser Ser Gln Asn Gly Ser Cys Arg Gln
965 970 975

Val Gln Tyr Pro Leu Thr Asp Met Ser Pro Ile Leu Thr Ser Gly Asp
980 985 990

Ser Asp Ile Ser Ser Pro Leu Leu Gln Asn Thr Val His Ile Asp Leu
995 1000 1005

Ser Ala Leu Asn Pro Glu Leu Val Gln Ala Val Gln His Val Val
1010 1015 1020

Ile Gly Pro Ser Ser Ile Val His Phe Asn Glu Val Ile Gly
1025 1030 1035

Arg Gly His Phe Gly Cys Val Tyr His Gly Thr Leu Leu Asp Asn
1040 1045 1050

Asp Gly Lys Lys Ile His Cys Ala Val Lys Ser Leu Asn Arg Ile
1055 1060 1065

Thr Asp Ile Gly Glu Val Ser Gln Phe Leu Thr Glu Gly Ile Ile
1070 1075 1080

Met Lys Asp Phe Ser His Pro Asn Val Leu Ser Leu Leu Gly Ile
1085 1090 1095

Cys Leu Arg Ser Glu Gly Ser Pro Leu Val Val Leu Pro Tyr Met
1100 1105 1110

Lys His Gly Asp Leu Arg Asn Phe Ile Arg Asn Glu Thr His Asn
1115 1120 1125

Pro Thr Val Lys Asp Leu Ile Gly Phe Gly Leu Gln Val Ala Lys
1130 1135 1140

Gly Met Lys Tyr Leu Ala Ser Lys Lys Phe Val His Arg Asp Leu
1145 1150 1155

Ala Ala Arg Asn Cys Met Leu Asp Glu Lys Phe Thr Val Lys Val
1160 1165 1170

Ala Asp Phe Gly Leu Ala Arg Asp Met Tyr Asp Lys Glu Tyr Tyr
1175 1180 1185

Ser Val His Asn Lys Thr Gly Ala Lys Leu Pro Val Lys Trp Met
1190 1195 1200

Ala Leu Glu Ser Leu Gln Thr Gln Lys Phe Thr Thr Lys Ser Asp
1205 1210 1215

Val Trp Ser Phe Gly Val Val Leu Trp Glu Leu Met Thr Arg Gly
1220 1225 1230

Ala Pro Pro Tyr Pro Asp Val Asn Thr Phe Asp Ile Thr Val Tyr
1235 1240 1245

Leu Leu Gln Gly Arg Arg Leu Leu Gln Pro Glu Tyr Cys Pro Asp
1250 1255 1260

Pro Leu Tyr Glu Val Met Leu Lys Cys Trp His Pro Lys Ala Glu
1265 1270 1275

Met Arg Pro Ser Phe Ser Glu Leu Val Ser Arg Ile Ser Ala Ile
1280 1285 1290

Phe Ser Thr Phe Ile Gly Glu His Tyr Val His Val Asn Ala Thr
1295 1300 1305

Tyr Val Asn Val Lys Cys Val Ala Pro Tyr Pro Ser Leu Leu Ser
1310 1315 1320

Ser Glu Asp Asn Ala Asp Asp Glu Val Asp Thr Arg Pro Ala Ser
1325 1330 1335

Phe Trp Glu Thr Ser
1340

<210> 42
<211> 1176
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 42

Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu Val Leu Leu Phe
1 5 10 15

Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys
20 25 30

Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn Phe Thr Ala
35 40 45

Glu Thr Pro Ile Gln Asn Val Ile Leu His His His Ile Phe Leu
50 55 60

Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu Asp Leu Gln Lys
65 70 75 80

Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His Pro Asp Cys Phe
85 90 95

Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Gly Val Trp
100 105 110

Lys Asp Asn Ile Asn Met Ala Leu Val Val Asp Thr Tyr Tyr Asp Asp
115 120 125

Gln Leu Ile Ser Cys Gly Ser Val Asn Arg Gly Thr Cys Gln Arg His
130 135 140

Val Phe Pro His Asn His Thr Ala Asp Ile Gln Ser Glu Val His Cys
145 150 155 160

Ile Phe Ser Pro Gln Ile Glu Glu Pro Ser Gln Cys Pro Asp Cys Val
165 170 175

Val Ser Ala Leu Gly Ala Lys Val Leu Ser Ser Val Lys Asp Arg Phe
180 185 190

Ile Asn Phe Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp
195 200 205

His Pro Leu His Ser Ile Ser Val Arg Arg Leu Lys Glu Thr Lys Asp
210 215 220

Gly Phe Met Phe Leu Thr Asp Gln Ser Tyr Ile Asp Val Leu Pro Glu
225 230 235 240

Phe Arg Asp Ser Tyr Pro Ile Lys Tyr Val His Ala Phe Glu Ser Asn
245 250 255

Asn Phe Ile Tyr Phe Leu Thr Val Gln Arg Glu Thr Leu Asp Ala Gln
260 265 270

Thr Phe His Thr Arg Ile Ile Arg Phe Cys Ser Ile Asn Ser Gly Leu
275 280 285

His Ser Tyr Met Glu Met Pro Leu Glu Cys Ile Leu Thr Glu Lys Arg
290 295 300

Lys Lys Arg Ser Thr Lys Glu Val Phe Asn Ile Leu Gln Ala Ala
305 310 315 320

Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser
325 330 335

Leu Asn Asp Asp Ile Leu Phe Gly Val Phe Ala Gln Ser Lys Pro Asp
340 345 350

Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys
355 360 365

Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg
370 375 380

Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His Cys Phe Asn Arg
385 390 395 400

Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg Arg Asp Glu Tyr
405 410 415

Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
420 425 430

Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr Phe Ile Lys Gly
435 440 445

Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
450 455 460

Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
465 470 475 480

Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
485 490 495

Asn Gln Asn Gly Tyr Thr Leu Val Ile Thr Gly Lys Lys Ile Thr Lys
500 505 510

Ile Pro Leu Asn Gly Leu Gly Cys Arg His Phe Gln Ser Cys Ser Gln
515 520 525

Cys Leu Ser Ala Pro Pro Phe Val Gln Cys Gly Trp Cys His Asp Lys
530 535 540

Cys Val Arg Ser Glu Glu Cys Leu Ser Gly Thr Trp Thr Gln Gln Ile
545 550 555 560

Cys Leu Pro Ala Ile Tyr Lys Val Phe Pro Asn Ser Ala Pro Leu Glu
565 570 575

Gly Gly Thr Arg Leu Thr Ile Cys Gly Trp Asp Phe Gly Phe Arg Arg
580 585 590

Asn Asn Lys Phe Asp Leu Lys Lys Thr Arg Val Leu Leu Gly Asn Glu
595 600 605

Ser Cys Thr Leu Thr Leu Ser Glu Ser Thr Met Asn Thr Leu Lys Cys
610 615 620

Thr Val Gly Pro Ala Met Asn Lys His Phe Asn Met Ser Ile Ile Ile
625 630 635 640

Ser Asn Gly His Gly Thr Thr Gln Tyr Ser Thr Phe Ser Tyr Val Asp
645 650 655

Pro Val Ile Thr Ser Ile Ser Pro Lys Tyr Gly Pro Met Ala Gly Gly
660 665 670

Thr Leu Leu Thr Leu Thr Gly Asn Tyr Leu Asn Ser Gly Asn Ser Arg
675 680 685

His Ile Ser Ile Gly Gly Lys Thr Cys Thr Leu Lys Ser Val Ser Asn
690 695 700

Ser Ile Leu Glu Cys Tyr Thr Pro Ala Gln Thr Ile Ser Thr Glu Phe
705 710 715 720

Ala Val Lys Leu Lys Ile Asp Leu Ala Asn Arg Glu Thr Ser Ile Phe
725 730 735

Ser Tyr Arg Glu Asp Pro Ile Val Tyr Glu Ile His Pro Thr Lys Ser
740 745 750

Phe Ile Ser Gly Gly Ser Thr Ile Thr Gly Val Gly Lys Asn Leu Asn
755 760 765

Ser Val Ser Val Pro Arg Met Val Ile Asn Val His Glu Ala Gly Arg
770 775 780

Asn Phe Thr Val Ala Cys Gln His Arg Ser Asn Ser Glu Ile Ile Cys
785 790 795 800

Cys Thr Thr Pro Ser Leu Gln Gln Leu Asn Leu Gln Leu Pro Leu Lys
805 810 815

Thr Lys Ala Phe Phe Met Leu Asp Gly Ile Leu Ser Lys Tyr Phe Asp
820 825 830

Leu Ile Tyr Val His Asn Pro Val Phe Lys Pro Phe Glu Lys Pro Val
835 840 845

Met Ile Ser Met Gly Asn Glu Asn Val Leu Glu Ile Lys Gly Asn Asp
850 855 860

Ile Asp Pro Glu Ala Val Lys Gly Glu Val Leu Lys Val Gly Asn Lys
 865 870 875 880

Ser Cys Glu Asn Ile His Leu His Ser Glu Ala Val Leu Cys Thr Val
 885 890 895

Pro Asn Asp Leu Leu Lys Leu Asn Ser Glu Leu Asn Ile Glu Trp Lys
 900 905 910

Gln Ala Ile Ser Ser Thr Val Leu Gly Lys Val Ile Val Gln Pro Asp
 915 920 925

Gln Asn Phe Thr Gly Leu Ile Ala Gly Val Val Ser Ile Ser Thr Ala
 930 935 940

Leu Leu Leu Leu Leu Gly Phe Phe Leu Trp Leu Lys Lys Arg Lys Gln
 945 950 955 960

Ile Lys Asp Leu Gly Ser Glu Leu Val Arg Tyr Asp Ala Arg Val His
 965 970 975

Thr Pro His Leu Asp Arg Leu Val Ser Ala Arg Ser Val Ser Pro Thr
 980 985 990

Thr Glu Met Val Ser Asn Glu Ser Val Asp Tyr Arg Ala Thr Phe Pro
 995 1000 1005

Glu Asp Gln Phe Pro Asn Ser Ser Gln Asn Gly Ser Cys Arg Gln
 1010 1015 1020

Val Gln Tyr Pro Leu Thr Asp Met Ser Pro Ile Leu Thr Ser Gly
 1025 1030 1035

Asp Ser Asp Ile Ser Ser Pro Leu Leu Gln Asn Thr Val His Ile
 1040 1045 1050

Asp Leu Ser Ala Leu Asn Pro Glu Leu Val Gln Ala Val Gln His
 1055 1060 1065

Val Val Ile Gly Pro Ser Ser Leu Ile Val His Phe Asn Glu Val
 1070 1075 1080

Ile Gly Arg Gly His Phe Gly Cys Val Tyr His Gly Thr Leu Leu
 1085 1090 1095

Asp Asn Asp Gly Lys Ile His Cys Ala Val Lys Ser Leu Asn
 1100 1105 1110

Arg Ile Thr Asp Ile Gly Glu Val Ser Gln Phe Leu Thr Glu Gly
 1115 1120 1125

Ile Ile Met Lys Asp Phe Ser His Pro Asn Val Leu Ser Leu Leu
 1130 1135 1140

Gly Ile Cys Leu Arg Ser Glu Gly Ser Pro Leu Val Val Leu Pro
 1145 1150 1155

Tyr Met Lys His Gly Asp Leu Arg Asn Phe Ile Arg Asn Glu Thr

1160

1165

1170

His Ala Gly
1175

<210> 43
<211> 672
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 43

Met Ala Leu Leu Leu Val Ser Leu Leu Ala Phe Leu Ser Leu Gly Ser
1 5 10 15

Gly Cys His His Arg Ile Cys His Cys Ser Asn Arg Val Phe Leu Cys
20 25 30

Gln Glu Ser Lys Val Thr Glu Ile Pro Ser Asp Leu Pro Arg Asn Ala
35 40 45

Ile Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Gln Lys Gly
50 55 60

Ala Phe Ser Gly Phe Gly Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn
65 70 75 80

Asp Val Leu Glu Val Ile Glu Ala Asp Val Phe Ser Asn Leu Pro Lys
85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asn
100 105 110

Pro Glu Ala Phe Gln Asn Leu Pro Asn Leu Gln Tyr Leu Leu Ile Ser
115 120 125

Asn Thr Gly Ile Lys His Leu Pro Asp Val His Lys Ile His Ser Leu
130 135 140

Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Thr Ile
145 150 155 160

Glu Arg Asn Ser Phe Val Gly Leu Ser Phe Glu Ser Val Ile Leu Asn
165 170 175

Leu Ser Asp Asn Asn Leu Glu Leu Pro Asn Asp Val Phe His
180 185 190

Gly Ala Ser Gly Pro Val Ile Leu Asp Ile Ser Arg Thr Arg Ile His
195 200 205

Ser Leu Pro Ser Tyr Gly Leu Glu Asn Leu Lys Lys Leu Arg Ala Arg
210 215 220

Ser Thr Tyr Asn Leu Lys Lys Leu Pro Thr Leu Glu Lys Leu Val Ala
225 230 235 240

Leu Met Glu Ala Ser Leu Thr Tyr Pro Ser His Cys Cys Ala Phe Ala
245 250 255

Asn Trp Arg Arg Gln Ile Ser Glu Leu His Pro Ile Cys Asn Lys Ser
260 265 270

Ile Leu Arg Gln Glu Val Asp Tyr Met Thr Gln Thr Arg Gly Gln Arg
275 280 285

Ser Ser Leu Ala Glu Asp Asn Glu Ser Ser Tyr Ser Arg Gly Phe Asp
290 295 300

Met Thr Tyr Thr Glu Phe Asp Tyr Asp Leu Cys Asn Glu Val Val Asp
305 310 315 320

Val Thr Cys Ser Pro Lys Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile
325 330 335

Met Gly Tyr Asn Ile Leu Arg Val Leu Ile Trp Phe Ile Ser Ile Leu
340 345 350

Ala Ile Thr Gly Asn Ile Ile Val Leu Val Ile Leu Thr Thr Ser Gln
355 360 365

Tyr Lys Leu Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala
370 375 380

Asp Leu Cys Ile Gly Ile Tyr Leu Leu Leu Ile Ala Ser Val Asp Ile
385 390 395 400

His Thr Lys Ser Gln Tyr His Asn Tyr Ala Ile Asp Trp Gln Thr Gly
405 410 415

Ala Gly Cys Asp Ala Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu
420 425 430

Ser Val Tyr Thr Leu Thr Ala Ile Thr Leu Glu Arg Trp His Thr Ile
435 440 445

Thr His Ala Met Gln Leu Asp Cys Lys Val Gln Leu Arg His Ala Ala
450 455 460

Ser Val Met Val Met Gly Trp Ile Phe Ala Phe Ala Ala Leu Phe
465 470 475 480

Pro Ile Phe Gly Ile Ser Ser Tyr Met Lys Val Ser Ile Cys Leu Pro
485 490 495

Met Asp Ile Asp Ser Pro Leu Ser Gln Leu Tyr Val Met Ser Leu Leu
500 505 510

Val Leu Asn Val Leu Ala Phe Val Val Ile Cys Gly Cys Tyr Ile His
515 520 525

Ile Tyr Leu Thr Val Arg Asn Pro Asn Ile Val Ser Ser Ser Asp
530 535 540

Thr Arg Ile Ala Lys Arg Met Ala Met Leu Ile Phe Thr Asp Phe Leu

545 550 555 560

Cys Met Ala Pro Ile Ser Phe Phe Ala Ile Ser Ala Ser Leu Lys Val
565 570 575

Pro Leu Ile Thr Val Ser Lys Ala Lys Ile Leu Leu Val Leu Phe His
580 585 590

Pro Ile Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys
595 600 605

Asn Phe Arg Arg Asp Phe Phe Ile Leu Leu Ser Lys Cys Gly Cys Tyr
610 615 620

Glu Met Gln Ala Gln Ile Tyr Arg Thr Glu Thr Ser Ser Thr Val His
625 630 635 640

Asn Thr His Pro Arg Asn Gly His Cys Ser Ser Ala Pro Arg Val Thr
645 650 655

Asn Gly Ser Thr Tyr Ile Leu Val Pro Leu Ser His Leu Ala Gln Asn
660 665 670

<210> 44

<211> 670

<212> PRT

<213> Artificial sequence ..

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 44

Met Ala Leu Leu Leu Val Ser Leu Leu Ala Phe Leu Ser Leu Gly Ser
1 5 10 15

Gly Cys His His Arg Ile Cys His Cys Ser Asn Arg Val Phe Leu Cys
20 25 30

Gln Glu Ser Lys Val Thr Glu Ile Pro Ser Asp Leu Pro Arg Asn Ala
35 40 45

Ile Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Gln Lys Gly
50 55 60

Ala Phe Ser Gly Phe Gly Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn
65 70 75 80

Asp Val Leu Glu Val Ile Glu Ala Asp Val Phe Ser Asn Leu Pro Lys
85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asn
100 105 110

Pro Glu Ala Phe Gln Asn Leu Pro Asn Leu Gln Tyr Leu Leu Ile Ser
115 120 125

Asn Thr Gly Ile Lys His Leu Pro Asp Val His Lys Ile His Ser Leu
130 135 140

Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Thr Ile
 145 150 155 160

Glu Arg Asn Ser Phe Val Gly Leu Ser Phe Glu Ser Val Ile Leu Trp
 165 170 175

Leu Asn Lys Asn Gly Ile Gln Glu Ile His Asn Cys Ala Phe Asn Gly
 180 185 190

Thr Gln Leu Asp Glu Leu Asp Ile Ser Arg Thr Arg Ile His Ser Leu
 195 200 205

Pro Ser Tyr Gly Leu Glu Asn Leu Lys Lys Leu Arg Ala Arg Ser Thr
 210 215 220

Tyr Asn Leu Lys Lys Leu Pro Thr Leu Glu Lys Leu Val Ala Leu Met
 225 230 235 240

Glu Ala Ser Leu Thr Tyr Pro Ser His Cys Cys Ala Phe Ala Asn Trp
 245 250 255

Arg Arg Gln Ile Ser Glu Leu His Pro Ile Cys Asn Lys Ser Ile Leu
 260 265 270

Arg Gln Glu Val Asp Tyr Met Thr Gln Thr Arg Gly Gln Arg Ser Ser
 275 280 285

Leu Ala Glu Asp Asn Glu Ser Ser Tyr Ser Arg Gly Phe Asp Met Thr
 290 295 300

Tyr Thr Glu Phe Asp Tyr Asp Leu Cys Asn Glu Val Val Asp Val Thr
 305 310 315 320

Cys Ser Pro Lys Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met Gly
 325 330 335

Tyr Asn Ile Leu Arg Val Leu Ile Trp Phe Ile Ser Ile Leu Ala Ile
 340 345 350

Thr Gly Asn Ile Ile Val Leu Val Ile Leu Thr Thr Ser Gln Tyr Lys
 355 360 365

Leu Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp Leu
 370 375 380

Cys Ile Gly Ile Tyr Leu Leu Ile Ala Ser Val Asp Ile His Thr
 385 390 395 400

Lys Ser Gln Tyr His Asn Tyr Ala Ile Asp Trp Gln Thr Gly Ala Gly
 405 410 415

Cys Asp Ala Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val
 420 425 430

Tyr Thr Leu Thr Ala Ile Thr Leu Glu Arg Trp His Thr Ile Thr His
 435 440 445

Ala Met Gin Leu Asp Cys Lys Val Gln Leu Arg His Ala Ala Ser Val

450 455 460
Met Val Met Gly Trp Ile Phe Ala Phe Ala Ala Ala Leu Phe Pro Ile
465 470 475 480

Phe Gly Ile Ser Ser Tyr Met Lys Val Ser Ile Cys Leu Pro Met Asp
485 490 495

Ile Asp Ser Pro Leu Ser Gln Leu Tyr Val Met Ser Leu Leu Val Leu
500 505 510

Asn Val Leu Ala Phe Val Val Ile Cys Gly Cys Tyr Ile His Ile Tyr
515 520 525

Leu Thr Val Arg Asn Pro Asn Ile Val Ser Ser Ser Asp Thr Arg
530 535 540

Ile Ala Lys Arg Met Ala Met Leu Ile Phe Thr Asp Phe Leu Cys Met
545 550 555 560

Ala Pro Ile Ser Phe Phe Ala Ile Ser Ala Ser Leu Lys Val Pro Leu
565 570 575

Ile Thr Val Ser Lys Ala Lys Ile Leu Leu Val Leu Phe His Pro Ile
580 585 590

Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Asn Phe
595 600 605

Arg Arg Asp Phe Phe Ile Leu Leu Ser Lys Cys Gly Cys Tyr Glu Met
610 615 620

Gln Ala Gln Ile Tyr Arg Thr Glu Thr Ser Ser Thr Val His Asn Thr
625 630 635 640

His Pro Arg Asn Gly His Cys Ser Ser Ala Pro Arg Val Thr Asn Gly
645 650 655

Ser Thr Tyr Ile Leu Val Pro Leu Ser His Leu Ala Gln Asn
660 665 670

<210> 45
<211> 198
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 45

Met Ala Leu Leu Leu Val Ser Leu Leu Ala Phe Leu Ser Leu Gly Ser
1 5 10 15

Gly Cys His His Arg Ile Cys His Cys Ser Asn Arg Val Phe Leu Cys
20 25 30

Gln Glu Ser Lys Val Thr Glu Ile Pro Ser Asp Leu Pro Arg Asn Ala
35 40 45

Ile Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Gln Lys Gly
50 55 60

Ala Phe Ser Gly Phe Gly Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn
65 70 75 80

Asp Val Leu Glu Val Ile Glu Ala Asp Val Phe Ser Asn Leu Pro Lys
85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asn
100 105 110

Pro Glu Ala Phe Gln Asn Leu Pro Asn Leu Gln Tyr Leu Leu Ile Ser
115 120 125

Asn Thr Gly Ile Lys His Leu Pro Asp Val His Lys Ile His Ser Leu
130 135 140

Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Thr Ile
145 150 155 160

Glu Arg Asn Ser Phe Val Gly Leu Ser Phe Glu Ser Val Ile Leu Trp
165 170 175

Leu Asn Lys Asn Gly Ile Gln Glu Ile His Asn Cys Ala Phe Asn Gly
180 185 190

Thr Gln Leu Asp Glu Leu
195

<210> 46

<211> 729

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 46

Met Ala Leu Leu Leu Val Ser Leu Leu Ala Phe Leu Ser Leu Gly Ser
1 5 10 15

Gly Cys His His Arg Ile Cys His Cys Ser Asn Arg Val Phe Leu Cys
20 25 30

Gln Glu Ser Lys Val Thr Glu Ile Pro Ser Asp Leu Pro Arg Asn Ala
35 40 45

Ile Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Gln Lys Gly
50 55 60

Ala Phe Ser Gly Phe Gly Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn
65 70 75 80

Asp Val Leu Glu Val Ile Glu Ala Asp Val Phe Ser Asn Leu Pro Lys
85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asn
100 105 110

Pro Glu Ala Phe Gln Asn Leu Pro Asn Leu Gln Tyr Leu Leu Ile Ser
115 120 125

Asn Thr Gly Ile Lys His Leu Pro Asp Val His Lys Ile His Ser Leu
130 135 140

Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Thr Ile
145 150 155 160

Glu Arg Asn Ser Phe Val Gly Leu Ser Phe Glu Ser Val Ile Leu Trp
165 170 175

Leu Asn Lys Asn Gly Ile Gln Glu Ile His Asn Cys Ala Phe Asn Gly
180 185 190

Thr Gln Leu Asp Glu Leu Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu
195 200 205

Leu Pro Asn Asp Val Phe His Gly Ala Ser Gly Pro Val Ile Leu Asn
210 215 220

Arg Arg Thr Arg Thr Pro Thr Glu Pro Asn Val Leu Leu Ala Lys Tyr
225 230 235 240

Pro Ser Gly Gln Gly Val Leu Glu Glu Pro Glu Ser Leu Ser Ser Ser
245 250 255

Ile Asp Ile Ser Arg Thr Arg Ile His Ser Leu Pro Ser Tyr Gly Leu
260 265 270

Glu Asn Leu Lys Lys Leu Arg Ala Arg Ser Thr Tyr Asn Leu Lys Lys
275 280 285

Leu Pro Thr Leu Glu Lys Leu Val Ala Leu Met Glu Ala Ser Leu Thr
290 295 300

Tyr Pro Ser His Cys Cys Ala Phe Ala Asn Trp Arg Arg Gln Ile Ser
305 310 315 320

Glu Leu His Pro Ile Cys Asn Lys Ser Ile Leu Arg Gln Glu Val Asp
325 330 335

Tyr Met Thr Gln Thr Arg Gly Gln Arg Ser Ser Leu Ala Glu Asp Asn
340 345 350

Glu Ser Ser Tyr Ser Arg Gly Phe Asp Met Thr Tyr Thr Glu Phe Asp
355 360 365

Tyr Asp Leu Cys Asn Glu Val Val Asp Val Thr Cys Ser Pro Lys Pro
370 375 380

Asp Ala Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Asn Ile Leu Arg
385 390 395 400

Val Leu Ile Trp Phe Ile Ser Ile Leu Ala Ile Thr Gly Asn Ile Ile
405 410 415

Val Leu Val Ile Leu Thr Thr Ser Gln Tyr Lys Leu Thr Val Pro Arg
420 425 430

Phe Leu Met Cys Asn Leu Ala Phe Ala Asp Leu Cys Ile Gly Ile Tyr
435 440 445

Leu Leu Leu Ile Ala Ser Val Asp Ile His Thr Lys Ser Gln Tyr His
450 455 460

Asn Tyr Ala Ile Asp Trp Gln Thr Gly Ala Gly Cys Asp Ala Ala Gly
465 470 475 480

Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu Thr Ala
485 490 495

Ile Thr Leu Glu Arg Trp His Thr Ile Thr His Ala Met Gln Leu Asp
500 505 510

Cys Lys Val Gln Leu Arg His Ala Ala Ser Val Met Val Met Gly Trp
515 520 525

Ile Phe Ala Phe Ala Ala Leu Phe Pro Ile Phe Gly Ile Ser Ser
530 535 540

Tyr Met Lys Val Ser Ile Cys Leu Pro Met Asp Ile Asp Ser Pro Leu
545 550 555 560

Ser Gln Leu Tyr Val Met Ser Leu Leu Val Leu Asn Val Leu Ala Phe
565 570 575

Val Val Ile Cys Gly Cys Tyr Ile His Ile Tyr Leu Thr Val Arg Asn
580 585 590

Pro Asn Ile Val Ser Ser Ser Asp Thr Arg Ile Ala Lys Arg Met
595 600 605

Ala Met Leu Ile Phe Thr Asp Phe Leu Cys Met Ala Pro Ile Ser Phe
610 615 620

Phe Ala Ile Ser Ala Ser Leu Lys Val Pro Leu Ile Thr Val Ser Lys
625 630 635 640

Ala Lys Ile Leu Leu Val Leu Phe His Pro Ile Asn Ser Cys Ala Asn
645 650 655

Pro Phe Leu Tyr Ala Ile Phe Thr Lys Asn Phe Arg Arg Asp Phe Phe
660 665 670

Ile Leu Leu Ser Lys Cys Gly Cys Tyr Glu Met Gln Ala Gln Ile Tyr
675 680 685

Arg Thr Glu Thr Ser Ser Thr Val His Asn Thr His Pro Arg Asn Gly
690 695 700

His Cys Ser Ser Ala Pro Arg Val Thr Asn Gly Ser Thr Tyr Ile Leu
705 710 715 720

Val Pro Leu Ser His Leu Ala Gln Asn

725

<210> 47
<211> 675
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 47

Met Lys Gln Arg Phe Ser Ala Leu Gln Leu Leu Lys Leu Leu Leu
1 5 10 15

Leu Gln Pro Pro Leu Pro Arg Ala Leu Arg Glu Ala Leu Cys Pro Glu
20 25 30

Pro Cys Asn Cys Val Pro Asp Gly Ala Leu Arg Cys Pro Gly Pro Thr
35 40 45

Ala Gly Leu Thr Arg Leu Glu Ile Ser Gln Ile Asp Ser Leu Glu Arg
50 55 60

Ile Glu Ala Asn Ala Phe Asp Asn Leu Leu Asn Leu Ser Glu Ile Leu
65 70 75 80

Ile Gln Asn Thr Lys Asn Leu Arg Tyr Ile Glu Pro Gly Ala Phe Ile
85 90 95

Asn Leu Pro Arg Leu Lys Tyr Leu Ser Ile Cys Asn Thr Gly Ile Arg
100 105 110

Lys Phe Pro Asp Val Thr Lys Val Phe Ser Ser Glu Ser Asn Phe Ile
115 120 125

Leu Glu Ile Cys Asp Asn Leu His Ile Thr Thr Ile Pro Gly Asn Ala
130 135 140

Phe Gln Gly Met Asn Asn Glu Ser Val Thr Leu Lys Leu Tyr Gly Asn
145 150 155 160

Gly Phe Glu Glu Val Gln Ser His Ala Phe Asn Gly Thr Thr Leu Thr
165 170 175

Ser Leu Glu Leu Lys Glu Asn Val His Leu Glu Lys Met His Asn Gly
180 185 190

Ala Phe Arg Gly Ala Thr Gly Pro Lys Thr Leu Asp Ile Ser Ser Thr
195 200 205

Lys Leu Gln Ala Leu Pro Ser Tyr Gly Leu Glu Ser Ile Gln Arg Leu
210 215 220

Ile Ala Thr Ser Ser Tyr Ser Leu Lys Lys Leu Pro Ser Arg Glu Thr
225 230 235 240

Phe Val Asn Leu Leu Glu Ala Thr Leu Thr Tyr Pro Ser His Cys Cys
245 250 255

Ala Phe Arg Asn Leu Pro Thr Lys Glu Gln Asn Phe Ser His Ser Ile
 260 265 270

Ser Glu Asn Phe Ser Lys Gln Cys Glu Ser Thr Val Arg Lys Val Ser
 275 280 285

Asn Lys Thr Leu Tyr Ser Ser Met Leu Ala Glu Ser Glu Leu Ser Gly
 290 295 300

Trp Asp Tyr Glu Tyr Gly Phe Cys Leu Pro Lys Thr Pro Arg Cys Ala
 305 310 315 320

Pro Glu Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Asp
 325 330 335

Phe Leu Arg Val Leu Ile Trp Leu Ile Asn Ile Leu Ala Ile Met Gly
 340 345 350

Asn Met Thr Val Leu Phe Val Leu Leu Thr Ser Arg Tyr Lys Leu Thr
 355 360 365

Val Pro Arg Phe Leu Met Cys Asn Leu Ser Phe Ala Asp Phe Cys Met
 370 375 380

Gly Leu Tyr Leu Leu Leu Ile Ala Ser Val Asp Ser Gln Thr Lys Gly
 385 390 395 400

Gln Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Ser Gly Cys Ser
 405 410 415

Thr Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr
 420 425 430

Leu Thr Val Ile Thr Leu Glu Arg Trp His Thr Ile Thr Tyr Ala Ile
 435 440 445

His Leu Asp Gln Lys Leu Arg Leu Arg His Ala Ile Leu Ile Met Leu
 450 455 460

Gly Gly Trp Leu Phe Ser Ser Leu Ile Ala Met Leu Pro Leu Val Gly
 465 470 475 480

Val Ser Asn Tyr Met Lys Val Ser Ile Cys Phe Pro Met Asp Val Glu
 485 490 495

Thr Thr Leu Ser Gln Val Tyr Ile Leu Thr Ile Leu Ile Leu Asn Val
 500 505 510

Val Ala Phe Phe Ile Ile Cys Ala Cys Tyr Ile Lys Ile Tyr Phe Ala
 515 520 525

Val Arg Asn Pro Glu Leu Met Ala Thr Asn Lys Asp Thr Lys Ile Ala
 530 535 540

Lys Lys Met Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys Met Ala Pro
 545 550 555 560

Ile Ser Phe Phe Ala Ile Ser Ala Ala Phe Lys Val Pro Leu Ile Thr

565 570 575

Val Thr Asn Ser Lys Val Leu Leu Val Leu Phe Tyr Pro Ile Asn Ser
 580 585 590

Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Thr Phe Gln Arg
 595 600 605

Asp Phe Phe Leu Leu Leu Ser Lys Phe Gly Cys Cys Lys Arg Arg Ala
 610 615 620

Glu Leu Tyr Arg Arg Lys Asp Phe Ser Ala Tyr Thr Ser Asn Cys Lys
 625 630 635 640

Asn Gly Phe Thr Gly Ser Asn Lys Pro Ser Gln Ser Thr Leu Lys Leu
 645 650 655

Ser Thr Leu His Cys Gln Gly Thr Ala Leu Leu Asp Lys Thr Arg Tyr
 660 665 670

Thr Glu Cys
 675

<210> 48

<211> 677

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 48

Met Lys Gln Arg Phe Ser Ala Leu Gln Leu Leu Lys Leu Leu Leu
 1 5 10 15

Leu Gln Pro Pro Leu Pro Arg Ala Leu Arg Glu Ala Leu Cys Pro Glu
 20 25 30

Pro Cys Asn Cys Val Pro Asp Gly Ala Leu Arg Cys Pro Gly Pro Thr
 35 40 45

Ala Gly Leu Thr Arg Leu Ser Leu Ala Tyr Leu Pro Val Lys Val Ile
 50 55 60

Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val Ile Lys Ile Ser Glu
 65 70 75 80

Ile Leu Ile Gln Asn Thr Lys Asn Leu Arg Tyr Ile Glu Pro Gly Ala
 85 90 95

Phe Ile Asn Leu Pro Arg Leu Lys Tyr Leu Ser Ile Cys Asn Thr Gly
 100 105 110

Ile Arg Lys Phe Pro Asp Val Thr Lys Val Phe Ser Ser Glu Ser Asn
 115 120 125

Phe Ile Leu Glu Ile Cys Asp Asn Leu His Ile Thr Thr Ile Pro Gly
 130 135 140

Asn Ala Phe Gln Gly Met Asn Asn Glu Ser Val Thr Leu Lys Leu Tyr
 145 150 155 160

Gly Asn Gly Phe Glu Glu Val Gln Ser His Ala Phe Asn Gly Thr Thr
 165 170 175

Leu Thr Ser Leu Glu Leu Lys Glu Asn Val His Leu Glu Lys Met His
 180 185 190

Asn Gly Ala Phe Arg Gly Ala Thr Gly Pro Lys Thr Leu Asp Ile Ser
 195 200 205

Ser Thr Lys Leu Gln Ala Leu Pro Ser Tyr Gly Leu Glu Ser Ile Gln
 210 215 220

Arg Leu Ile Ala Thr Ser Ser Tyr Ser Leu Lys Lys Leu Pro Ser Arg
 225 230 235 240

Glu Thr Phe Val Asn Leu Leu Glu Ala Thr Leu Thr Tyr Pro Ser His
 245 250 255

Cys Cys Ala Phe Arg Asn Leu Pro Thr Lys Glu Gln Asn Phe Ser His
 260 265 270

Ser Ile Ser Glu Asn Phe Ser Lys Gln Cys Glu Ser Thr Val Arg Lys
 275 280 285

Val Ser Asn Lys Thr Leu Tyr Ser Ser Met Leu Ala Glu Ser Glu Leu
 290 295 300

Ser Gly Trp Asp Tyr Glu Tyr Gly Phe Cys Leu Pro Lys Thr Pro Arg
 305 310 315 320

Cys Ala Pro Glu Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met Gly
 325 330 335

Tyr Asp Phe Leu Arg Val Leu Ile Trp Leu Ile Asn Ile Leu Ala Ile
 340 345 350

Met Gly Asn Met Thr Val Leu Phe Val Leu Leu Thr Ser Arg Tyr Lys
 355 360 365

Leu Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ser Phe Ala Asp Phe
 370 375 380

Cys Met Gly Leu Tyr Leu Leu Ile Ala Ser Val Asp Ser Gln Thr
 385 390 395 400

Lys Gly Gin Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Ser Gly
 405 410 415

Cys Ser Thr Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val
 420 425 430

Tyr Thr Leu Thr Val Ile Thr Leu Glu Arg Trp His Thr Ile Thr Tyr
 435 440 445

Ala Ile His Leu Asp Gln Lys Leu Arg Leu Arg His Ala Ile Leu Ile

450 455 460
Met Leu Gly Gly Trp Leu Phe Ser Ser Leu Ile Ala Met Leu Pro Leu
465 470 475 480

Val Gly Val Ser Asn Tyr Met Lys Val Ser Ile Cys Phe Pro Met Asp
485 490 495

Val Glu Thr Thr Leu Ser Gln Val Tyr Ile Leu Thr Ile Leu Ile Leu
500 505 510

Asn Val Val Ala Phe Phe Ile Ile Cys Ala Cys Tyr Ile Lys Ile Tyr
515 520 525

Phe Ala Val Arg Asn Pro Glu Leu Met Ala Thr Asn Lys Asp Thr Lys
530 535 540

Ile Ala Lys Lys Met Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys Met
545 550 555 560

Ala Pro Ile Ser Phe Phe Ala Ile Ser Ala Ala Phe Lys Val Pro Leu
565 570 575

Ile Thr Val Thr Asn Ser Lys Val Leu Leu Val Val Leu Phe Tyr Pro Ile
580 585 590

Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Thr Phe
595 600 605

Gln Arg Asp Phe Phe Leu Leu Ser Lys Phe Gly Cys Cys Lys Arg
610 615 620

Arg Ala Glu Leu Tyr Arg Arg Lys Asp Phe Ser Ala Tyr Thr Ser Asn
625 630 635 640

Cys Lys Asn Gly Phe Thr Gly Ser Asn Lys Pro Ser Gln Ser Thr Leu
645 650 655

Lys Leu Ser Thr Leu His Cys Gln Gly Thr Ala Leu Leu Asp Lys Thr
660 665 670

Arg Tyr Thr Glu Cys
675

<210> 49
<211> 678
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 49
Ala Met Lys Gln Arg Phe Ser Ala Leu Gln Leu Leu Lys Leu Leu Leu
1 5 10 15

Leu Leu Gln Pro Pro Leu Pro Arg Ala Leu Arg Glu Ala Leu Cys Pro
20 25 30

Glu Pro Cys Asn Cys Val Pro Asp Gly Ala Leu Arg Cys Pro Gly Pro
35 40 45

Thr Ala Gly Leu Thr Arg Leu Ser Leu Ala Tyr Leu Pro Val Lys Val
50 55 60

Ile Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val Ile Lys Ile Glu
65 70 75 80

Ile Ser Gln Ile Asp Ser Leu Glu Arg Ile Glu Ala Asn Ala Phe Asp
85 90 95

Asn Leu Leu Asn Leu Ser Glu Ile Leu Ile Gln Asn Thr Lys Asn Leu
100 105 110

Arg Tyr Ile Glu Pro Gly Ala Phe Ile Asn Leu Pro Arg Leu Lys Tyr
115 120 125

Leu Phe Ile Leu Glu Ile Cys Asp Asn Leu His Ile Thr Thr Ile Pro
130 135 140

Gly Asn Ala Phe Gln Gly Met Asn Asn Glu Ser Val Thr Leu Lys Leu
145 150 155 160

Tyr Gly Asn Gly Phe Glu Glu Val Gln Ser His Ala Phe Asn Gly Thr
165 170 175

Thr Leu Thr Ser Leu Glu Leu Lys Glu Asn Val His Leu Glu Lys Met
180 185 190

His Asn Gly Ala Phe Arg Gly Ala Thr Gly Pro Lys Thr Leu Asp Ile
195 200 205

Ser Ser Thr Lys Leu Gln Ala Leu Pro Ser Tyr Gly Leu Glu Ser Ile
210 215 220

Gln Arg Leu Ile Ala Thr Ser Ser Tyr Ser Leu Lys Lys Leu Pro Ser
225 230 235 240

Arg Glu Thr Phe Val Asn Leu Glu Ala Thr Leu Thr Tyr Pro Ser
245 250 255

His Cys Cys Ala Phe Arg Asn Leu Pro Thr Lys Glu Gln Asn Phe Ser
260 265 270

His Ser Ile Ser Glu Asn Phe Ser Lys Gln Cys Glu Ser Thr Val Arg
275 280 285

Lys Val Ser Asn Lys Thr Leu Tyr Ser Ser Met Leu Ala Glu Ser Glu
290 295 300

Leu Ser Gly Trp Asp Tyr Glu Tyr Gly Phe Cys Leu Pro Lys Thr Pro
305 310 315 320

Arg Cys Ala Pro Glu Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met
325 330 335

Gly Tyr Asp Phe Leu Arg Val Leu Ile Trp Leu Ile Asn Ile Leu Ala

340	345	350
Ile Met Gly Asn Met Thr Val Leu Phe Val Leu Leu Thr Ser Arg Tyr		
355	360	365
Lys Leu Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ser Phe Ala Asp		
370	375	380
Phe Cys Met Gly Leu Tyr Leu Leu Ile Ala Ser Val Asp Ser Gln		
385	390	395
400		
Thr Lys Gly Gln Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr GLY Ser		
405	410	415
Gly Cys Ser Thr Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser		
420	425	430
Val Tyr Thr Leu Thr Val Ile Thr Leu Glu Arg Trp His Thr Ile Thr		
435	440	445
Tyr Ala Ile His Leu Asp Gln Lys Leu Arg Leu Arg His Ala Ile Leu		
450	455	460
Ile Met Leu Gly Gly Trp Leu Phe Ser Ser Leu Ile Ala Met Leu Pro		
465	470	475
480		
Leu Val Gly Val Ser Asn Tyr Met Lys Val Ser Ile Cys Phe Pro Met		
485	490	495
Asp Val Glu Thr Thr Leu Ser Gln Val Tyr Ile Leu Thr Ile Leu Ile		
500	505	510
Leu Asn Val Val Ala Phe Phe Ile Ile Cys Ala Cys Tyr Ile Lys Ile		
515	520	525
Tyr Phe Ala Val Arg Asn Pro Glu Leu Met Ala Thr Asn Lys Asp Thr		
530	535	540
Lys Ile Ala Lys Lys Met Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys		
545	550	555
560		
Met Ala Pro Ile Ser Phe Phe Ala Ile Ser Ala Ala Phe Lys Val Pro		
565	570	575
Leu Ile Thr Val Thr Asn Ser Lys Val Leu Leu Val Leu Phe Tyr Pro		
580	585	590
Ile Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Thr		
595	600	605
Phe Gln Arg Asp Phe Phe Leu Leu Leu Ser Lys Phe Gly Cys Cys Lys		
610	615	620
Arg Arg Ala Glu Leu Tyr Arg Arg Lys Asp Phe Ser Ala Tyr Thr Ser		
625	630	635
640		
Asn Cys Lys Asn Gly Phe Thr Gly Ser Asn Lys Pro Ser Gln Ser Thr		
645	650	655

Leu Lys Leu Ser Thr Leu His Cys Gln Gly Thr Ala Leu Leu Asp Lys
 660 665 670

Thr Arg Tyr Thr Glu Cys
 675

<210> 50

<211> 673

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 50

Met Lys Gln Arg Phe Ser Ala Leu Gln Leu Leu Lys Leu Leu Leu
 1 5 10 15

Leu Gln Pro Pro Leu Pro Arg Ala Leu Arg Glu Ala Leu Cys Pro Glu
 20 25 30

Pro Cys Asn Cys Val Pro Asp Gly Ala Leu Arg Cys Pro Gly Pro Thr
 35 40 45

Ala Gly Leu Thr Arg Leu Ser Leu Ala Tyr Leu Pro Val Lys Val Ile
 50 55 60

Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val Ile Lys Ile Glu Ile
 65 70 75 80

Ser Gln Ile Asp Ser Leu Glu Arg Ile Glu Ala Asn Ala Phe Asp Asn
 85 90 95

Leu Leu Asn Leu Ser Glu Ile Leu Ile Gln Asn Thr Lys Asn Leu Arg
 100 105 110

Tyr Ile Glu Pro Gly Ala Phe Ile Asn Leu Pro Arg Leu Lys Tyr Leu
 115 120 125

Ser Ile Cys Asn Thr Gly Ile Arg Lys Phe Pro Asp Val Thr Lys Val
 130 135 140

Phe Ser Ser Glu Ser Asn Phe Ile Leu Lys Leu Tyr Gly Asn Gly Phe
 145 150 155 160

Glu Glu Val Gln Ser His Ala Phe Asn Gly Thr Thr Leu Thr Ser Leu
 165 170 175

Glu Leu Lys Glu Asn Val His Leu Glu Lys Met His Asn Gly Ala Phe
 180 185 190

Arg Gly Ala Thr Gly Pro Lys Thr Leu Asp Ile Ser Ser Thr Lys Leu
 195 200 205

Gln Ala Leu Pro Ser Tyr Gly Leu Glu Ser Ile Gln Arg Leu Ile Ala
 210 215 220

Thr Ser Ser Tyr Ser Leu Lys Lys Leu Pro Ser Arg Glu Thr Phe Val

225 230 235 240

Asn Leu Leu Glu Ala Thr Leu Thr Tyr Pro Ser His Cys Cys Ala Phe
245 250 255

Arg Asn Leu Pro Thr Lys Glu Gln Asn Phe Ser His Ser Ile Ser Glu
260 265 270

Asn Phe Ser Lys Gln Cys Glu Ser Thr Val Arg Lys Val Ser Asn Lys
275 280 285

Thr Leu Tyr Ser Ser Met Leu Ala Glu Ser Glu Leu Ser Gly Trp Asp
290 295 300

Tyr Glu Tyr Gly Phe Cys Leu Pro Lys Thr Pro Arg Cys Ala Pro Glu
305 310 315 320

Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Asp Phe Leu
325 330 335

Arg Val Leu Ile Trp Leu Ile Asn Ile Leu Ala Ile Met Gly Asn Met
340 345 350

Thr Val Leu Phe Val Leu Leu Thr Ser Arg Tyr Lys Leu Thr Val Pro
355 360 365

Arg Phe Leu Met Cys Asn Leu Ser Phe Ala Asp Phe Cys Met Gly Leu
370 375 380

Tyr Leu Leu Leu Ile Ala Ser Val Asp Ser Gln Thr Lys Gly Gln Tyr
385 390 395 400

Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Ser Gly Cys Ser Thr Ala
405 410 415

Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu Thr
420 425 430

Val Ile Thr Leu Glu Arg Trp His Thr Ile Thr Tyr Ala Ile His Leu
435 440 445

Asp Gln Lys Leu Arg Leu Arg His Ala Ile Leu Ile Met Leu Gly Gly
450 455 460

Trp Leu Phe Ser Ser Leu Ile Ala Met Leu Pro Leu Val Gly Val Ser
465 470 475 480

Asn Tyr Met Lys Val Ser Ile Cys Phe Pro Met Asp Val Glu Thr Thr
485 490 495

Leu Ser Gln Val Tyr Ile Leu Thr Ile Leu Ile Leu Asn Val Val Ala
500 505 510

Phe Phe Ile Ile Cys Ala Cys Tyr Ile Lys Ile Tyr Phe Ala Val Arg
515 520 525

Asn Pro Glu Leu Met Ala Thr Asn Lys Asp Thr Lys Ile Ala Lys Lys
530 535 540

Met Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys Met Ala Pro Ile Ser
545 550 555 560

Phe Phe Ala Ile Ser Ala Ala Phe Lys Val Pro Leu Ile Thr Val Thr
565 570 575

Asn Ser Lys Val Leu Leu Val Leu Phe Tyr Pro Ile Asn Ser Cys Ala
580 585 590

Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Thr Phe Gln Arg Asp Phe
595 600 605

Phe Leu Leu Leu Ser Lys Phe Gly Cys Cys Lys Arg Arg Ala Glu Leu
610 615 620

Tyr Arg Arg Lys Asp Phe Ser Ala Tyr Thr Ser Asn Cys Lys Asn Gly
625 630 635 640

Phe Thr Gly Ser Asn Lys Pro Ser Gln Ser Thr Leu Lys Leu Ser Thr
645 650 655

Leu His Cys Gln Gly Thr Ala Leu Leu Asp Lys Thr Arg Tyr Thr Glu
650 655 665 670

Cys

<210> 51

<211> 678

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 51

Met Lys Gln Arg Phe Ser Ala Leu Gln Leu Leu Lys Leu Leu Leu
1 5 10 15

Leu Gln Pro Pro Leu Pro Arg Ala Leu Arg Glu Ala Leu Cys Pro Glu
20 25 30

Pro Cys Asn Cys Val Pro Asp Gly Ala Leu Arg Cys Pro Gly Pro Thr
35 40 45

Ala Gly Leu Thr Arg Leu Ser Leu Ala Tyr Leu Pro Val Lys Val Ile
50 55 60

Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val Ile Lys Ile Glu Ile
65 70 75 80

Ser Gln Ile Asp Ser Leu Glu Arg Ile Glu Ala Asn Ala Phe Asp Asn
85 90 95

Leu Leu Asn Leu Ser Glu Ile Leu Ile Gln Asn Thr Lys Asn Leu Arg
100 105 110

Tyr Ile Glu Pro Gly Ala Phe Ile Asn Leu Pro Arg Leu Lys Tyr Leu

115 120 125

Ser Ile Cys Asn Thr Gly Ile Arg Lys Phe Pro Asp Val Thr Lys Val
130 135 140

Phe Ser Ser Glu Ser Asn Phe Ile Leu Glu Ile Cys Asp Asn Leu His
145 150 155 160

Ile Thr Thr Ile Pro Gly Asn Ala Phe Gln Gly Met Asn Asn Glu Ser
165 170 175

Val Thr Leu Ser Leu Glu Leu Lys Glu Asn Val His Leu Glu Lys Met
180 185 190

His Asn Gly Ala Phe Arg Gly Ala Thr Gly Pro Lys Thr Leu Asp Ile
195 200 205

Ser Ser Thr Lys Leu Gln Ala Leu Pro Ser Tyr Gly Leu Glu Ser Ile
210 215 220

Gln Arg Leu Ile Ala Thr Ser Ser Tyr Ser Leu Lys Lys Leu Pro Ser
225 230 235 240

Arg Glu Thr Phe Val Asn Leu Leu Glu Ala Thr Leu Thr Tyr Pro Ser
245 250 255

His Cys Cys Ala Phe Arg Asn Leu Pro Thr Lys Glu Gln Asn Phe Ser
260 265 270

His Ser Ile Ser Glu Asn Phe Ser Lys Gln Cys Glu Ser Thr Val Arg
275 280 285

Lys Val Ser Asn Lys Thr Leu Tyr Ser Ser Met Leu Ala Glu Ser Glu
290 295 300

Leu Ser Gly Trp Asp Tyr Glu Tyr Gly Phe Cys Leu Pro Lys Thr Pro
305 310 315 320

Arg Cys Ala Pro Glu Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met
325 330 335

Gly Tyr Asp Phe Leu Arg Val Leu Ile Trp Leu Ile Asn Ile Leu Ala
340 345 350

Ile Met Gly Asn Met Thr Val Leu Phe Val Leu Leu Thr Ser Arg Tyr
355 360 365

Lys Leu Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ser Phe Ala Asp
370 375 380

Phe Cys Met Gly Leu Tyr Leu Leu Leu Ile Ala Ser Val Asp Ser Gln
385 390 395 400

Thr Lys Gly Gln Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Ser
405 410 415

Gly Cys Ser Thr Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser
420 425 430

Val Tyr Thr Leu Thr Val Ile Thr Leu Glu Arg Trp His Thr Ile Thr
 435 440 445

Tyr Ala Ile His Leu Asp Gln Lys Leu Arg Leu Arg His Ala Ile Leu
 450 455 460

Ile Met Leu Gly Gly Trp Leu Phe Ser Ser Leu Ile Ala Met Leu Pro
 465 470 475 480

Leu Val Gly Val Ser Asn Tyr Met Lys Val Ser Ile Cys Phe Pro Met
 485 490 495

Asp Val Glu Thr Thr Leu Ser Gln Val Tyr Ile Leu Thr Ile Leu Ile
 500 505 510

Leu Asn Val Val Ala Phe Phe Ile Ile Cys Ala Cys Tyr Ile Lys Ile
 515 520 525

Tyr Phe Ala Val Arg Asn Pro Glu Leu Met Ala Thr Asn Lys Asp Thr
 530 535 540

Lys Ile Ala Lys Lys Met Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys
 545 550 555 560

Met Ala Pro Ile Ser Phe Phe Ala Ile Ser Ala Ala Phe Lys Val Pro
 565 570 575

Leu Ile Thr Val Thr Asn Ser Lys Val Leu Leu Val Leu Phe Tyr Pro
 580 585 590

Ile Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Thr
 595 600 605

Phe Gln Arg Asp Phe Phe Leu Leu Leu Ser Lys Phe Gly Cys Cys Lys
 610 615 620

Arg Arg Ala Glu Leu Tyr Arg Arg Lys Asp Phe Ser Ala Tyr Thr Ser
 625 630 635 640

Asn Cys Lys Asn Gly Phe Thr Gly Ser Asn Lys Pro Ser Gln Ser Thr
 645 650 655

Leu Lys Leu Ser Thr Leu His Cys Gln Gly Thr Ala Leu Leu Asp Lys
 660 665 670

Thr Arg Tyr Thr Glu Cys
 675

<210> 52

<211> 672

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 52

Met Lys Gln Arg Phe Ser Ala Leu Gln Leu Leu Lys Leu Leu Leu

1	5	10	15
Leu Gln Pro Pro Leu Pro Arg Ala Leu Arg Glu Ala Leu Cys Pro Glu			
20.	25	30	
Pro Cys Asn Cys Val Pro Asp Gly Ala Leu Arg Cys Pro Gly Pro Thr			
35	40	45	
Ala Gly Leu Thr Arg Leu Ser Leu Ala Tyr Leu Pro Val Lys Val Ile			
50	55	60	
Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val Ile Lys Ile Glu Ile			
65	70	75	80
Ser Gln Ile Asp Ser Leu Glu Arg Ile Glu Ala Asn Ala Phe Asp Asn			
85	90	95	
Leu Leu Asn Leu Ser Glu Ile Leu Ile Gln Asn Thr Lys Asn Leu Arg			
100	105	110	
Tyr Ile Glu Pro Gly Ala Phe Ile Asn Leu Pro Arg Leu Lys Tyr Leu			
115	120	125	
Ser Ile Cys Asn Thr Gly Ile Arg Lys Phe Pro Asp Val Thr Lys Val			
130	135	140	
Phe Ser Ser Glu Ser Asn Phe Ile Leu Glu Ile Cys Asp Asn Leu His			
145	150	155	160
Ile Thr Thr Ile Pro Gly Asn Ala Phe Gln Gly Met Asn Asn Glu Ser			
165	170	175	
Val Thr Leu Lys Leu Tyr Gly Asn Gly Phe Glu Glu Val Gln Ser His			
180	185	190	
Ala Phe Asn Gly Thr Thr Leu Thr Ser Leu Glu Leu Lys Glu Asn Val			
195	200	205	
His Leu Glu Lys Met His Asn Gly Ala Phe Arg Gly Ala Thr Gly Pro			
210	215	220	
Lys Thr Leu Asp Ile Ser Ser Thr Lys Leu Gln Ala Leu Pro Ser Tyr			
225	230	235	240
Gly Leu Glu Ser Ile Gln Arg Leu Ile Ala Thr Ser Ser Tyr Ser Leu			
245	250	255	
Lys Lys Leu Pro Ser Arg Glu Thr Phe Val Asn Leu Leu Glu Ala Thr			
260	265	270	
Leu Thr Tyr Pro Ser His Cys Cys Ala Phe Arg Asn Leu Pro Thr Lys			
275	280	285	
Glu Tyr Ser Ser Met Leu Ala Glu Ser Glu Leu Ser Gly Trp Asp Tyr			
290	295	300	
Glu Tyr Gly Phe Cys Leu Pro Lys Thr Pro Arg Cys Ala Pro Glu Pro			
305	310	315	320

Asp Ala Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Asp Phe Leu Arg
325 330 335

Val Leu Ile Trp Leu Ile Asn Ile Leu Ala Ile Met Gly Asn Met Thr
340 345 350

Val Leu Phe Val Leu Leu Thr Ser Arg Tyr Lys Leu Thr Val Pro Arg
355 360 365

Phe Leu Met Cys Asn Leu Ser Phe Ala Asp Phe Cys Met Gly Leu Tyr
370 375 380

Leu Leu Leu Ile Ala Ser Val Asp Ser Gln Thr Lys Gly Gln Tyr Tyr
385 390 395 400

Asn His Ala Ile Asp Trp Gln Thr Gly Ser Gly Cys Ser Thr Ala Gly
405 410 415

Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu Thr Val
420 425 430

Ile Thr Leu Glu Arg Trp His Thr Ile Thr Tyr Ala Ile His Leu Asp
435 440 445

Gln Lys Leu Arg Leu Arg His Ala Ile Leu Ile Met Leu Gly Gly Trp
450 455 460

Leu Phe Ser Ser Leu Ile Ala Met Leu Pro Leu Val Gly Val Ser Asn
465 470 475 480

Tyr Met Lys Val Ser Ile Cys Phe Pro Met Asp Val Glu Thr Thr Leu
485 490 495

Ser Gln Val Tyr Ile Leu Thr Ile Leu Ile Leu Asn Val Val Ala Phe
500 505 510

Phe Ile Ile Cys Ala Cys Tyr Ile Lys Ile Tyr Phe Ala Val Arg Asn
515 520 525

Pro Glu Leu Met Ala Thr Asn Lys Asp Thr Lys Ile Ala Lys Lys Met
530 535 540

Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys Met Ala Pro Ile Ser Phe
545 550 555 560

Phe Ala Ile Ser Ala Ala Phe Lys Val Pro Leu Ile Thr Val Thr Asn
565 570 575

Ser Lys Val Leu Leu Val Leu Phe Tyr Pro Ile Asn Ser Cys Ala Asn
580 585 590

Pro Phe Leu Tyr Ala Ile Phe Thr Lys Thr Phe Gln Arg Asp Phe Phe
595 600 605

Leu Leu Leu Ser Lys Phe Gly Cys Cys Lys Arg Arg Ala Glu Leu Tyr
610 615 620

Arg Arg Lys Asp Phe Ser Ala Tyr Thr Ser Asn Cys Lys Asn Gly Phe
 625 630 635 640

Thr Gly Ser Asn Lys Pro Ser Gln Ser Thr Leu Lys Leu Ser Thr Leu
 645 650 655

His Cys Gln Gly Thr Ala Leu Leu Asp Lys Thr Arg Tyr Thr Glu Cys
 660 665 670

<210> 53

<211> 153

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 53

Met Lys Gln Arg Phe Ser Ala Leu Gln Leu Leu Lys Leu Leu Leu
 1 5 10 15

Leu Gln Pro Pro Leu Pro Arg Ala Leu Arg Glu Ala Leu Cys Pro Glu
 20 25 30

Pro Cys Asn Cys Val Pro Asp Gly Ala Leu Arg Cys Pro Gly Pro Thr
 35 40 45

Ala Gly Leu Thr Arg Leu Ser Leu Ala Tyr Leu Pro Val Lys Val Ile
 50 55 60

Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val Ile Lys Ile Glu Ile
 65 70 75 80

Ser Gln Ile Asp Ser Leu Glu Arg Ile Glu Ala Asn Ala Phe Asp Asn
 85 90 95

Leu Leu Asn Leu Ser Glu Ile Leu Ile Gln Asn Thr Lys Asn Leu Arg
 100 105 110

Tyr Ile Glu Pro Gly Ala Phe Ile Asn Leu Pro Arg Leu Lys Tyr Leu
 115 120 125

Ser Ile Cys Asn Thr Gly Ile Arg Lys Phe Pro Asp Val Thr Lys Val
 130 135 140

Phe Ser Ser Glu Ser Asn Phe Ile Leu
 145 150

<210> 54

<211> 190

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 54

Met Ala Ala Leu Ala Ser Ser Leu Ile Arg Gln Lys Arg Glu Val Arg
 1 5 10 15

Glu Pro Gly Gly Ser Arg Pro Val Ser Ala Gln Arg Arg Val Cys Pro
20 25 30

Arg Gly Thr Lys Ser Leu Cys Gln Lys Gln Leu Leu Ile Leu Ser
35 40 45

Lys Val Arg Leu Cys Gly Arg Pro Ala Arg Pro Asp Arg Gly Pro
50 55 60

Ala Phe Thr His Phe Asn Leu Ile Pro Val Gly Leu Arg Val Val Thr
65 70 75 80

Ile Gln Ser Ala Lys Leu Gly His Tyr Met Ala Met Asn Ala Glu Gly
85 90 95

Leu Leu Tyr Ser Ser Pro His Phe Thr Ala Glu Cys Arg Phe Lys Glu
100 105 110

Cys Val Phe Glu Asn Tyr Tyr Val Leu Tyr Ala Ser Ala Leu Tyr Arg
115 120 125

Gln Arg Arg Ser Gly Arg Ala Trp Tyr Leu Gly Leu Asp Lys Glu Gly
130 135 140

Gln Val Met Lys Gly Asn Arg Val Lys Lys Thr Lys Ala Ala Ala His
145 150 155 160

Phe Leu Pro Lys Leu Leu Glu Val Ala Met Tyr Gln Glu Pro Ser Leu
165 170 175

His Ser Val Pro Glu Ala Ser Pro Ser Ser Pro Pro Ala Pro
180 185 190

<210> 55

<211> 206

<212> PRT

<213> Artificial sequence:

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 55

Met Ala Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln Ala
1 5 10 15

Arg Glu Ser Asn Ser Asp Arg Val Ser Ala Ser Lys Arg Arg Ser Ser
20 25 30

Pro Ser Lys Asp Gly Arg Ser Leu Cys Glu Arg His Val Leu Gly Val
35 40 45

Phe Ser Lys Val Arg Phe Cys Ser Gly Arg Lys Arg Pro Val Arg Arg
50 55 60

Arg Pro Ala Leu Phe Asn Leu Ile Pro Val Gly Leu Arg Val Val Ala
65 70 75 80

Ile Gln Gly Val Lys Ala Ser Leu Tyr Val Ala Met Asn Gly Glu Gly
85 90 95

Tyr Leu Tyr Ser Ser Asp Val Phe Thr Pro Glu Cys Lys Phe Lys Glu
100 105 110

Ser Val Phe Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Thr Leu Tyr Arg
115 120 125

Gln Gln Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys Glu Gly
130 135 140

Gln Ile Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ser Ser His
145 150 155 160

Phe Val Pro Lys Pro Ile Glu Val Cys Met Tyr Arg Glu Pro Ser Leu
165 170 175

His Glu Ile Gly Glu Lys Gln Gly Arg Ser Arg Lys Ser Ser Gly Thr
180 185 190

Pro Thr Met Asn Gly Gly Lys Val Val Asn Gln Asp Ser Thr
195 200 205

<210> 56

<211> 144

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 56

Met Glu Ser Lys Ala Leu Phe Asn Leu Ile Pro Val Gly Leu Arg Val
1 5 10 15

Val Ala Ile Gln Gly Val Lys Ala Ser Leu Tyr Val Ala Met Asn Gly
20 25 30

Glu Gly Tyr Leu Tyr Ser Ser Asp Val Phe Thr Pro Glu Cys Lys Phe
35 40 45

Lys Glu Ser Val Phe Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Thr Leu
50 55 60

Tyr Arg Gln Gln Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys
65 70 75 80

Glu Gly Gln Ile Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ser
85 90 95

Ser His Phe Val Pro Lys Pro Ile Glu Val Cys Met Tyr Arg Glu Pro
100 105 110

Ser Leu His Glu Ile Gly Glu Lys Gln Gly Arg Ser Arg Lys Ser Ser
115 120 125

Gly Thr Pro Thr Met Asn Gly Gly Lys Val Val Asn Gln Asp Ser Thr
130 135 140

<210> 57

<211> 208

<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 57

Met Ala Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln Ala
1 5 10 15

Arg Glu Arg Glu Lys Ser Asn Ala Cys Lys Cys Val Ser Ser Pro Ser
20 25 30

Lys Gly Lys Thr Ser Cys Asp Lys Asn Lys Leu Asn Val Phe Ser Arg
35 40 45

Val Lys Leu Phe Gly Ser Lys Lys Arg Arg Arg Arg Pro Ala Leu
50 55 60

Phe Asn Leu Ile Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val
65 70 75 80

Gln Thr Lys Leu Tyr Leu Ala Met Asn Ser Glu Gly Tyr Leu Tyr Thr
85 90 95

Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe Glu
100 105 110

Asn Tyr Tyr Val Thr Tyr Ser Ser Met Ile Tyr Arg Gln Gln Gln Ser
115 120 125

Gly Arg Gly Trp Tyr Leu Gly Leu Asn Lys Glu Gly Glu Ile Met Lys
130 135 140

Gly Asn His Val Lys Lys Asn Lys Pro Ala Ala His Phe Leu Pro Lys
145 150 155 160

Pro Leu Lys Val Ala Met Tyr Lys Glu Pro Ser Leu His Asp Leu Thr
165 170 175

Glu Phe Ser Arg Ser Gly Ser Gly Thr Pro Thr Lys Ser Arg Ser Val
180 185 190

Ser Gly Val Leu Asn Gly Gly Lys Ser Met Ser His Asn Glu Ser Thr
195 200 205

<210> 58
<211> 155
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 58

Met Ala Leu Leu Arg Lys Ser Tyr Ser Ala Leu Phe Asn Leu Ile Pro
1 5 10 15

Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Gln Thr Lys Leu Tyr
20 25 30

Leu Ala Met Asn Ser Glu Gly Tyr Leu Tyr Thr Ser Glu Leu Phe Thr
 35 40 45

Pro Glu Cys Lys Phe Lys Glu Ser Val Phe Glu Asn Tyr Tyr Val Thr
 50 55 60

Tyr Ser Ser Met Ile Tyr Arg Gln Gln Ser Gly Arg Gly Trp Tyr
 65 70 75 80

Leu Gly Leu Asn Lys Glu Gly Glu Ile Met Lys Gly Asn His Val Lys
 85 90 95

Lys Asn Lys Pro Ala Ala His Phe Leu Pro Lys Pro Leu Lys Val Ala
 100 105 110

Met Tyr Lys Glu Pro Ser Leu His Asp Leu Thr Glu Phe Ser Arg Ser
 115 120 125

Gly Ser Gly Thr Pro Thr Lys Ser Arg Ser Val Ser Gly Val Leu Asn
 130 135 140

Gly Gly Lys Ser Met Ser His Asn Glu Ser Thr
 145 150 155

<210> 59
<211> 104
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 59

Met Ala Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln Ala
 1 5 10 15

Arg Glu Arg Glu Lys Ser Asn Ala Cys Lys Cys Val Ser Ser Pro Ser
 20 25 30

Lys Gly Lys Thr Ser Cys Asp Lys Asn Lys Leu Asn Val Phe Ser Arg
 35 40 45

Val Lys Leu Phe Gly Ser Lys Lys Arg Arg Arg Arg Pro Glu Pro
 50 55 60

Gln Leu Lys Gly Ile Val Thr Lys Leu Tyr Ser Arg Gln Gly Tyr His
 65 70 75 80

Leu Gln Leu Gln Ala Asp Gly Thr Ile Asp Gly Thr Lys Asp Glu Asp
 85 90 95

Ser Thr Tyr Arg Thr Phe His Thr
 100

<210> 60
<211> 51
<212> PRT
<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 60

Met Ala Leu Leu Arg Lys Ser Tyr Ser Glu Pro Gln Leu Lys Gly Ile
1. 5 10 15

Val Thr Lys Leu Tyr Ser Arg Gln Gly Tyr His Leu Gln Leu Gln Ala
20 25 30

Asp Gly Thr Ile Asp Gly Thr Lys Asp Glu Asp Ser Thr Tyr Arg Thr
35 40 45

Phe His Thr
50

<210> 61

<211> 183

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 61

Met Glu Phe Leu Trp Ala Pro Leu Leu Gly Leu Cys Cys Ser Leu Ala
1 5 10 15

Ala Ala Asp Arg His Thr Val Phe Trp Asn Ser Ser Asn Pro Lys Phe
20 25 30

Arg Asn Glu Asp Tyr Thr Ile His Val Gln Leu Asn Asp Tyr Val Asp
35 40 45

Ile Ile Cys Pro His Tyr Glu Asp His Ser Val Ala Asp Ala Ala Met
50 55 60

Glu Gln Tyr Ile Leu Tyr Leu Val Glu His Glu Glu Tyr Gln Leu Cys
65 70 75 80

Gln Pro Gln Ser Lys Asp Gln Val Arg Trp Gln Cys Asn Arg Pro Ser
85 90 95

Ala Lys His Gly Pro Glu Lys Leu Ser Glu Lys Phe Gln Arg Phe Thr
100 105 110

Pro Phe Thr Leu Gly Lys Glu Phe Lys Glu Gly His Ser Tyr Tyr Tyr
115 120 125

Ile Ser His Ser Pro Gln Ala His Val Asn Pro Gln Glu Lys Arg Leu
130 135 140

Ala Ala Asp Asp Pro Glu Val Arg Val Leu His Ser Ile Gly His Ser
145 150 155 160

Ala Ala Pro Arg Leu Phe Pro Leu Ala Trp Thr Val Leu Leu Leu Pro
165 170 175

Leu Leu Leu Leu Gln Thr Pro
180

<210> 62
<211> 216
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 62

Met Ala Ala Ala Pro Leu Leu Leu Leu Leu Val Pro Val Pro
1 5 10 15

Leu Leu Pro Leu Leu Ala Gln Gly Pro Gly Gly Ala Leu Gly Asn Arg
20 25 30

His Ala Val Tyr Trp Asn Ser Ser Asn Gln His Leu Arg Arg Glu Gly
35 40 45

Tyr Thr Val Gln Val Asn Val Asn Asp Tyr Leu Asp Ile Tyr Cys Pro
50 55 60

His Tyr Asn Ser Ser Gly Val Gly Pro Gly Ala Gly Pro Gly Pro Gly
65 70 75 80

Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met Val Ser Arg Asn Gly Tyr
85 90 95

Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys Arg Trp Glu Cys Asn Arg
100 105 110

Pro His Ala Pro His Ser Pro Ile Lys Phe Ser Glu Lys Phe Gln Arg
115 120 125

Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe His Ala Gly His Glu Tyr
130 135 140

Tyr Tyr Ile Ser Ser His Ser Gly Glu Lys Pro Val Pro Thr Leu Pro
145 150 155 160

Gln Phe Thr Met Gly Pro Asn Val Lys Ile Asn Val Leu Glu Asp Phe
165 170 175

Glu Gly Glu Asn Pro Gln Val Pro Lys Leu Glu Lys Ser Ile Ser Gly
180 185 190

Thr Ser Pro Lys Arg Glu His Leu Pro Leu Ala Val Gly Ile Ala Phe
195 200 205

Phe Leu Met Thr Phe Leu Ala Ser
210 215

<210> 63
<211> 212
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 63

Met Ala Ala Ala Pro Leu Leu Leu Leu Leu Val Pro Val Pro
 1 5 10 15

Leu Leu Pro Leu Leu Ala Gln Gly Pro Gly Gly Ala Leu Gly Asn Arg
 20 25 30

His Ala Val Tyr Trp Asn Ser Ser Asn Gln His Leu Arg Arg Glu Gly
 35 40 45

Tyr Thr Val Gln Val Asn Val Asn Asp Tyr Leu Asp Ile Tyr Cys Pro
 50 55 60

His Tyr Asn Ser Ser Gly Val Gly Pro Gly Ala Gly Pro Gly Pro Gly
 65 70 75 80

Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met Val Ser Arg Asn Gly Tyr
 85 90 95

Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys Arg Trp Glu Cys Asn Arg
 100 105 110

Pro His Ala Pro His Ser Pro Ile Lys Phe Ser Glu Lys Phe Gln Arg
 115 120 125

Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe His Ala Gly His Glu Tyr
 130 135 140

Tyr Tyr Ile Ser Thr Pro Thr His Asn Leu His Trp Lys Cys Leu Arg
 145 150 155 160

Met Lys Val Phe Val Cys Cys Ala Ser Lys Asp Phe Glu Gly Glu Asn
 165 170 175

Pro Gln Val Pro Lys Leu Glu Lys Ser Ile Ser Gly Thr Ser Pro Lys
 180 185 190

Arg Glu His Leu Pro Leu Ala Val Gly Ile Ala Phe Phe Leu Met Thr
 195 200 205

Phe Leu Ala Ser
 210

<210> 64
 <211> 206
 <212> PRT
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant protein product
 <400> 64

Met Leu His Val Glu Met Leu Thr Leu Val Phe Leu Val Leu Trp Met
 1 5 10 15

Cys Val Phe Ser Gln Asp Pro Gly Ser Lys Ala Val Ala Asp Arg Tyr
 20 25 30

Ala Val Tyr Trp Asn Ser Ser Asn Pro Arg Phe Gln Arg Gly Asp Tyr
 35 40 45

His Ile Asp Val Cys Ile Asn Asp Tyr Leu Asp Val Phe Cys Pro His
50 55 60

Tyr Glu Asp Ser Val Pro Glu Asp Lys Thr Glu Arg Tyr Val Leu Tyr
65 70 75 80

Met Val Asn Phe Asp Gly Tyr Ser Ala Cys Asp His Thr Ser Lys Gly
85 90 95

Phe Lys Arg Trp Glu Cys Asn Arg Pro His Ser Pro Asn Gly Pro Leu
100 105 110

Lys Phe Ser Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe
115 120 125

Glu Phe Arg Pro Gly Arg Glu Tyr Phe Tyr Ile Tyr Ser Cys Met Lys
130 135 140

Thr Ile Gly Val His Asp Arg Val Phe Asp Val Asn Asp Lys Val Glu
145 150 155 160

Asn Ser Leu Glu Pro Ala Asp Asp Thr Val His Glu Ser Ala Glu Pro
165 170 175

Ser Arg Gly Glu Asn Ala Ala Gln Thr Pro Arg Ile Pro Ser Arg Leu
180 185 190

Leu Ala Ile Leu Leu Phe Leu Leu Ala Met Leu Leu Thr Leu
195 200 205

<210> 65

<211> 202

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 65

Met Leu His Val Glu Met Leu Thr Leu Val Phe Leu Val Leu Trp Met
1 5 10 15

Cys Val Phe Ser Gln Asp Pro Gly Ser Lys Ala Val Ala Asp Arg Tyr
20 25 30

Ala Val Tyr Trp Asn Ser Ser Asn Pro Arg Phe Gln Arg Gly Asp Tyr
35 40 45

His Ile Asp Val Cys Ile Asn Asp Tyr Leu Asp Val Phe Cys Pro His
50 55 60

Tyr Glu Asp Ser Val Pro Glu Asp Lys Thr Glu Arg Tyr Val Leu Tyr
65 70 75 80

Met Val Asn Phe Asp Gly Tyr Ser Ala Cys Asp His Thr Ser Lys Gly
85 90 95

Phe Lys Arg Trp Glu Cys Asn Arg Pro His Ser Pro Asn Gly Pro Leu
100 105 110

Lys Phe Ser Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe
 115 120 125

Glu Phe Arg Pro Gly Arg Glu Tyr Phe Tyr Ile Ser Ser Ala Ile Pro
 130 135 140

Asp Asn Gly Arg Arg Ser Cys Leu Lys Leu Lys Val Phe Val Arg Pro
 145 150 155 160

Thr Asn Asp Asp Thr Val His Glu Ser Ala Glu Pro Ser Arg Gly Glu
 165 170 175

Asn Ala Ala Gln Thr Pro Arg Ile Pro Ser Arg Leu Leu Ala Ile Leu
 180 185 190

Leu Phe Leu Leu Ala Met Leu Leu Thr Leu
 195 200

<210> 66

<211> 51

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 66

Met Ala Val Arg Arg Asp Ser Val Trp Lys Tyr Cys Trp Gly Val Leu
 1 5 10 15

Met Val Leu Cys Arg Thr Ala Ile Ser Lys Ser Ile Val Leu Glu Pro
 20 25 30

Ile Tyr Trp Asn Ser Ser Asn Ser Asn Tyr Ile Lys Trp Val Phe Gly
 35 40 45

Gly Pro Gly

50

<210> 67

<211> 302

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 67

Met Ala Val Arg Arg Asp Ser Val Trp Lys Tyr Cys Trp Gly Val Leu
 1 5 10 15

Met Val Leu Cys Arg Thr Ala Ile Ser Lys Ser Ile Val Leu Glu Pro
 20 25 30

Ile Tyr Trp Asn Ser Ser Asn Ser Lys Phe Leu Pro Gly Gln Gly Leu
 35 40 45

Val Leu Tyr Pro Gin Ile Gly Asp Lys Leu Asp Ile Ile Cys Pro Lys
 50 55 60

Val Asp Ser Lys Thr Val Gly Gln Tyr Glu Tyr Tyr Lys Val Tyr Met
65 70 75 80

Val Asp Lys Asp Gln Ala Asp Arg Cys Thr Ile Lys Lys Glu Asn Thr
85 90 95

Pro Leu Leu Asn Cys Ala Lys Pro Asp Gln Asp Ile Lys Phe Thr Ile
100 105 110

Lys Phe Gln Glu Phe Ser Pro Asn Leu Trp Gly Leu Glu Phe Gln Lys
115 120 125

Asn Lys Asp Tyr Tyr Ile Ile Tyr Ala Ser Ser Ala Gly Ser Thr Arg
130 135 140

Asn Lys Asp Pro Thr Arg Arg Pro Glu Leu Glu Ala Gly Thr Asn Gly
145 150 155 160

Arg Ser Ser Thr Thr Ser Pro Phe Val Lys Pro Asn Pro Gly Ser Ser
165 170 175

Thr Asp Gly Asn Ser Ala Gly His Ser Gly Asn Asn Ile Leu Gly Ser
180 185 190

Glu Val Ala Leu Phe Ala Gly Ile Ala Ser Gly Cys Ile Ile Phe Ile
195 200 205

Val Ile Ile Ile Thr Leu Val Val Leu Leu Leu Lys Tyr Arg Arg Arg
210 215 220

His Arg Lys His Ser Pro Gln His Thr Thr Leu Ser Leu Ser Thr
225 230 235 240

Leu Ala Thr Pro Lys Arg Ser Gly Asn Asn Asn Gly Ser Glu Pro Ser
245 250 255

Asp Ile Ile Ile Pro Leu Arg Thr Ala Asp Ser Val Phe Cys Pro His
260 265 270

Tyr Glu Lys Val Ser Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln
275 280 285

Glu Met Pro Pro Gln Ser Pro Ala Asn Ile Tyr Tyr Lys Val
290 295 300

<210> 68

<211> 295

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 68

Met Ala Val Arg Arg Asp Ser Val Trp Lys Tyr Cys Trp Gly Val Leu
1 5 10 15

Met Val Leu Cys Arg Thr Ala Ile Ser Lys Ser Ile Val Leu Glu Pro
20 25 30

Ile Tyr Trp Asn Ser Ser Asn Ser Lys Phe Leu Pro Gly Gln Gly Leu
35 40 45

Val Leu Tyr Pro Gln Ile Gly Asp Lys Leu Asp Ile Ile Cys Pro Lys
50 55 60

Val Asp Ser Iys Thr Val Gly Gln Tyr Glu Tyr Tyr Lys Val Tyr Met
65 70 75 80

Val Asp Lys Asp Gln Ala Asp Arg Cys Thr Ile Lys Lys Glu Asn Thr
85 90 95

Pro Leu Leu Asn Cys Ala Lys Pro Asp Gln Asp Ile Lys Phe Thr Ile
100 105 110

Lys Phe Gln Glu Phe Ser Pro Asn Leu Trp Gly Leu Glu Phe Gln Lys
115 120 125

Asn Lys Asp Tyr Tyr Ile Ile Ser Thr Ser Asn Gly Ser Leu Glu Gly
130 135 140

Leu Asp Asn Gln Glu Gly Val Cys Gln Thr Arg Ala Met Lys Ile
145 150 155 160

Leu Met Lys Val Gly Gln Gly Ser Ser Thr Asp Gly Asn Ser Ala Gly
165 170 175

His Ser Gly Asn Asn Ile Leu Gly Ser Glu Val Ala Leu Phe Ala Gly
180 185 190

Ile Ala Ser Gly Cys Ile Ile Phe Ile Val Ile Ile Ile Thr Leu Val
195 200 205

Val Leu Leu Lys Tyr Arg Arg Arg His Arg Lys His Ser Pro Gln
210 215 220

His Thr Thr Thr Leu Ser Leu Ser Thr Leu Ala Thr Pro Lys Arg Ser
225 230 235 240

Gly Asn Asn Asn Gly Ser Glu Pro Ser Asp Ile Ile Ile Pro Leu Arg
245 250 255

Thr Ala Asp Ser Val Phe Cys Pro His Tyr Glu Lys Val Ser Gly Asp
260 265 270

Tyr Gly His Pro Val Tyr Ile Val Gln Glu Met Pro Pro Gln Ser Pro
275 280 285

Ala Asn Ile Tyr Tyr Lys Val
290 295

<210> 69

<211> 38

<212> PRT

<213> Artificial sequence.

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 69

Met Ala Gly Ile Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile
1 5 10 15

Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Gly
20 25 30

Gly Ser Glu Tyr His Gly
35

<210> 70

<211> 111

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 70

Met Ala Gly Ile Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile
1 5 10 15

Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr
20 25 30

Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser
35 40 45

Pro Leu Glu Gly Gly Leu Ala Lys Leu Asp Ile Thr Arg Leu Ser Pro
50 55 60

Arg Met Pro Pro Val Pro Ser Ala His Pro Thr Ala Thr Leu Ser Gly
65 70 75 80

Lys Glu Pro Pro Arg Ala Pro Val Thr Glu Ala Phe Ser Glu Leu Thr
85 90 95

Thr Met Leu Pro Leu Cys Pro Ala Pro Val His His Leu Leu Pro
100 105 110

<210> 71

<211> 934

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 71

Met Ala Gly Ile Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile
1 5 10 15

Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr
20 25 30

Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser
35 40 45

Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
50 55 60

Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln
 65 70 75 80

Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
 85 90 95

Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
 100 105 110

Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
 115 120 125

Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys
 130 135 140

Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
 145 150 155 160

Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
 165 170 175

Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
 180 185 190

Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
 195 200 205

Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
 210 215 220

Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
 225 230 235 240

Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255

Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu
 260 265 270

Cys Gln Gly Pro Pro Ser Ala Pro Leu Asn Leu Ile Ser Asn Val Asn
 275 280 285

Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln Asn Thr Gly Gly
 290 295 300

Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys Cys Gly Ala Gly
 305 310 315 320

Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val His Tyr Thr Pro
 325 330 335

Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile Thr Asp Leu Leu
 340 345 350

Ala His Thr Asn Tyr Thr phe Glu Ile Trp Ala Val Asn Gly Val Ser
 355 360 365

Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val Thr Val Thr Thr
 370 375 380

Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln Ala Lys Glu Val
 385 390 395 400

Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro Asp Arg Pro Asn
 405 410 415

Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys Asp Gln Asn
 420 425 430

Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg Asn Thr Asp Ile
 435 440 445

Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His Val Arg Ala Arg
 450 455 460

Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu Glu Val Thr Thr
 465 470 475 480

Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala Asn Ser Thr Val
 485 490 495

Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val Val Ile Leu Ile
 500 505 510

Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr Ser Lys Ala Lys
 515 520 525

Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly Val Arg Thr Tyr
 530 535 540

Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val Arg Glu Phe
 545 550 555 560

Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys Val Ile Gly
 565 570 575

Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Val Pro Gly
 580 585 590

Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr
 595 600 605

Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met Gly Gln
 610 615 620

Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val Thr Lys Cys
 625 630 635 640

Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp
 645 650 655

Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile Gln Leu Val
 660 665 670

Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu Ser Asp Met
 675 680 685

Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser
 690 695 700

Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg Val Leu Glu
 705 710 715 720

Asp Asp Pro Glu Ala Ala Tyr Thr Arg Gly Gly Lys Ile Pro Ile
 725 730 735

Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser Ala
 740 745 750

Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr
 755 760 765

Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala
 770 775 780

Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ile Ala
 785 790 795 800

Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp Arg
 805 810 815

Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn
 820 825 830

Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser Arg Pro Asn Thr
 835 840 845

Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala Val Val Ser Val
 850 855 860

Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr Lys Asp Asn Phe
 865 870 875 880

Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val His Val Asn Gln
 885 890 895

Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr His Gln Asn Lys
 900 905 910

Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln Met His
 915 920 925

Gly Arg Met Val Pro Val
 930

<210> 72

<211> 691

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 72

Met Ala Gly Ile Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile
 1 5 10 15

Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr
 20 25 30

Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser
 35 40 45

Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
 50 55 60

Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln
 65 70 75 80

Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
 85 90 95

Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
 100 105 110

Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
 115 120 125

Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys
 130 135 140

Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
 145 150 155 160

Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
 165 170 175

Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
 180 185 190

Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
 195 200 205

Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
 210 215 220

Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
 225 230 235 240

Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255

Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu
 260 265 270

Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
 275 280 285

Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
 290 295 300

Thr Ser Cys Thr Cys Asp Arg Gly Phe Arg Ala Asp Asn Asp Ala
 305 310 315 320

Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
 325 330 335

Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln
 340 345 350

Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys
 355 360 365

Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val
 370 375 380

His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile
 385 390 395 400

Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
 405 410 415

Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Gln Ser Val Ser Val
 420 425 430

Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
 435 440 445

Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
 450 455 460

Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu
 465 470 475 480

Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg
 485 490 495

Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His
 500 505 510

Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
 515 520 525

Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala
 530 535 540

Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val
 545 550 555 560

Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
 565 570 575

Ser Lys Ala Lys Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
 580 585 590

Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala
 595 600 605

Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu

610 615 620

Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
625 630 635 640

Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys
645 650 655

Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
660 665 670

Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
675 680 685

Val Thr Lys
690

<210> 73
<211> 985

<212> PRT

<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 73

Met Arg Gly Ser Gly Pro Arg Gly Ala Gly His Arg Arg Pro Pro Ser
1 5 10 15

Gly Gly Gly Asp Thr Pro Ile Thr Pro Ala Ser Leu Ala Gly Cys Tyr
20 25 30

Ser Ala Pro Arg Arg Ala Pro Leu Trp Thr Cys Leu Leu Cys Ala
35 40 45

Ala Leu Arg Thr Leu Leu Ala Ser Pro Ser Asn Glu Val Asn Leu Leu
50 55 60

Asp Ser Arg Thr Val Met Gly Asp Leu Gly Trp Ile Ala Phe Pro Lys
65 70 75 80

Asn Gly Trp Glu Glu Ile Gly Glu Val Asp Glu Asn Tyr Ala Pro Ile
85 90 95

His Thr Tyr Gln Val Cys Lys Val Met Glu Gln Asn Gln Asn Trp
100 105 110

Leu Leu Thr Ser Trp Ile Ser Asn Glu Gly Ala Ser Arg Ile Phe Ile
115 120 125

Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Gly Leu
130 135 140

Gly Thr Cys Lys Glu Thr Phe Asn Met Tyr Tyr Phe Glu Ser Asp Asp
145 150 155 160

Gln Asn Gly Arg Asn Ile Lys Glu Asn Gln Tyr Ile Lys Ile Asp Thr
165 170 175

Ile Ala Ala Asp Glu Ser Phe Thr Glu Leu Asp Leu Gly Asp Arg Val
180 185 190

Met Lys Leu Asn Thr Glu Val Arg Asp Val Gly Pro Leu Ser Lys Lys
195 200 205

Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile Ala Leu Val
210 215 220

Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Ser Val Val Arg His Leu
225 230 235 240

Ala Val Phe Pro Asp Thr Ile Thr Gly Ala Asp Ser Ser Gln Leu Leu
245 250 255

Glu Val Ser Gly Ser Cys Val Asn His Ser Val Thr Asp Glu Pro Pro
260 265 270

Lys Met His Cys Ser Ala Glu Gly Glu Trp Leu Val Pro Ile Gly Lys
275 280 285

Cys Met Cys Lys Ala Gly Tyr Glu Glu Lys Asn Gly Thr Cys Gln Gly
290 295 300

Pro Pro Ser Ala Pro Arg Asn Ala Ile Ser Asn Val Asn Glu Thr Ser
305 310 315 320

Val Phe Leu Glu Trp Ile Pro Pro Ala Asp Thr Gly Gly Arg Lys Asp
325 330 335

Val Ser Tyr Tyr Ile Ala Cys Lys Cys Asn Ser His Ala Gly Val
340 345 350

Cys Glu Glu Cys Gly Gly His Val Arg Tyr Leu Pro Arg Gln Ser Gly
355 360 365

Leu Lys Asn Thr Ser Val Met Met Val Asp Leu Leu Ala His Thr Asn
370 375 380

Tyr Thr Phe Glu Ile Glu Ala Val Asn Gly Val Ser Asp Leu Ser Pro
385 390 395 400

Gly Ala Arg Gln Tyr Val Ser Val Asn Val Thr Thr Asn Gln Ala Ala
405 410 415

Pro Ser Pro Val Thr Asn Val Lys Lys Gly Lys Ile Ala Lys Asn Ser
420 425 430

Ile Ser Leu Ser Trp Gin Glu Pro Asp Arg Pro Asn Gly Ile Ile Leu
435 440 445

Glu Tyr Glu Ile Lys His Phe Glu Lys Asp Gln Glu Thr Ser Tyr Thr
450 455 460

Ile Ile Lys Ser Lys Glu Thr Thr Ile Thr Ala Glu Gly Leu Lys Pro
465 470 475 480

Ala Ser Val Tyr Val Phe Gln Ile Arg Ala Arg Thr Ala Ala Gly Tyr

485 490 495

Gly Val Phe Ser Arg Arg Phe Glu Phe Glu Thr Thr Pro Val Phe Ala
 500 505 510

Ala Ser Ser Asp Gln Ser Gln Ile Pro Val Ile Ala Val Ser Val Thr
 515 520 525

Val Gly Val Ile Leu Leu Ala Val Val Ile Gly Val Leu Leu Ser Gly
 530 535 540

Ser Cys Cys Glu Cys Gly Cys Gly Arg Ala Ser Ser Leu Cys Ala Val
 545 550 555 560

Ala His Pro Ile Leu Ile Trp Arg Cys Gly Tyr Ser Lys Ala Lys Gln
 565 570 575

Asp Pro Glu Glu Glu Lys Met His Phe His Asn Gly His Ile Lys Leu
 580 585 590

Pro Gly Val Arg Thr Tyr Ile Asp Pro His Thr Tyr Glu Asp Pro Asn
 595 600 605

Gln Ala Val His Glu Phe Ala Lys Glu Ile Glu Ala Ser Cys Ile Thr
 610 615 620

Ile Glu Arg Val Ile Gly Ala Gly Glu Phe Gly Glu Val Cys Ser Gly
 625 630 635 640

Arg Leu Lys Leu Pro Gly Lys Arg Glu Leu Pro Val Ala Ile Lys Thr
 645 650 655

Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg Arg Asp Phe Leu Gly Glu
 660 665 670

Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu
 675 680 685

Gly Val Val Thr Lys Ser Lys Pro Val Met Ile Val Thr Glu Tyr Met
 690 695 700

Glu Asn Gly Ser Leu Asp Thr Phe Leu Lys Lys Asn Asp Gly Gln Phe
 705 710 715 720

Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ser Ala Gly Met
 725 730 735

Lys Tyr Leu Ser Asp Met Gly Tyr Val His Arg Asp Leu Ala Ala Arg
 740 745 750

Asn Ile Leu Ile Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly
 755 760 765

Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg
 770 775 780

Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Phe
 785 790 795 800

Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met
 805 810 815

Trp Glu Val Val Ser Tyr Gly Glu Arg Pro Tyr Trp Glu Met Thr Asn
 820 825 830

Gln Asp Val Ile Lys Ala Val Glu Glu Gly Tyr Arg Leu Pro Ser Pro
 835 840 845

Met Asp Cys Pro Ala Ala Leu Tyr Gln Leu Met Leu Asp Cys Trp Gln
 850 855 860

Lys Glu Arg Asn Ser Arg Pro Lys Phe Asp Glu Ile Val Asn Met Leu
 865 870 875 880

Asp Lys Leu Ile Arg Asn Pro Ser Ser Leu Lys Thr Leu Val Asn Ala
 885 890 895

Ser Cys Arg Val Ser Asn Leu Leu Ala Glu His Ser Pro Leu Gly Ser
 900 905 910

Gly Ala Tyr Arg Ser Val Gly Glu Trp Leu Glu Ala Ile Lys Met Gly
 915 920 925

Arg Tyr Thr Glu Ile Phe Met Glu Asn Gly Tyr Ser Ser Met Asp Ala
 930 935 940

Val Ala Gln Val Thr Leu Glu Asp Leu Arg Arg Leu Gly Val Thr Leu
 945 950 955 960

Val Gly His Gln Lys Ile Met Asn Ser Leu Gln Glu Met Lys Val
 965 970 975

Gln Leu Val Asn Gly Met Val Pro Leu
 980 985

<210> 74

<211> 925

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 74

Met Arg Gly Ser Gly Pro Arg Gly Ala Gly His Arg Arg Pro Pro Ser
 1 5 10 15

Gly Gly Gly Asp Thr Pro Ile Thr Pro Ala Ser Leu Ala Gly Cys Tyr
 20 25 30

Ser Ala Pro Arg Arg Ala Pro Leu Trp Thr Cys Leu Leu Cys Ala
 35 40 45

Ala Leu Arg Thr Leu Leu Ala Ser Pro Ser Asn Glu Val Asn Leu Leu
 50 55 60

Asp Ser Arg Thr Val Met Gly Asp Leu Gly Trp Ile Ala Phe Pro Lys

65	70	75	80
Asn Gly Trp Glu Glu Ile Gly Glu Val Asp Glu Asn Tyr Ala Pro Ile			
85	90		95
His Thr Tyr Gln Val Cys Lys Val Met Glu Gln Asn Gln Asn Asn Trp			
100	105		110
Leu Leu Thr Ser Trp Ile Ser Asn Glu Gly Ala Ser Arg Ile Phe Ile			
115	120		125
Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Gly Leu			
130	135		140
Gly Thr Cys Lys Glu Thr Phe Asn Met Tyr Tyr Phe Glu Ser Asp Asp			
145	150		155
160			
Gln Asn Gly Arg Asn Ile Lys Glu Asn Gln Tyr Ile Lys Ile Asp Thr			
165		170	
175			
Ile Ala Ala Asp Glu Ser Phe Thr Glu Leu Asp Leu Gly Asp Arg Val			
180		185	
190			
Met Lys Leu Asn Thr Glu Val Arg Asp Val Gly Pro Leu Ser Lys Lys			
195		200	
205			
Gly Phe Tyr Leu Ala Phe Glu Asp Val Gly Ala Cys Ile Ala Leu Val			
210		215	
220			
Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Ser Val Val Arg His Leu			
225		230	
235			240
Ile Val Phe Pro Asp Thr Ile Thr Gly Ala Asp Ser Ser Gln Leu Leu			
245		250	
255			
Ile Val Ser Gly Ser Cys Val Asn His Ser Val Thr Asp Glu Pro Pro			
260		265	
270			
Lys Met His Cys Ser Ala Glu Gly Glu Trp Leu Val Pro Ile Gly Lys			
275		280	
285			
Lys Met Cys Lys Ala Gly Tyr Glu Glu Lys Asn Gly Thr Cys Gln Val			
290		295	
300			
Arg Pro Gly Phe Lys Ala Ser Pro His Ile Gln Ser Cys Gly			
305		310	
315			320
Cys Pro Pro His Ser Tyr Thr His Glu Glu Ala Ser Thr Ser Cys			
325		330	
335			
Ile Cys Glu Lys Asp Tyr Phe Arg Arg Glu Ser Asp Pro Pro Thr Met			
340		345	
350			
Ile Cys Thr Thr Pro Ser Pro Val Thr Asn Val Lys Lys Gly Lys Ile			
355		360	
365			
Ile Lys Asn Ser Ile Ser Leu Ser Trp Gln Glu Pro Asp Arg Pro Asn			
370		375	
380			

Gly Ile Ile Leu Glu Tyr Glu Ile Lys His Phe Glu Lys Asp Gln Glu
385 390 395 400

Thr Ser Tyr Thr Ile Ile Lys Ser Lys Glu Thr Thr Ile Thr Ala Glu
405 410 415

Gly Leu Lys Pro Ala Ser Val Tyr Val Phe Gln Ile Arg Ala Arg Thr
420 425 430

Ala Ala Gly Tyr Gly Val Phe Ser Arg Arg Phe Glu Phe Glu Thr Thr
435 440 445

Pro Val Phe Ala Ala Ser Ser Asp Gln Ser Gln Ile Pro Val Ile Ala
450 455 460

Val Ser Val Thr Val Gly Val Ile Leu Leu Ala Val Val Ile Gly Val
465 470 475 480

Leu Leu Ser Gly Ser Cys Cys Glu Cys Gly Cys Gly Arg Ala Ser Ser
485 490 495

Leu Cys Ala Val Ala His Pro Ile Leu Ile Trp Arg Cys Gly Tyr Ser
500 505 510

Lys Ala Lys Gln Asp Pro Glu Glu Glu Lys Met His Phe His Asn Gly
515 520 525

His Ile Lys Leu Pro Gly Val Arg Thr Tyr Ile Asp Pro His Thr Tyr
530 535 540

Glu Asp Pro Asn Gln Ala Val His Glu Phe Ala Lys Glu Ile Glu Ala
545 550 555 560

Ser Cys Ile Thr Ile Glu Arg Val Ile Gly Ala Gly Glu Phe Gly Glu
565 570 575

Val Cys Ser Gly Arg Ile Lys Leu Pro Gly Lys Arg Glu Leu Pro Val
580 585 590

Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg Arg Asp
595 600 605

Phe Leu Gly Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile
610 615 620

Ile His Leu Glu Gly Val Val Thr Lys Ser Lys Pro Val Met Ile Val
625 630 635 640

Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Thr Phe Leu Lys Lys Asn
645 650 655

Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile
660 665 670

Ser Ala Gly Met Lys Tyr Leu Ser Asp Met Gly Tyr Val His Arg Asp
675 680 685

Leu Ala Ala Arg Asn Ile Leu Ile Asn Ser Asn Leu Val Cys Lys Val
690 695 700

Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Ala
705 710 715 720

Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu
725 730 735

Ala Ile Ala Phe Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr
740 745 750

Gly Ile Val Met Trp Glu Val Val Ser Tyr Gly Glu Arg Pro Tyr Trp
755 760 765

Glu Met Thr Asn Gln Asp Val Ile Lys Ala Val Glu Glu Gly Tyr Arg
770 775 780

Leu Pro Ser Pro Met Asp Cys Pro Ala Ala Leu Tyr Gln Leu Met Leu
785 790 795 800

Asp Cys Trp Gln Lys Glu Arg Asn Ser Arg Pro Lys Phe Asp Glu Ile
805 810 815

Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Ser Ser Leu Lys Thr
820 825 830

Leu Val Asn Ala Ser Cys Arg Val Ser Asn Leu Leu Ala Glu His Ser
835 840 845

Pro Leu Gly Ser Gly Ala Tyr Arg Ser Val Gly Glu Trp Leu Glu Ala
850 855 860

Ile Lys Met Gly Arg Tyr Thr Glu Ile Phe Met Glu Asn Gly Tyr Ser
865 870 875 880

Ser Met Asp Ala Val Ala Gln Val Thr Leu Glu Asp Leu Arg Arg Leu
885 890 895

Gly Val Thr Leu Val Gly His Gln Lys Lys Ile Met Asn Ser Leu Gln
900 905 910

Glu Met Lys Val Gln Leu Val Asn Gly Met Val Pro Leu
915 920 925

<210> 75

<211> 582

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 75

Met Arg Gly Ser Gly Pro Arg Gly Ala Gly His Arg Arg Pro Pro Ser
1 5 10 15

Gly Gly Gly Asp Thr Pro Ile Thr Pro Ala Ser Leu Ala Gly Cys Tyr
20 25 30

Ser Ala Pro Arg Arg Ala Pro Leu Trp Thr Cys Leu Leu Leu Cys Ala
35 40 45

Ala Leu Arg Thr Leu Leu Ala Ser Pro Ser Asn Glu Val Asn Leu Leu
50 55 60

Asp Ser Arg Thr Val Met Gly Asp Leu Gly Trp Ile Ala Phe Pro Lys
65 70 75 80

Asn Gly Trp Glu Glu Ile Gly Glu Val Asp Glu Asn Tyr Ala Pro Ile
85 90 95

His Thr Tyr Gln Val Cys Lys Val Met Glu Gln Asn Gln Asn Asn Trp
100 105 110

Leu Leu Thr Ser Trp Ile Ser Asn Glu Gly Ala Ser Arg Ile Phe Ile
115 120 125

Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Gly Leu
130 135 140

Gly Thr Cys Lys Glu Thr Phe Asn Met Tyr Tyr Phe Glu Ser Asp Asp
145 150 155 160

Gln Asn Gly Arg Asn Ile Lys Glu Asn Gln Tyr Ile Lys Ile Asp Thr
165 170 175

Ile Ala Ala Asp Glu Ser Phe Thr Glu Leu Asp Leu Gly Asp Arg Val
180 185 190

Met Lys Leu Asn Thr Glu Val Arg Asp Val Gly Pro Leu Ser Lys Lys
195 200 205

Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile Ala Leu Val
210 215 220

Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Ser Val Val Arg His Leu
225 230 235 240

Ala Val Phe Pro Asp Thr Ile Thr Gly Ala Asp Ser Ser Gln Leu Leu
245 250 255

Glu Val Ser Gly Ser Cys Val Asn His Ser Val Thr Asp Glu Pro Pro
260 265 270

Lys Met His Cys Ser Ala Glu Gly Glu Trp Leu Val Pro Ile Gly Lys
275 280 285

Cys Met Cys Lys Ala Gly Tyr Glu Glu Lys Asn Gly Thr Cys Gln Val
290 295 300

Cys Arg Pro Gly Phe Phe Lys Ala Ser Pro His Ile Gln Ser Cys Gly
305 310 315 320

Lys Cys Pro Pro His Ser Tyr His Glu Glu Ala Ser Thr Ser Cys
325 330 335

Val Cys Glu Lys Asp Tyr Phe Arg Arg Glu Ser Asp Pro Pro Thr Met
 340 345 350

Ala Cys Thr Arg Pro Pro Ser Ala Pro Arg Asn Ala Ile Ser Asn Val
 355 360 365

Asn Glu Thr Ser Val Phe Leu Glu Trp Ile Pro Pro Ala Asp Thr Gly
 370 375 380

Gly Arg Lys Asp Val Ser Tyr Tyr Ile Ala Cys Lys Lys Cys Asn Ser
 385 390 395 400

His Ala Gly Val Cys Glu Glu Cys Gly His Val Arg Tyr Leu Pro
 405 410 415

Arg Gln Ser Gly Leu Lys Asn Thr Ser Val Met Met Val Asp Leu Leu
 420 425 430

Ala His Thr Asn Tyr Thr Phe Glu Ile Glu Ala Val Asn Gly Val Ser
 435 440 445

Asp Leu Ser Pro Gly Ala Arg Gln Tyr Val Ser Val Asn Val Thr Thr
 450 455 460

Asn Gln Ala Ala Pro Ser Pro Val Thr Asn Val Lys Lys Gly Lys Ile
 465 470 475 480

Ala Lys Asn Ser Ile Ser Leu Ser Trp Gln Glu Pro Asp Arg Pro Asn
 485 490 495

Gly Ile Ile Leu Glu Tyr Glu Ile Lys His Phe Glu Lys Asp Gln Glu
 500 505 510

Thr Ser Tyr Thr Ile Ile Lys Ser Lys Glu Thr Thr Ile Thr Ala Glu
 515 520 525

Gly Leu Lys Pro Ala Ser Val Tyr Val Phe Gln Ile Arg Ala Arg Thr
 530 535 540

Ala Ala Gly Tyr Gly Val Phe Ser Arg Arg Phe Glu Phe Glu Thr Thr
 545 550 555 560

Pro Val Phe Ala Ala Ile Val Ala Val Gly Gly Leu Leu Pro Cys Ala
 565 570 575

Leu Leu Pro Ile Gln Ala
 580

<210> 76

<211> 619

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 76

Met Arg Gly Ser Gly Pro Arg Gly Ala Gly His Arg Arg Pro Pro Ser
 1 5 10 15

Gly Gly Gly Asp Thr Pro Ile Thr Pro Ala Ser Leu Ala Gly Cys Tyr
 20 25 30

Ser Ala Pro Arg Arg Ala Pro Leu Trp Thr Cys Leu Leu Cys Ala
 35 40 45

Ala Leu Arg Thr Leu Leu Ala Ser Pro Ser Asn Glu Val Asn Leu Leu
 50 55 60

Asp Ser Arg Thr Val Met Gly Asp Leu Gly Trp Ile Ala Phe Pro Lys
 65 70 75 80

Asn Gly Trp Glu Glu Ile Gly Glu Val Asp Glu Asn Tyr Ala Pro Ile
 85 90 95

His Thr Tyr Gln Val Cys Lys Val Met Glu Gln Asn Gln Asn Asn Trp
 100 105 110

Leu Ile Thr Ser Trp Ile Ser Asn Glu Gly Ala Ser Arg Ile Phe Ile
 115 120 125

Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Leu
 130 135 140

Gly Thr Cys Lys Glu Thr Phe Asn Met Tyr Tyr Phe Glu Ser Asp Asp
 145 150 155 160

Gln Asn Gly Arg Asn Ile Lys Glu Asn Gln Tyr Ile Lys Ile Asp Thr
 165 170 175

Ile Ala Ala Asp Glu Ser Phe Thr Glu Leu Asp Leu Gly Asp Arg Val
 180 185 190

Met Lys Leu Asn Thr Glu Val Arg Asp Val Gly Pro Leu Ser Lys Lys
 195 200 205

Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile Ala Leu Val
 210 215 220

Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Ser Val Val Arg His Leu
 225 230 235 240

Ala Val Phe Pro Asp Thr Ile Thr Gly Ala Asp Ser Ser Gln Leu Leu
 245 250 255

Glu Val Ser Gly Ser Cys Val Asn His Ser Val Thr Asp Glu Pro Pro
 260 265 270

Lys Met His Cys Ser Ala Glu Gly Glu Trp Leu Val Pro Ile Gly Lys.
 275 280 285

Cys Met Cys Lys Ala Gly Tyr Glu Glu Lys Asn Gly Thr Cys Gln Val
 290 295 300

Cys Arg Pro Gly Phe Phe Lys Ala Ser Pro His Ile Gln Ser Cys Gly
 305 310 315 320

Lys Cys Pro Pro His Ser Tyr Thr His Glu Glu Ala Ser Thr Ser Cys
 325 330 335

Val Cys Glu Lys Asp Tyr Phe Arg Arg Glu Ser Asp Pro Pro Thr Met
 340 345 350

Ala Cys Thr Arg Pro Pro Ser Ala Pro Arg Asn Ala Ile Ser Asn Val
 355 360 365

Asn Glu Thr Ser Val Phe Leu Glu Trp Ile Pro Pro Ala Asp Thr Gly
 370 375 380

Gly Arg Lys Asp Val Ser Tyr Tyr Ile Ala Cys Lys Lys Cys Asn Ser
 385 390 395 400

His Ala Gly Val Cys Glu Glu Cys Gly Gly His Val Arg Tyr Leu Pro
 405 410 415

Arg Gln Ser Gly Leu Lys Asn Thr Ser Val Met Met Val Asp Leu Leu
 420 425 430

Ala His Thr Asn Tyr Thr Phe Glu Ile Glu Ala Val Asn Gly Val Ser
 435 440 445

Asp Leu Ser Pro Gly Ala Arg Gln Tyr Val Ser Val Asn Val Thr Thr
 450 455 460

Asn Gln Ala Ala Pro Ser Pro Val Thr Asn Val Lys Lys Gly Lys Ile
 465 470 475 480

Ala Lys Asn Ser Ile Ser Leu Ser Trp Gln Glu Pro Asp Arg Pro Asn
 485 490 495

Gly Ile Ile Leu Glu Tyr Glu Ile Lys His Phe Glu Lys Asp Gln Glu
 500 505 510

Thr Ser Tyr Thr Ile Ile Lys Ser Lys Glu Thr Thr Ile Thr Ala Glu
 515 520 525

Gly Leu Lys Pro Ala Ser Val Tyr Val Phe Gln Ile Arg Ala Arg Thr
 530 535 540

Ala Ala Gly Tyr Gly Val Phe Ser Arg Arg Phe Glu Phe Glu Thr Thr
 545 550 555 560

Pro Val Phe Ala Ala Ser Ser Asp Gln Ser Gln Ile Pro Val Ile Ala
 565 570 575

Val Ser Val Thr Val Gly Val Ile Leu Leu Ala Val Val Ile Gly Val
 580 585 590

Leu Leu Ser Gly Ser Cys Cys Glu Cys Gly Cys Gly Arg Ala Ser Ser
 595 600 605

Leu Cys Ala Val Ala His Pro Ile Leu Ile Cys
 610 615

<210> 77

<211> 967

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 77

Met	Arg	Gly	Ser	Gly	Pro	Arg	Gly	Ala	Gly	His	Arg	Arg	Pro	Pro	Ser
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								5		10			15		

Gly	Gly	Gly	Asp	Thr	Pro	Ile	Thr	Pro	Ala	Ser	Leu	Ala	Gly	Cys	Tyr
								20		25			30		

Ser	Ala	Pro	Arg	Arg	Ala	Pro	Leu	Trp	Thr	Cys	Leu	Leu	Cys	Ala	
								35		40		45			

Ala	Leu	Arg	Thr	Leu	Leu	Ala	Ser	Pro	Ser	Asn	Glu	Val	Asn	Leu	Leu
								50		55		60			

Asp	Ser	Arg	Thr	Val	Met	Gly	Asp	Leu	Gly	Trp	Ile	Ala	Phe	Pro	Lys
								65		70		75		80	

Asn	Gly	Trp	Glü	Glü	Ile	Gly	Glu	Val	Asp	Glu	Asn	Tyr	Ala	Pro	Ile
								85		90		95			

His	Thr	Tyr	Gln	Val	Cys	Lys	Val	Met	Glu	Gln	Asn	Gln	Asn	Asn	Trp
								100		105		110			

Leu	Leu	Thr	Ser	Trp	Ile	Ser	Asn	Glu	Gly	Ala	Ser	Arg	Ile	Phe	Ile
								115		120		125			

Glu	Leu	Lys	Phe	Thr	Ieu	Arg	Asp	Cys	Asn	Ser	Leu	Pro	Gly	Gly	Leu
								130		135		140			

Gly	Thr	Cys	Lys	Glu	Thr	Phe	Asn	Met	Tyr	Tyr	Phe	Glu	Ser	Asp	Asp
								145		150		155		160	

Gln	Asn	Gly	Arg	Asn	Ile	Lys	Glu	Asn	Gln	Tyr	Ile	Lys	Ile	Asp	Thr
								165		170		175			

Ile	Ala	Ala	Asp	Glu	Ser	Phe	Thr	Glu	Ieu	Asp	Leu	Gly	Asp	Arg	Val
								180		185		190			

Met	Lys	Leu	Asn	Thr	Glu	Val	Arg	Asp	Val	Gly	Pro	Leu	Ser	Lys	Lys
								195		200		205			

Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	Val	Gly	Ala	Cys	Ile	Ala	Leu	Val
								210		215		220			

Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Ser	Val	Val	Arg	His	Leu
								225		230		235		240	

Ala	Val	Phe	Pro	Asp	Thr	Ile	Thr	Gly	Ala	Asp	Ser	Ser	Gln	Leu	Leu
								245		250		255			

Glu	Val	Ser	Gly	Ser	Cys	Val	Asn	His	Ser	Val	Thr	Asp	Glu	Pro	Pro
								260		265		270			

Lys Met His Cys Ser Ala Glu Gly Glu Trp Leu Val Pro Ile Gly Lys
275 280 285

Cys Met Cys Lys Ala Gly Tyr Glu Glu Lys Asn Gly Thr Cys Gln Val
290 295 300

Cys Arg Pro Gly Phe Ile Lys Ala Ser Pro His Ile Gln Ser Cys Gly
305 310 315 320

Lys Cys Pro Pro His Ser Tyr Thr His Glu Glu Ala Ser Thr Ser Cys
325 330 335

Val Cys Glu Lys Asp Tyr Phe Arg Arg Glu Ser Asp Pro Pro Thr Met
340 345 350

Ala Cys Thr Arg Pro Pro Ser Ala Pro Arg Asn Ala Ile Ser Asn Val
355 360 365

Asn Glu Thr Ser Val Phe Leu Glu Trp Ile Pro Pro Ala Asp Thr Gly
370 375 380

Gly Arg Lys Asp Val Ser Tyr Tyr Ile Ala Cys Lys Lys Cys Asn Ser
385 390 395 400

His Ala Gly Val Cys Glu Glu Cys Gly His Val Arg Tyr Leu Pro
405 410 415

Arg Gln Ser Gly Leu Lys Asn Thr Ser Val Met Met Val Asp Leu Leu
420 425 430

Ala His Thr Asn Tyr Thr Phe Glu Ile Glu Ala Val Asn Gly Val Ser
435 440 445

Asp Leu Ser Pro Gly Ala Arg Gln Tyr Val Ser Val Asn Val Thr Thr
450 455 460

Asn Gln Ala Ala Pro Ser Pro Val Thr Asn Val Lys Lys Gly Lys Ile
465 470 475 480

Ala Lys Asn Ser Ile Ser Leu Ser Trp Gln Glu Pro Asp Arg Pro Asn
485 490 495

Gly Ile Ile Leu Glu Tyr Glu Ile Lys His Phe Glu Lys Asp Gln Glu
500 505 510

Thr Ser Tyr Thr Ile Ile Lys Ser Lys Glu Thr Thr Ile Thr Ala Glu
515 520 525

Gly Leu Lys Pro Ala Ser Val Tyr Val Phe Gln Ile Arg Ala Arg Thr
530 535 540

Ala Ala Gly Tyr Gly Val Phe Ser Arg Arg Phe Glu Phe Glu Thr Thr
545 550 555 560

Pro Val Phe Ala Ala Ser Ser Asp Gln Ser Gln Ile Pro Val Ile Ala
565 570 575

Val Ser Val Thr Val Gly Val Ile Leu Leu Ala Val Val Ile Gly Val
 580 585 590

Leu Leu Ser Gly Ser Cys Cys Glu Cys Gly Arg Ala Ser Ser
 595 600 605

Leu Cys Ala Val Ala His Pro Ile Leu Ile Trp Arg Cys Gly Tyr Ser
 610 615 620

Lys Ala Lys Gln Asp Pro Glu Glu Glu Lys Met His Phe His Asn Gly
 625 630 635 640

His Ile Lys Leu Pro Gly Val Arg Thr Tyr Ile Asp Pro His Thr Tyr
 645 650 655

Glu Asp Pro Asn Gln Ala Val His Glu Phe Ala Lys Glu Ile Glu Ala
 660 665 670

Ser Cys Ile Thr Ile Glu Arg Val Ile Gly Ala Gly Glu Phe Gly Glu
 675 680 685

Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Lys Arg Glu Leu Pro Val
 690 695 700

Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg Arg Asp
 705 710 715 720

Phe Leu Gly Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile
 725 730 735

Ile His Leu Glu Gly Val Val Thr Lys Ser Lys Pro Val Met Ile Val
 740 745 750

Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Thr Phe Leu Lys Gly Gly
 755 760 765

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Phe Arg Lys
 770 775 780

Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu
 785 790 795 800

Val Val Ser Tyr Gly Glu Arg Pro Tyr Trp Glu Met Thr Asn Gln Asp
 805 810 815

Val Ile Lys Ala Val Glu Glu Gly Tyr Arg Leu Pro Ser Pro Met Asp
 820 825 830

Cys Pro Ala Ala Leu Tyr Gln Ile Met Leu Asp Cys Trp Gln Lys Glu
 835 840 845

Arg Asn Ser Arg Pro Lys Phe Asp Glu Ile Val Asn Met Leu Asp Lys
 855 860

Leu Ile Arg Asn Pro Ser Ser Leu Lys Thr Leu Val Asn Ala Ser Cys
 865 870 875 880

Arg Val Ser Asn Leu Leu Ala Glu His Ser Pro Leu Gly Ser Gly Ala

885 890 895

Tyr Arg Ser Val Gly Glu Trp Leu Glu Ala Ile Lys Met Gly Arg Tyr
900 905 910

Thr Glu Ile Phe Met Glu Asn Gly Tyr Ser Ser Met Asp Ala Val Ala
915 920 925

Gln Val Thr Leu Glu Asp Leu Arg Arg Leu Gly Val Thr Leu Val Gly
930 935 940

His Gln Lys Lys Ile Met Asp Ser Leu Gln Glu Met Lys Val Gln Leu
945 950 955 960

Val Asn Gly Met Val Pro Leu
965

<210> 78

<211> 888

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 78

Met Arg Gly Ser Gly Pro Arg Gly Ala Gly His Arg Arg Pro Pro Ser
1 5 10 15

Gly Gly Gly Asp Thr Pro Ile Thr Pro Ala Ser Leu Ala Gly Cys Tyr
20 25 30

Ser Ala Pro Arg Arg Ala Pro Leu Trp Thr Cys Leu Leu Leu Cys Ala
35 40 45

Ala Leu Arg Thr Leu Leu Ala Ser Pro Ser Asn Glu Val Asn Leu Leu
50 55 60

Asp Ser Arg Thr Val Met Gly Asp Leu Gly Trp Ile Ala Phe Pro Lys
65 70 75 80

Asn Gly Trp Glu Glu Ile Gly Glu Val Asp Glu Asn Tyr Ala Pro Ile
85 90 95

His Thr Tyr Gln Val Cys Lys Val Met Glu Gln Asn Gln Asn Trp
100 105 110

Leu Leu Thr Ser Trp Ile Ser Asn Glu Gly Ala Ser Arg Ile Phe Ile
115 120 125

Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Gly Leu
130 135 140

Gly Thr Cys Lys Glu Thr Phe Asn Met Tyr Tyr Phe Glu Ser Asp Asp
145 150 155 160

Gln Asn Gly Arg Asn Ile Lys Glu Asn Gln Tyr Ile Lys Ile Asp Thr
165 170 175

Ile Ala Ala Asp Glu Ser Phe Thr Glu Leu Asp Leu Gly Asp Arg Val
180 185 190

Met Lys Leu Asn Thr Glu Val Arg Asp Val Gly Pro Leu Ser Lys Lys
195 200 205

Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile Ala Leu Val
210 215 220

Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Ser Val Val Arg His Leu
225 230 235 240

Ala Val Phe Pro Asp Thr Ile Thr Gly Ala Asp Ser Ser Gln Leu Leu
245 250 255

Glu Val Ser Gly Ser Cys Val Asn His Ser Val Thr Asp Glu Pro Pro
260 265 270

Lys Met His Cys Ser Ala Glu Gly Glu Trp Leu Val Pro Ile Gly Lys
275 280 285

Cys Met Cys Lys Ala Gly Tyr Glu Glu Lys Asn Gly Thr Cys Gln Val
290 295 300

Cys Arg Pro Gly Phe Phe Lys Ala Ser Pro His Ile Gln Ser Cys Gly
305 310 315 320

Lys Cys Pro Pro His Ser Tyr Thr His Glu Glu Ala Ser Thr Ser Cys
325 330 335

Val Cys Glu Lys Asp Tyr Phe Arg Arg Glu Ser Asp Pro Pro Thr Met
340 345 350

Ala Cys Thr Arg Pro Pro Ser Ala Pro Arg Asn Ala Ile Ser Asn Val
355 360 365

Asn Glu Thr Ser Val Phe Leu Glu Trp Ile Pro Pro Ala Asp Thr Gly
370 375 380

Gly Arg Lys Asp Val Ser Tyr Tyr Ile Ala Cys Lys Lys Cys Asn Ser
385 390 395 400

His Ala Gly Val Cys Glu Glu Cys Gly Gly His Val Arg Tyr Leu Pro
405 410 415

Arg Gln Ser Gly Leu Lys Asn Thr Ser Val Met Met Val Asp Leu Leu
420 425 430

Ala His Thr Asn Tyr Thr Phe Glu Ile Glu Ala Val Asn Gly Val Ser
435 440 445

Asp Leu Ser Pro Gly Ala Arg Gln Tyr Val Ser Val Asn Val Thr Thr
450 455 460

Asn Gln Ala Ala Pro Ser Pro Val Thr Asn Val Lys Lys Gly Lys Ile
465 470 475 480

Ala Lys Asn Ser Ile Ser Leu Ser Trp Gln Glu Pro Asp Arg Pro Asn

485 490 495

Gly Ile Ile Leu Glu Tyr Glu Ile Lys His Phe Glu Lys Asp Gln Glu
 500 505 510

Thr Ser Tyr Thr Ile Ile Lys Ser Lys Glu Thr Thr Ile Thr Ala Glu
 515 520 525

Gly Leu Lys Pro Ala Ser Val Tyr Val Phe Gln Ile Arg Ala Arg Thr
 530 535 540

Ala Ala Gly Tyr Gly Val Phe Ser Arg Arg Phe Glu Phe Glu Thr Thr
 545 550 555 560

Pro Val Phe Ala Ala Ser Ser Asp Gln Ser Gln Ile Pro Val Ile Ala
 565 570 575

Val Ser Val Thr Val Gly Val Ile Leu Leu Ala Val Val Ile Gly Val
 580 585 590

Leu Leu Ser Gly Ser Cys Cys Glu Cys Gly Cys Gly Arg Ala Ser Ser
 595 600 605

Leu Cys Ala Val Ala His Pro Ile Leu Ile Trp Arg Cys Gly Tyr Ser
 610 615 620

Lys Ala Lys Gln Asp Pro Glu Glu Lys Met His Phe His Asn Gly
 625 630 635 640

His Ile Lys Leu Pro Gly Val Arg Thr Tyr Ile Asp Pro His Thr Tyr
 645 650 655

Glu Asp Pro Asn Gln Ala Val His Glu Phe Ala Lys Glu Ile Glu Ala
 660 665 670

Ser Cys Ile Thr Ile Glu Arg Val Ile Gly Ala Gly Glu Phe Gly Glu
 675 680 685

Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Lys Arg Glu Leu Pro Val
 690 695 700

Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg Arg Asp
 705 710 715 720

Phe Leu Gly Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile
 725 730 735

Ile His Leu Glu Gly Val Val Thr Lys Ser Lys Pro Val Met Ile Val
 740 745 750

Thr Glu Tyr Met Gly Asn Gly Ser Leu Asp Thr Phe Leu Lys Lys Asn
 755 760 765

Asp Gly Gln Phe Thr Val Ile Gin Leu Val Gly Met Leu Arg Gly Ile
 770 775 780

Ser Ala Gly Met Lys Tyr Leu Ser Asp Met Gly Tyr Val His Arg Asp
 785 790 795 800

Leu Ala Ala Arg Asn Ile Leu Ile Asn Ser Asn Leu Val Cys Lys Val
 805 810 815

Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Ala
 820 825 830

Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu
 835 840 845

Ala Ile Ala Phe Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr
 850 855 860

Gly Ile Val Met Trp Glu Val Val Ser Tyr Gly Glu Arg Pro Tyr Trp
 865 870 875 880

Glu Met Thr Asn Gln Asp Ser Ile
 885

<210> 79
<211> 985
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 79.

Met Arg Gly Ser Gly Pro Arg Gly Ala Gly His Arg Arg Pro Pro Ser
 1 5 10 15

Gly Gly Gly Asp Thr Pro Ile Thr Pro Ala Ser Leu Ala Gly Cys Tyr
 20 25 30

Ser Ala Pro Arg Arg Ala Pro Leu Trp Thr Cys Leu Leu Cys Ala
 35 40 45

Ala Leu Arg Thr Leu Leu Ala Ser Pro Ser Asn Glu Val Asn Leu Leu
 50 55 60

Asp Ser Arg Thr Val Met Gly Asp Leu Gly Trp Ile Ala Phe Pro Lys
 65 70 75 80

Asn Gly Trp Glu Glu Ile Gly Glu Val Asp Glu Asn Tyr Ala Pro Ile
 85 90 95

His Thr Tyr Gln Val Cys Lys Val Met Glu Gln Asn Gln Asn Asn Trp
 100 105 110

Leu Leu Thr Ser Trp Ile Ser Asn Glu Gly Ala Ser Arg Ile Phe Ile
 115 120 125

Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Leu
 130 135 140

Gly Thr Cys Lys Glu Thr Phe Asn Met Tyr Tyr Phe Glu Ser Asp Asp
 145 150 155 160

Gln Asn Gly Arg Asn Ile Lys Glu Asn Gln Tyr Ile Lys Ile Asp Thr

165

170

175

Ile Ala Ala Asp Glu Ser Phe Thr Glu Leu Asp Leu Gly Asp Arg Val
 180 185 190

Met Lys Leu Asn Thr Glu Val Arg Asp Val Gly Pro Leu Ser Lys Lys
 195 200 205

Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile Ala Leu Val
 210 215 220

Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Ser Val Val Arg His Leu
 225 230 235 240

Ala Val Phe Pro Asp Thr Ile Thr Gly Ala Asp Ser Ser Gln Leu Leu
 245 250 255

Glu Val Ser Gly Ser Cys Val Asn His Ser Val Thr Asp Glu Pro Pro
 260 265 270

Lys Met His Cys Ser Ala Glu Gly Glu Trp Leu Val Pro Ile Gly Lys
 275 280 285

Cys Met Cys Lys Ala Gly Tyr Glu Glu Lys Asn Gly Thr Cys Gln Val
 290 295 300

Cys Arg Pro Gly Phe Phe Lys Ala Ser Pro His Ile Gln Ser Cys Gly
 305 310 315 320

Lys Cys Pro Pro His Ser Tyr Thr His Glu Glu Ala Ser Thr Ser Cys
 325 330 335

Val Cys Glu Lys Asp Tyr Phe Arg Arg Glu Ser Asp Pro Pro Thr Met
 340 345 350

Ala Cys Thr Arg Pro Pro Ser Ala Pro Arg Asn Ala Ile Ser Asn Val
 355 360 365

Asn Glu Thr Ser Val Phe Leu Glu Trp Ile Pro Pro Ala Asp Thr Gly
 370 375 380

Gly Arg Lys Asp Val Ser Tyr Tyr Ile Ala Cys Lys Lys Cys Asn Ser
 385 390 395 400

His Ala Gly Val Cys Glu Glu Cys Gly His Val Arg Tyr Leu Pro
 405 410 415

Arg Gln Ser Gly Leu Lys Asn Thr Ser Val Met Met Val Asp Leu Leu
 420 425 430

Ala His Thr Asn Tyr Thr Phe Glu Ile Glu Ala Val Asn Gly Val Ser
 435 440 445

Asp Leu Ser Pro Gly Ala Arg Gln Tyr Val Ser Val Asn Val Thr Thr
 450 455 460

Asn Gln Ala Ala Pro Ser Pro Val Thr Asn Val Lys Lys Gly Lys Ile
 465 470 475 480

Ala Lys Asn Ser Ile Ser Leu Ser Trp Gln Glu Pro Asp Arg Pro Asn
 485 490 495

Gly Ile Ile Leu Glu Tyr Glu Ile Lys His Phe Glu Lys Asp Gln Glu
 500 505 510

Thr Ser Tyr Thr Ile Ile Lys Ser Lys Glu Thr Thr Ile Thr Ala Glu
 515 520 525

Gly Leu Lys Pro Ala Ser Val Tyr Val Phe Gln Ile Arg Ala Arg Thr
 530 535 540

Ala Ala Gly Tyr Gly Val Phe Ser Arg Arg Phe Glu Phe Glu Thr Thr
 545 550 555 560

Pro Val Phe Ala Ala Ser Ser Asp Gln Ser Gln Ile Pro Val Ile Ala
 565 570 575

Val Ser Val Thr Val Gly Val Ile Leu Leu Ala Val Val Ile Gly Val
 580 585 590

Leu Leu Ser Gly Ser Cys Cys Glu Cys Gly Cys Gly Arg Ala Ser Ser
 595 600 605

Leu Cys Ala Val Ala His Pro Ile Leu Ile Trp Arg Cys Gly Tyr Ser
 610 615 620

Lys Ala Lys Gln Asp Pro Glu Glu Lys Met His Phe His Asn Gly
 625 630 635 640

His Ile Lys Leu Pro Gly Val Arg Thr Tyr Ile Asp Pro His Thr Tyr
 645 650 655

Glu Asp Pro Asn Gln Ala Val His Glu Phe Ala Lys Glu Ile Glu Ala
 660 665 670

Ser Cys Ile Thr Ile Glu Arg Val Ile Gly Ala Gly Glu Phe Gly Glu
 675 680 685

Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Lys Arg Glu Leu Pro Val
 690 695 700

Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg Arg Asp
 705 710 715 720

Phe Leu Gly Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile
 725 730 735

Ile His Leu Glu Gly Val Val Thr Lys Ser Lys Pro Val Met Ile Val
 740 745 750

Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Thr Phe Leu Lys Lys Asn
 755 760 765

Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile
 770 775 780

Ser Ala Gly Met Lys Tyr Leu Ser Asp Met Gly Tyr Val His Arg Asp
 785 790 795 800

Leu Ala Ala Arg Asn Ile Leu Ile Asn Ser Asn Leu Val Cys Lys Val
 805 810 815

Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Ala
 820 825 830

Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu
 835 840 845

Ala Ile Ala Phe Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr
 850 855 860

Gly Ile Val Met Trp Glu Val Val Ser Tyr Gly Glu Arg Pro Tyr Trp
 865 870 875 880

Glu Met Thr Asn Gln Asp Val Ile Lys Ala Val Glu Glu Gly Tyr Arg
 885 890 895

Leu Pro Ser Pro Met Asp Cys Pro Ala Ala Leu Tyr Gln Leu Met Leu
 900 905 910

Asp Cys Trp Gln Lys Glu Arg Asn Ser Arg Pro Lys Phe Asp Glu Ile
 915 920 925

Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Ser Ser Leu Lys Thr
 930 935 940

Leu Val Asn Ala Ser Cys Arg Asp Leu Arg Arg Leu Gly Val Thr Leu
 945 950 955 960

Val Gly His Gln Lys Lys Ile Met Asn Ser Leu Gln Glu Met Lys Val
 965 970 975

Gln Leu Val Asn Gly Met Val Pro Leu
 980 985

<210> 80

<211> 599

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 80

Met Val Phe Gln Thr Arg Tyr Pro Ser Trp Ile Ile Leu Cys Tyr Ile
 1 5 10 15

Trp Leu Leu Arg Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
 20 25 30

Val Ile Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
 35 40 45

Ser Ser Pro Pro Asn Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
 50 55 60

Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
 65 70 75 80

Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
 85 90 95

Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
 100 105 110

Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
 115 120 125

Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
 130 135 140

Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
 145 150 155 160

Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
 165 170 175

Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
 180 185 190

Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Ser Ile
 195 200 205

Ile Glu Asn Leu Ala Ile Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210 215 220

Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225 230 235 240

Glu Ala Glu Asn Ala Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
 245 250 255

Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
 260 265 270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Gly Phe Tyr Lys Ser Ser Ser
 275 280 285

Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Lys
 290 295 300

Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
 305 310 315 320

Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
 325 330 335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
 340 345 350

Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
 355 360 365

Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
 370 375 380

Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
 385 390 395 400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
 405 410 415

Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
 420 425 430

Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
 435 440 445

Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Glu Leu Ser Trp Gln
 450 455 460

Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
 465 470 475 480

Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Val Lys Thr Lys
 485 490 495

Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
 500 505 510

Phe Gln Ile Arg Ala Phe Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
 515 520 525

Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Thr Gly Lys Met Phe Glu
 530 535 540

Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
 545 550 555 560

Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
 565 570 575

Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
 580 585 590

Asp Glu Glu Leu Tyr Phe His
 595

<210> 81

<211> 855

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 81

Met Val Phe Gln Thr Arg Tyr Pro Ser Trp Ile Ile Leu Cys Tyr Ile
 1 5 10 15

Trp Leu Leu Arg Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
 20 25 30

Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
 35 40 45

Ser Ser Pro Pro Asn Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
 50 55 60

Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
 65 70 75 80

Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
 85 90 95

Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
 100 105 110

Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
 115 120 125

Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
 130 135 140

Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
 145 150 155 160

Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
 165 170 175

Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
 180 185 190

Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Ser Ile
 195 200 205

Ile Glu Asn Leu Ala Ile Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210 215 220

Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225 230 235 240

Glu Ala Glu Asn Ala Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
 245 250 255

Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
 260 265 270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Gly Phe Tyr Lys Ser Ser Ser
 275 280 285

Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Lys
 290 295 300

Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
 305 310 315 320

Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
 325 330 335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
 340 345 350

Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
 355 360 365

Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
 370 375 380

Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
 385 390 395 400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
 405 410 415

Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
 420 425 430

Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
 435 440 445

Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Glu Leu Ser Trp Gln
 450 455 460

Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
 465 470 475 480

Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Val Lys Thr Lys
 485 490 495

Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
 500 505 510

Phe Gln Ile Arg Ala Phe Thr Ala Ala Gly Tyr Asn Tyr Ser Pro
 515 520 525

Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Thr Gly Lys Met Phe Glu
 530 535 540

Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
 545 550 555 560

Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
 565 570 575

Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
 580 585 590

Asp Glu Glu Leu Tyr Phe His Phe Lys Phe Pro Gly Thr Lys Thr Tyr
 595 600 605

Ile Asp Pro Glu Thr Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe
 610 615 620

Ala Lys Glu Leu Asp Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly
 625 630 635 640

Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly
645 650 655

Lys Arg Asp Val Ala Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr
660 665 670

Glu Lys Gln Arg Arg Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln
675 680 685

Phe Asp His Pro Asn Val Val His Leu Glu Gly Val Val Thr Arg Gly
690 695 700

Lys Pro Val Met Ile Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp
705 710 715 720

Ala Phe Leu Arg Lys His Asp Gly Gln Phe Thr Val Ile Gln Leu Val
725 730 735

Gly Met Leu Arg Gly Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met
740 745 750

Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser
755 760 765

Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu
770 775 780

Asp Asp Pro Glu Ala Val Tyr Thr Thr Gly Gly Lys Ile Pro Val
785 790 795 800

Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala
805 810 815

Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr
820 825 830

Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Ala Asn Lys Pro
835 840 845

Ser Ser Gly Ser Lys His Ser
850 855

<210> 82

<211> 435

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 82

Met Ala Leu Asp Tyr Leu Leu Leu Leu Leu Ala Ser Ala Val Ala
1 5 10 15

Ala Met Glu Glu Thr Leu Met Asp Thr Arg Thr Ala Thr Ala Glu Leu
20 25 30

Gly Trp Thr Ala Asn Pro Ala Ser Gly Trp Glu Glu Val Ser Gly Tyr
35 40 45

Asp Glu Asn Leu Asn Thr Ile Arg Thr Tyr Gln Val Cys Asn Val Phe
50 55 60

Glu Pro Asn Gln Asn Asn Trp Leu Leu Thr Thr Phe Ile Asn Arg Arg
65 70 75 80

Gly Ala His Arg Ile Tyr Thr Glu Met Arg Phe Thr Val Arg Asp Cys
85 90 95

Ser Ser Leu Pro Asn Val Pro Gly Ser Cys Lys Glu Thr Phe Asn Leu
100 105 110

Tyr Tyr Tyr Glu Thr Asp Ser Val Ile Ala Thr Lys Lys Ser Ala Phe
115 120 125

Trp Ser Glu Ala Pro Tyr Ile Lys Val Asp Thr Ile Ala Ala Asp Glu
130 135 140

Ser Phe Ser Gln Val Asp Phe Gly Gly Arg Leu Met Lys Val Asn Thr
145 150 155 160

Glu Val Arg Ser Phe Gly Pro Leu Thr Arg Asn Gly Phe Tyr Leu Ala
165 170 175

Phe Gln Asp Tyr Gly Ala Cys Met Ser Leu Leu Ser Val Arg Val Phe
180 185 190

Phe Lys Lys Cys Pro Ser Ile Val Gln Asn Phe Ala Val Phe Pro Glu
195 200 205

Thr Met Thr Gly Ala Glu Ser Thr Ser Leu Val Ile Ala Arg Gly Thr
210 215 220

Cys Ile Pro Asn Ala Glu Glu Val Asp Val Pro Ile Lys Leu Tyr Cys
225 230 235 240

Asn Gly Asp Gly Glu Trp Met Val Pro Ile Gly Arg Cys Thr Cys Lys
245 250 255

Pro Gly Tyr Glu Pro Glu Asn Ser Val Ala Cys Lys Ala Cys Pro Ala
260 265 270

Gly Thr Phe Lys Ala Ser Gln Glu Ala Glu Gly Cys Ser His Cys Pro
275 280 285

Ser Asn Ser Arg Ser Pro Ala Glu Ala Ser Pro Ile Cys Thr Cys Arg
290 295 300

Thr Gly Tyr Tyr Arg Ala Asp Phe Asp Pro Pro Glu Val Ala Cys Thr
305 310 315 320

Ser Val Pro Ser Gly Pro Arg Asn Val Ile Ser Ile Val Asn Glu Thr
325 330 335

Ser Ile Ile Leu Glu Trp His Pro Pro Arg Glu Thr Gly Gly Arg Asp
340 345 350

Asp Val Thr Tyr Asn Ile Ile Cys Lys Lys Cys Arg Ala Asp Arg Arg
 355 360 365

Ser Cys Ser Arg Cys Asp Asp Asn Val Glu Phe Val Pro Arg Gln Leu
 370 375 380

Gly Leu Thr Glu Cys Arg Val Ser Ile Ser Ser Leu Trp Ala His Thr
 385 390 395 400

Pro Tyr Thr Phe Asp Ile Gln Ala Ile Asn Gly Val Ser Ser Lys Ser
 405 410 415

Pro Phe Pro Pro Gln His Val Ser Val Asn Ile Thr Thr Asn Gln Ala
 420 425 430

Gly Thr Gly
 435

<210> 83

<211> 560

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 83

Met Ala Leu Asp Tyr Leu Leu Leu Leu Leu Ala Ser Ala Val Ala
 1 5 10 15

Ala Met Glu Glu Thr Leu Met Asp Thr Arg Thr Ala Thr Ala Glu Leu
 20 25 30

Gly Trp Thr Ala Asn Pro Ala Ser Gly Trp Glu Glu Val Ser Gly Tyr
 35 40 45

Asp Glu Asn Leu Asn Thr Ile Arg Thr Tyr Gln Val Cys Asn Val Phe
 50 55 60

Glu Pro Asn Gln Asn Asn Trp Leu Leu Thr Thr Phe Ile Asn Arg Arg
 65 70 75 80

Gly Ala His Arg Ile Tyr Thr Glu Met Arg Phe Thr Val Arg Asp Cys
 85 90 95

Ser Ser Leu Pro Asn Val Pro Gly Ser Cys Lys Glu Thr Phe Asn Leu
 100 105 110

Tyr Tyr Tyr Glu Thr Asp Ser Val Ile Ala Thr Lys Lys Ser Ala Phe
 115 120 125

Trp Ser Glu Ala Pro Tyr Leu Lys Val Asp Thr Ile Ala Ala Asp Glu
 130 135 140

Ser Phe Ser Gln Val Asp Phe Gly Gly Arg Leu Met Lys Val Asn Thr
 145 150 155 160

Glu Val Arg Ser Phe Gly Pro Leu Thr Arg Asn Gly Phe Tyr Leu Ala
 165 170 175

Phe Gln Asp Tyr Gly Ala Cys Met Ser Leu Leu Ser Val Arg Val Phe
 180 185 190

Phe Lys Lys Cys Pro Ser Ile Val Gln Asn Phe Ala Val Phe Pro Glu
 195 200 205

Thr Met Thr Gly Ala Glu Ser Thr Ser Leu Val Ile Ala Arg Gly Thr
 210 215 220

Cys Ile Pro Asn Ala Glu Glu Val Asp Val Pro Ile Lys Leu Tyr Cys
 225 230 235 240

Asn Gly Asp Gly Glu Trp Met Val Pro Ile Gly Arg Cys Thr Cys Lys
 245 250 255

Pro Gly Tyr Glu Pro Glu Asn Ser Val Ala Cys Lys Ala Cys Pro Ala
 260 265 270

Gly Thr Phe Lys Ala Ser Gln Glu Ala Glu Gly Cys Ser His Cys Pro
 275 280 285

Ser Asn Ser Arg Ser Pro Ala Glu Ala Ser Pro Ile Cys Thr Cys Arg
 290 295 300

Thr Gly Tyr Tyr Arg Ala Asp Phe Asp Pro Pro Glu Val Ala Cys Thr
 305 310 315 320

Ser Val Pro Ser Gly Pro Arg Asn Val Ile Ser Ile Val Asn Glu Thr
 325 330 335

Ser Ile Ile Leu Glu Trp His Pro Pro Arg Glu Thr Gly Gly Arg Asp
 340 345 350

Asp Val Thr Tyr Asn Ile Ile Cys Lys Lys Cys Arg Ala Asp Arg Arg
 355 360 365

Ser Cys Ser Arg Cys Asp Asp Asn Val Glu Phe Val Pro Arg Gln Leu
 370 375 380

Gly Leu Thr Glu Cys Arg Val Ser Ile Ser Ser Leu Trp Ala His Thr
 385 390 395 400

Pro Tyr Thr Phe Asp Ile Gln Ala Ile Asn Gly Val Ser Ser Lys Ser
 405 410 415

Pro Phe Pro Pro Gln His Val Ser Val Asn Ile Thr Thr Asn Gln Ala
 420 425 430

Ala Pro Ser Thr Val Pro Ile Met His Gln Val Ser Ala Thr Met Arg
 435 440 445

Ser Ile Thr Leu Ser Trp Pro Gln Pro Glu Gln Pro Asn Gly Ile Ile
 450 455 460

Leu Asp Tyr Glu Ile Arg Tyr Tyr Glu Lys Glu His Asn Glu Phe Asn
 465 470 475 480

Ser Ser Met Ala Arg Ser Gln Thr Asn Thr Ala Arg Ile Asp Gly Leu
 485 490 495

Arg Pro Gly Met Val Tyr Val Val Gln Val Arg Ala Arg Thr Val Ala
 500 505 510

Gly Tyr Gly Lys Phe Ser Gly Lys Met Cys Phe Gln Thr Leu Thr Asp
 515 520 525

Gly Asn Gly Leu Ile Ala Lys Arg Leu Cys Thr Ala Ile Ser Ser Ser
 530 535 540

Ile Thr Ala Gln Ala Glu Gly Ser Leu Glu Lys Cys Thr Arg Gly Val
 545 550 555 560

<210> 84

<211> 943

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 84

Met Ala Leu Asp Tyr Leu Leu Leu Leu Ala Ser Ala Val Ala
 1 5 10 15

Ala Met Glu Glu Thr Leu Met Asp Thr Arg Thr Ala Thr Ala Glu Leu
 20 25 30

Gly Trp Thr Ala Asn Pro Ala Ser Gly Trp Glu Glu Val Ser Gly Tyr
 35 40 45

Asp Glu Asn Leu Asn Thr Ile Arg Thr Tyr Gln Val Cys Asn Val Phe
 50 55 60

Glu Pro Asn Gln Asn Asn Trp Leu Leu Thr Thr Phe Ile Asn Arg Arg
 65 70 75 80

Gly Ala His Arg Ile Tyr Thr Glu Met Arg Phe Thr Val Arg Asp Cys
 85 90 95

Ser Ser Leu Pro Asn Val Pro Gly Ser Cys Lys Glu Thr Phe Asn Leu
 100 105 110

Tyr Tyr Tyr Glu Thr Asp Ser Val Ile Ala Thr Lys Lys Ser Ala Phe
 115 120 125

Trp Ser Glu Ala Pro Tyr Leu Lys Val Asp Thr Ile Ala Ala Asp Glu
 130 135 140

Ser Phe Ser Gln Val Asp Phe Gly Gly Arg Leu Met Lys Val Asn Thr
 145 150 155 160

Glu Val Arg Ser Phe Gly Pro Leu Thr Arg Asn Gly Phe Tyr Leu Ala
 165 170 175

Phe Gln Asp Tyr Gly Ala Cys Met Ser Leu Leu Ser Val Arg Val Phe
 180 185 190

Phe Lys Lys Cys Pro Ser Ile Val Gln Asn Phe Ala Val Phe Pro Glu
195 200 205

Thr Met Thr Gly Ala Glu Ser Thr Ser Leu Val Ile Ala Arg Gly Thr
210 215 220

Cys Ile Pro Asn Ala Glu Glu Val Asp Val Pro Ile Lys Leu Tyr Cys
225 230 235 240

Asn Gly Asp Gly Glu Trp Met Val Pro Ile Gly Arg Cys Thr Cys Lys
245 250 255

Pro Gly Tyr Glu Pro Glu Asn Ser Val Ala Cys Lys Ala Cys Pro Ala
260 265 270

Gly Thr Phe Lys Ala Ser Gln Glu Ala Glu Gly Cys Ser His Cys Pro
275 280 285

Ser Asn Ser Arg Ser Pro Ala Glu Ala Ser Pro Ile Cys Thr Cys Arg
290 295 300

Thr Gly Tyr Tyr Arg Ala Asp Phe Asp Pro Pro Glu Val Ala Cys Thr
305 310 315 320

Ser Val Pro Ser Gly Pro Arg Asn Val Ile Ser Ile Val Asn Glu Thr
325 330 335

Ser Ile Ile Leu Glu Trp His Pro Pro Arg Glu Thr Gly Gly Arg Asp
340 345 350

Asp Val Thr Tyr Asn Ile Ile Cys Lys Lys Cys Arg Ala Asp Arg Arg
355 360 365

Ser Cys Ser Arg Cys Asp Asp Asn Val Glu Phe Val Pro Arg Gln Leu
370 375 380

Gly Leu Thr Glu Cys Arg Val Ser Ile Ser Ser Leu Trp Ala His Thr
385 390 395 400

Pro Tyr Thr Phe Asp Ile Gln Ala Ile Asn Gly Val Ser Ser Lys Ser
405 410 415

Pro Phe Pro Pro Gln His Val Ser Val Asn Ile Thr Thr Asn Gln Ala
420 425 430

Ala Pro Ser Thr Val Pro Ile Met His Gln Val Ser Ala Thr Met Arg
435 440 445

Ser Ile Thr Leu Ser Trp Pro Gln Pro Glu Gln Pro Asn Gly Ile Ile
450 455 460

Leu Asp Tyr Glu Ile Arg Tyr Tyr Glu Lys Glu His Asn Glu Phe Asn
465 470 475 480

Ser Ser Met Ala Arg Ser Gln Thr Asn Thr Ala Arg Ile Asp Gly Leu
485 490 495

Arg Pro Gly Met Val Tyr Val Val Gln Val Arg Ala Arg Thr Val Ala
500 505 510

Gly Tyr Gly Lys Phe Ser Gly Lys Met Cys Phe Gln Thr Leu Thr Asp
515 520 525

Asp Asp Tyr Lys Ser Glu Ile Arg Glu Gln Leu Pro Leu Ile Ala Gly
530 535 540

Ser Ala Ala Ala Gly Val Val Phe Val Val Ser Leu Val Ala Ile Ser
545 550 555 560

Ile Val Cys Ser Arg Lys Arg Ala Tyr Ser Lys Glu Ala Val Tyr Ser
565 570 575

Asp Lys Leu Gln His Tyr Ser Thr Gly Arg Gly Glu Phe Gly Glu Val
580 585 590

Tyr Lys Gly Arg Leu Lys Leu Pro Gly Lys Arg Glu Ile Tyr Val Ala
595 600 605

Ile Lys Thr Leu Lys Ala Gly Tyr Ser Glu Lys Gln Arg Arg Asp Phe
610 615 620

Leu Ser Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile
625 630 635 640

Arg Leu Glu Gly Val Val Thr Lys Ser Arg Pro Val Met Ile Ile Thr
645 650 655

Glu Phe Met Glu Asn Gly Ala Leu Asp Ser Phe Leu Arg Gln Asn Asp
660 665 670

Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala
675 680 685

Ala Gly Met Lys Tyr Leu Ala Glu Met Asn Tyr Val His Arg Asp Leu
690 695 700

Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser
705 710 715 720

Asp Phe Gly Leu Ser Arg Tyr Leu Gln Asp Asp Thr Ser Asp Pro Thr
725 730 735

Tyr Thr Ser Ser Leu Gly Gly Lys Ile Pro Val Arg Trp Thr Ala Pro
740 745 750

Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser
755 760 765

Tyr Gly Ile Val Met Trp Glu Val Met Ser Phe Gly Glu Arg Pro Tyr
770 775 780

Trp Asp Met Ser Asn Gln Asp Val Ile Asn Ala Ile Glu Gln Asp Tyr
785 790 795 800

Arg Leu Pro Pro Pro Met Asp Cys Pro Ala Ala Leu His Gln Leu Met

805

810

815

Leu Asp Cys Trp Gln Lys Asp Arg Asn Ser Arg Pro Arg Phe Ala Glu
 820 825 830

Ile Val Asn Thr Leu Asp Lys Met Ile Arg Asn Pro Ala Ser Leu Lys
 835 840 845

Thr Val Ala Thr Ile Thr Ala Val Pro Ser Gln Pro Leu Leu Asp Arg
 850 855 860

Ser Ile Pro Asp Phe Thr Ala Phe Thr Thr Val Asp Asp Trp Leu Ser
 865 870 875 880

Ala Ile Lys Met Val Gln Tyr Arg Asp Ser Phe Leu Thr Ala Gly Phe
 885 890 895

Thr Ser Leu Gln Leu Val Thr Gln Met Thr Ser Glu Asp Leu Leu Arg
 900 905 910

Ile Gly Ile Thr Leu Ala Gly His Gln Lys Lys Ile Leu Asn Ser Ile
 915 920 925

His Ser Met Arg Val Gln Ile Ser Gln Ser Pro Thr Ala Met Ala
 930 935 940

<210> 85

<211> 223

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 85

Met Arg Ile Leu Lys Arg Phe Leu Ala Cys Ile Gln Leu Leu Cys Val
 1 5 10 15

Cys Arg Leu Asp Trp Ala Asn Gly Tyr Tyr Arg Gln Gln Arg Lys Leu
 20 25 30

Val Glu Glu Ile Gly Trp Ser Tyr Thr Gly Ala Leu Asn Gln Lys Asn
 35 40 45

Trp Gly Lys Lys Tyr Pro Thr Cys Asn Ser Pro Lys Gln Ser Pro Ile
 50 55 60

Asn Ile Asp Glu Asp Leu Thr Gln Val Asn Val Asn Leu Lys Lys Leu
 65 70 75 80

Lys Phe Gln Gly Trp Asp Lys Thr Ser Leu Glu Asn Thr Phe Ile His
 85 90 95

Asn Thr Gly Lys Thr Val Glu Ile Asn Leu Thr Asn Asp Tyr Arg Val
 100 105 110

Ser Gly Gly Val Ser Glu Met Val Phe Lys Ala Ser Lys Ile Thr Phe
 115 120 125

His Trp Gly Lys Cys Asn Met Ser Ser Asp Gly Ser Glu His Ser Leu
 130 135 140

Glu Gly Gln Lys Phe Pro Leu Glu Met Gln Ile Tyr Cys Phe Asp Ala
 145 150 155 160

Asp Arg Phe Ser Ser Phe Glu Glu Ala Val Lys Gly Lys Gly Lys Leu
 165 170 175

Arg Ala Leu Ser Ile Leu Phe Glu Val Gly Thr Glu Glu Asn Leu Asp
 180 185 190

Phe Lys Ala Ile Ile Asp Gly Val Glu Ser Val Ser Arg Phe Val Gly
 195 200 205

Cys Phe Cys Glu Val Leu Thr Cys Asn Asn Leu Val Met Ser Cys
 210 215 220

<210> 86

<211> 421

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 86

Met Arg Ile Leu Lys Arg Phe Leu Ala Cys Ile Gln Leu Leu Cys Val
 1 5 10 15

Cys Arg Leu Asp Trp Ala Asn Gly Tyr Tyr Arg Gln Gln Arg Lys Leu
 20 25 30

Val Glu Glu Ile Gly Trp Ser Tyr Thr Gly Ala Leu Asn Gln Lys Asn
 35 40 45

Trp Gly Lys Lys Tyr Pro Thr Cys Asn Ser Pro Lys Gln Ser Pro Ile
 50 55 60

Asn Ile Asp Glu Asp Leu Thr Gln Val Asn Val Asn Leu Lys Leu
 65 70 75 80

Lys Phe Gln Gly Trp Asp Lys Thr Ser Leu Glu Asn Thr Phe Ile His
 85 90 95

Asn Thr Gly Iys Thr Val Glu Ile Asn Leu Thr Asn Asp Tyr Arg Val
 100 105 110

Ser Gly Gly Val Ser Glu Met Val Phe Lys Ala Ser Lys Ile Thr Phe
 115 120 125

His Trp Gly Lys Cys Asn Met Ser Ser Asp Gly Ser Glu His Ser Leu
 130 135 140

Glu Gly Gln Lys Phe Pro Leu Glu Met Gln Ile Tyr Cys Phe Asp Ala
 145 150 155 160

Asp Arg Phe Ser Ser Phe Glu Glu Ala Val Lys Gly Lys Gly Lys Leu
 165 170 175

Arg Ala Leu Ser Ile Leu Phe Glu Val Gly Thr Glu Glu Asn Leu Asp
 180 185 190

Phe Lys Ala Ile Ile Asp Gly Val Glu Ser Val Ser Arg Phe Gly Lys
 195 200 205

Gln Ala Ala Leu Asp Pro Phe Ile Leu Leu Asn Leu Leu Pro Asn Ser
 210 215 220

Thr Asp Lys Tyr Tyr Ile Tyr Asn Gly Ser Leu Thr Ser Pro Pro Cys
 225 230 235 240

Thr Asp Thr Val Asp Trp Ile Val Phe Lys Asp Thr Val Ser Ile Ser
 245 250 255

Glu Ser Gln Leu Ala Val Phe Cys Glu Val Leu Thr Met Gln Gln Ser
 260 265 270

Gly Tyr Val Met Leu Met Asp Tyr Leu Gln Asn Asn Phe Arg Glu Gln
 275 280 285

Gln Tyr Lys Phe Ser Arg Gln Val Phe Ser Ser Tyr Thr Gly Lys Glu
 290 295 300

Glu Ile His Glu Ala Val Cys Ser Ser Glu Pro Glu Asn Val Gln Ala
 305 310 315 320

Asp Pro Glu Asn Tyr Thr Ser Leu Leu Val Thr Trp Glu Arg Pro Arg
 325 330 335

Val Val Tyr Asp Thr Met Ile Glu Lys Phe Ala Val Leu Tyr Gln Gln
 340 345 350

Leu Asp Gly Glu Asp Gln Thr Lys His Glu Phe Leu Thr Asp Gly Tyr
 355 360 365

Gln Asp Leu Gly Ala Ile Leu Asn Asn Leu Leu Pro Asn Met Ser Tyr
 370 375 380

Val Leu Gln Ile Val Ala Ile Cys Thr Asn Gly Leu Tyr Gly Lys Tyr
 385 390 395 400

Ser Asp Gln Leu Ile Val Asp Met Pro Thr Asp Asn Pro Gly Gly Gly
 405 410 415

Arg Gly Lys Arg His
 420

<210> 87

<211> 1623

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 87

Met Arg Ile Leu Lys Arg Phe Leu Ala Cys Ile Gln Leu Leu Cys Val
 1 5 10 15

Cys Arg Leu Asp Trp Ala Asn Gly Tyr Tyr Arg Gln Gln Arg Lys Leu
 20 25 30

Val Glu Glu Ile Gly Trp Ser Tyr Thr Gly Ala Leu Asn Gln Lys Asn
 35 40 45

Trp Gly Lys Lys Tyr Pro Thr Cys Asn Ser Pro Lys Gln Ser Pro Ile
 50 55 60

Asn Ile Asp Glu Asp Leu Thr Gln Val Asn Val Asn Leu Lys Lys Leu
 65 70 75 80

Lys Phe Gln Gly Trp Asp Lys Thr Ser Leu Glu Asn Thr Phe Ile His
 85 90 95

Asn Thr Gly Lys Thr Val Glu Ile Asn Leu Thr Asn Asp Tyr Arg Val
 100 105 110

Ser Gly Gly Val Ser Glu Met Val Phe Lys Ala Ser Lys Ile Thr Phe
 115 120 125

His Trp Gly Lys Cys Asn Met Ser Ser Asp Gly Ser Glu His Ser Leu
 130 135 140

Glu Gly Gln Lys Phe Pro Leu Glu Met Gln Ile Tyr Cys Phe Asp Ala
 145 150 155 160

Asp Arg Phe Ser Ser Phe Glu Glu Ala Val Lys Gly Lys Gly Lys Leu
 165 170 175

Arg Ala Leu Ser Ile Leu Phe Glu Val Gly Thr Glu Glu Asn Leu Asp
 180 185 190

Phe Lys Ala Ile Ile Asp Gly Val Glu Ser Val Ser Arg Phe Gly Lys
 195 200 205

Gln Ala Ala Leu Asp Pro Phe Ile Leu Leu Asn Leu Leu Pro Asn Ser
 210 215 220

Thr Asp Lys Tyr Tyr Ile Tyr Asn Gly Ser Leu Thr Ser Pro Pro Cys
 225 230 235 240

Thr Asp Thr Val Asp Trp Ile Val Phe Lys Asp Thr Val Ser Ile Ser
 245 250 255

Glu Ser Gln Leu Ala Val Phe Cys Glu Val Leu Thr Met Gln Gln Ser
 260 265 270

Gly Tyr Val Met Leu Met Asp Tyr Leu Gln Asn Asn Phe Arg Glu Gln
 275 280 285

Gln Tyr Lys Phe Ser Arg Gln Val Phe Ser Ser Tyr Thr Gly Lys Glu
 290 295 300

Glu Ile His Glu Ala Val Cys Ser Ser Glu Pro Glu Asn Val Gln Ala
 305 310 315 320

Asp Pro Glu Asn Tyr Thr Ser Leu Leu Val Thr Trp Glu Arg Pro Arg
 325 330 335

Val Val Tyr Asp Thr Met Ile Glu Lys Phe Ala Val Leu Tyr Gln Gln
 340 345 350

Leu Asp Gly Glu Asp Gln Thr Lys His Glu Phe Leu Thr Asp Gly Tyr
 355 360 365

Gln Asp Leu Gly Ala Ile Leu Asn Asn Leu Leu Pro Asn Met Ser Tyr
 370 375 380

Val Leu Gln Ile Val Ala Ile Cys Thr Asn Gly Leu Tyr Gly Lys Tyr
 385 390 395 400

Ser Asp Gln Leu Ile Val Asp Met Pro Thr Asp Asn Pro Glu Leu Asp
 405 410 415

Leu Phe Pro Glu Leu Ile Gly Thr Glu Glu Ile Ile Lys Glu Glu Glu
 420 425 430

Glu Gly Lys Asp Ile Glu Glu Gly Ala Ile Val Asn Pro Gly Arg Asp
 435 440 445

Ser Ala Thr Asn Gln Ile Arg Lys Lys Glu Pro Gln Ile Ser Thr Thr
 450 455 460

Thr His Tyr Asn Arg Ile Gly Thr Lys Tyr Asn Glu Ala Lys Thr Asn
 465 470 475 480

Arg Ser Pro Thr Arg Gly Ser Glu Phe Ser Gly Lys Gly Asp Val Pro
 485 490 495

Asn Thr Ser Leu Asn Ser Thr Ser Gln Pro Val Thr Lys Leu Ala Thr
 500 505 510

Glu Lys Asp Ile Ser Leu Thr Ser Gln Thr Val Thr Glu Leu Pro Pro
 515 520 525

His Thr Val Glu Gly Thr Ser Ala Ser Leu Asn Asp Gly Ser Lys Thr
 530 535 540

Val Leu Arg Ser Pro His Met Asn Leu Ser Gly Thr Ala Glu Ser Leu
 545 550 555 560

Asn Thr Val Ser Ile Thr Glu Tyr Glu Glu Ser Leu Leu Thr Ser
 565 570 575

Phe Lys Leu Asp Thr Gly Ala Glu Asp Ser Ser Gly Ser Ser Pro Ala
 580 585 590

Thr Ser Ala Ile Pro Phe Ile Ser Glu Asn Ile Ser Gln Gly Tyr Ile
 595 600 605

Phe Ser Ser Glu Asn Pro Glu Thr Ile Thr Tyr Asp Val Leu Ile Pro
 610 615 620

Glu Ser Ala Arg Asn Ala Ser Glu Asp Ser Thr Ser Ser Gly Ser Glu
 625 630 635 640

Glu Ser Leu Lys Asp Pro Ser Met Glu Gly Asn Val Trp Phe Pro Ser
 645 650 655

Ser Thr Asp Ile Thr Ala Gln Pro Asp Val Gly Ser Gly Arg Glu Ser
 660 665 670

Phe Leu Gln Thr Asn Tyr Thr Glu Ile Arg Val Asp Glu Ser Glu Lys
 675 680 685

Thr Thr Lys Ser Phe Ser Ala Gly Pro Val Met Ser Gln Gly Pro Ser
 690 695 700

Val Thr Asp Leu Glu Met Pro His Tyr Ser Thr Phe Ala Tyr Phe Pro
 705 710 715 720

Thr Glu Val Thr Pro His Ala Phe Thr Pro Ser Ser Arg Gln Gln Asp
 725 730 735

Leu Val Ser Thr Val Asn Val Val Tyr Ser Gln Thr Thr Gln Pro Val
 740 745 750

Tyr Asn Gly Glu Thr Pro Leu Gln Pro Ser Tyr Ser Ser Glu Val Phe
 755 760 765

Pro Leu Val Thr Pro Leu Leu Asp Asn Gln Ile Leu Asn Thr Thr
 770 775 780

Pro Ala Ala Ser Ser Ser Asp Ser Ala Leu His Ala Thr Pro Val Phe
 785 790 795 800

Pro Ser Val Asp Val Ser Phe Glu Ser Ile Leu Ser Ser Tyr Asp Gly
 805 810 815

Ala Pro Leu Leu Pro Phe Ser Ser Ala Ser Phe Ser Ser Glu Leu Phe
 820 825 830

Arg His Leu His Thr Val Ser Gln Ile Leu Pro Gln Val Thr Ser Ala
 835 840 845

Thr Glu Ser Asp Lys Val Pro Leu His Ala Ser Leu Pro Val Ala Gly
 850 855 860

Gly Asp Leu Leu Leu Glu Pro Ser Leu Ala Gln Tyr Ser Asp Val Leu
 865 870 875 880

Ser Thr Thr His Ala Ala Ser Glu Thr Leu Glu Phe Gly Ser Glu Ser
 885 890 895

Gly Val Leu Tyr Lys Thr Ile Met Phe Ser Gln Val Glu Pro Pro Ser
 900 905 910

Ser Asp Ala Met Met His Ala Arg Ser Ser Gly Pro Glu Pro Ser Tyr
 915 920 925

Ala Leu Ser Asp Asn Glu Gly Ser Gln His Ile Phe Thr Val Ser Tyr

930

935

940

Ser Ser Ala Ile Pro Val His Asp Ser Val Gly Val Thr Tyr Gln Gly
945 950 955 960

Ser Leu Phe Ser Gly Pro Ser His Ile Pro Ile Pro Lys Ser Ser Leu
965 970 975

Ile Thr Pro Thr Ala Ser Leu Leu Gln Pro Thr His Ala Leu Ser Gly
980 985 990

Asp Gly Glu Trp Ser Gly Ala Ser Ser Asp Ser Glu Phe Leu Leu Pro
995 1000 1005

Asp Thr Asp Gly Leu Thr Ala Leu Asn Ile Ser Ser Pro Val Ser
1010 1015 1020

Val Ala Glu Phe Thr Tyr Thr Ser Val Phe Gly Asp Asp Asn
1025 1030 1035

Lys Ala Leu Ser Lys Ser Glu Ile Ile Tyr Gly Asn Glu Thr Glu
1040 1045 1050

Leu Gln Ile Pro Ser Phe Asn Glu Met Val Tyr Pro Ser Glu Ser
1055 1060 1065

Thr Val Met Pro Asn Met Tyr Asp Asn Val Asn Lys Leu Asn Ala
1070 1075 1080

Ser Leu Gln Glu Thr Ser Val Ser Ile Ser Ser Thr Lys Gly Met
1085 1090 1095

Phe Pro Gly Ser Leu Ala His Thr Thr Thr Lys Val Phe Asp His
1100 1105 1110

Glu Ile Ser Gln Val Pro Glu Asn Asn Phe Ser Val Gln Pro Thr
1115 1120 1125

His Thr Val Ser Gln Ala Ser Gly Asp Thr Ser Leu Lys Pro Val
1130 1135 1140

Leu Ser Ala Asn Ser Glu Pro Ala Ser Ser Asp Pro Ala Ser Ser
1145 1150 1155

Glu Met Leu Ser Pro Ser Thr Gln Leu Leu Phe Tyr Glu Thr Ser
1160 1165 1170

Ala Ser Phe Ser Thr Glu Val Leu Leu Gln Pro Ser Phe Gln Ala
1175 1180 1185

Ser Asp Val Asp Thr Leu Leu Lys Thr Val Leu Pro Ala Val Pro
1190 1195 1200

Ser Asp Pro Ile Leu Val Glu Thr Pro Lys Val Asp Lys Ile Ser
1205 1210 1215

Ser Thr Met Leu His Leu Ile Val Ser Asn Ser Ala Ser Ser Glu
1220 1225 1230

Asn Met Leu His Ser Thr Ser Val Pro Val Phe Asp Val Ser Pro
1235 1240 1245

Thr Ser His Met His Ser Ala Ser Leu Gln Gly Leu Thr Ile Ser
1250 1255 1260

Tyr Ala Ser Glu Lys Tyr Glu Pro Val Leu Leu Lys Ser Glu Ser
1265 1270 1275

Ser His Gln Val Val Pro Ser Leu Tyr Ser Asn Asp Glu Leu Phe
1280 1285 1290

Gln Thr Ala Asn Leu Glu Ile Asn Gln Ala His Pro Pro Lys Gly
1295 1300 1305

Arg His Val Phe Ala Thr Pro Val Leu Ser Ile Asp Glu Pro Leu
1310 1315 1320

Asn Thr Leu Ile Asn Lys Leu Ile His Ser Asp Glu Ile Leu Thr
1325 1330 1335

Ser Thr Lys Ser Ser Val Thr Gly Lys Val Phe Ala Gly Ile Pro
1340 1345 1350

Thr Val Ala Ser Asp Thr Phe Val Ser Thr Asp His Ser Val Pro
1355 1360 1365

Ile Gly Asn Gly His Val Ala Ile Thr Ala Val Ser Pro His Arg
1370 1375 1380

Asp Gly Ser Val Thr Ser Thr Lys Leu Leu Phe Pro Ser Lys Ala
1385 1390 1395

Thr Ser Glu Leu Ser His Ser Ala Lys Ser Asp Ala Gly Leu Val
1400 1405 1410

Gly Gly Gly Glu Asp Gly Asp Thr Asp Asp Asp Gly Asp Asp Asp
1415 1420 1425

Asp Asp Arg Asp Ser Asp Gly Leu Ser Ile His Lys Cys Met Ser
1430 1435 1440

Cys Ser Ser Tyr Arg Glu Ser Gln Glu Lys Val Met Asn Asp Ser
1445 1450 1455

Asp Thr His Glu Asn Ser Leu Met Asp Gln Asn Asn Pro Ile Ser
1460 1465 1470

Tyr Ser Leu Ser Glu Asn Ser Glu Glu Asp Asn Arg Val Thr Ser
1475 1480 1485

Val Ser Ser Asp Ser Gln Thr Gly Met Asp Arg Ser Pro Gly Lys
1490 1495 1500

Ser Pro Ser Ala Asn Gly Leu Ser Gln Lys His Asn Asp Gly Lys
1505 1510 1515

Glu Glu Asn Asp Ile Gln Thr Gly Ser Ala Leu Leu Pro Leu Ser
 1520 1525 1530

Pro Glu Ser Lys Ala Trp Ala Val Leu Thr Ser Asp Glu Glu Ser
 1535 1540 1545

Gly Ser Gly Gln Gly Thr Ser Asp Ser Leu Asn Glu Asn Glu Thr
 1550 1555 1560

Ser Thr Asp Phe Ser Phe Ala Asp Thr Asn Glu Lys Asp Ala Asp
 1565 1570 1575

Gly Ile Leu Ala Ala Gly Asp Ser Glu Ile Thr Pro Gly Phe Pro
 1580 1585 1590

Gln Ser Pro Thr Ser Ser Val Thr Ser Glu Asn Ser Glu Val Phe
 1595 1600 1605

His Val Ser Glu Ala Gly Asn Ala Ser Arg Leu His Thr Phe Thr
 1610 1615 1620

<210> 88
 <211> 1725
 <212> PRT
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant protein product

<400> 88

Met Arg Ile Leu Lys Arg Phe Leu Ala Cys Ile Gln Leu Leu Cys Val
 1 5 10 15

Cys Arg Leu Asp Trp Ala Asn Gly Tyr Tyr Arg Gln Gln Arg Lys Leu
 20 25 30

Val Glu Glu Ile Gly Trp Ser Tyr Thr Gly Ala Leu Asn Gln Lys Asn
 35 40 45

Trp Gly Lys Lys Tyr Pro Thr Cys Asn Ser Pro Lys Gln Ser Pro Ile
 50 55 60

Asn Ile Asp Glu Asp Leu Thr Gln Val Asn Val Asn Leu Lys Leu
 65 70 75 80

Lys Phe Gln Gly Trp Asp Lys Thr Ser Leu Glu Asn Thr Phe Ile His
 85 90 95

Asn Thr Gly Lys Thr Val Glu Ile Asn Leu Thr Asn Asp Tyr Arg Val
 100 105 110

Ser Gly Gly Val Ser Glu Met Val Phe Lys Ala Ser Lys Ile Thr Phe
 115 120 125

His Trp Gly Lys Cys Asn Met Ser Ser Asp Gly Ser Glu His Ser Leu
 130 135 140

Glu Gly Gln Lys Phe Pro Leu Glu Met Gln Ile Tyr Cys Phe Asp Ala
 145 150 155 160

Asp Arg Phe Ser Ser Phe Glu Glu Ala Val Lys Gly Lys Gly Lys Leu
 165 170 175

Arg Ala Leu Ser Ile Leu Phe Glu Val Gly Thr Glu Glu Asn Leu Asp
 180 185 190

Phe Lys Ala Ile Ile Asp Gly Val Glu Ser Val Ser Arg Phe Gly Lys
 195 200 205

Gln Ala Ala Leu Asp Pro Phe Ile Leu Leu Asn Leu Leu Pro Asn Ser
 210 215 220

Thr Asp Lys Tyr Tyr Ile Tyr Asn Gly Ser Leu Thr Ser Pro Pro Cys
 225 230 235 240

Thr Asp Thr Val Asp Trp Ile Val Phe Lys Asp Thr Val Ser Ile Ser
 245 250 255

Glu Ser Gln Leu Ala Val Phe Cys Glu Val Leu Thr Met Gln Gln Ser
 260 265 270

Gly Tyr Val Met Leu Met Asp Tyr Leu Gln Asn Asn Phe Arg Glu Gln
 275 280 285

Gln Tyr Lys Phe Ser Arg Gln Val Phe Ser Ser Tyr Thr Gly Lys Glu
 290 295 300

Glu Ile His Glu Ala Val Cys Ser Ser Glu Pro Glu Asn Val Gln Ala
 305 310 315 320

Asp Pro Glu Asn Tyr Thr Ser Leu Leu Val Thr Trp Glu Arg Pro Arg
 325 330 335

Val Val Tyr Asp Thr Met Ile Glu Lys Phe Ala Val Leu Tyr Gln Gln
 340 345 350

Leu Asp Gly Glu Asp Gln Thr Lys His Glu Phe Leu Thr Asp Gly Tyr
 355 360 365

Gln Asp Leu Gly Ala Ile Leu Asn Asn Leu Leu Pro Asn Met Ser Tyr
 370 375 380

Val Leu Gln Ile Val Ala Ile Cys Thr Asn Gly Leu Tyr Gly Lys Tyr
 385 390 395 400

Ser Asp Gln Leu Ile Val Asp Met Pro Thr Asp Asn Pro Glu Leu Asp
 405 410 415

Leu Phe Pro Glu Leu Ile Gly Thr Glu Glu Ile Ile Lys Glu Glu Glu
 420 425 430

Glu Gly Lys Asp Ile Glu Glu Gly Ala Ile Val Asn Pro Gly Arg Asp
 435 440 445

Ser Ala Thr Asn Gln Ile Arg Lys Lys Glu Pro Gln Ile Ser Thr Thr
 450 455 460

Thr His Tyr Asn Arg Ile Gly Thr Lys Tyr Asn Glu Ala Lys Thr Asn
465 470 475 480

Arg Ser Pro Thr Arg Gly Ser Glu Phe Ser Gly Lys Gly Asp Val Pro
485 490 495

Asn Thr Ser Leu Asn Ser Thr Ser Gln Pro Val Thr Lys Leu Ala Thr
500 505 510

Glu Lys Asp Ile Ser Leu Thr Ser Gln Thr Val Thr Glu Leu Pro Pro
515 520 525

His Thr Val Glu Gly Thr Ser Ala Ser Leu Asn Asp Gly Ser Lys Thr
530 535 540

Val Leu Arg Ser Pro His Met Asn Leu Ser Gly Thr Ala Glu Ser Leu
545 550 555 560

Asn Thr Val Ser Ile Thr Glu Tyr Glu Glu Ser Leu Leu Thr Ser
565 570 575

Phe Lys Leu Asp Thr Gly Ala Glu Asp Ser Ser Gly Ser Ser Pro Ala
580 585 590

Thr Ser Ala Ile Pro Phe Ile Ser Glu Asn Ile Ser Gln Gly Tyr Ile
595 600 605

Phe Ser Ser Glu Asn Pro Glu Thr Ile Thr Tyr Asp Val Leu Ile Pro
610 615 620

Glu Ser Ala Arg Asn Ala Ser Glu Asp Ser Thr Ser Ser Gly Ser Glu
625 630 635 640

Glu Ser Leu Lys Asp Pro Ser Met Glu Gly Asn Val Trp Phe Pro Ser
645 650 655

Ser Thr Asp Ile Thr Ala Gln Pro Asp Val Gly Ser Gly Arg Glu Ser
660 665 670

Phe Leu Gln Thr Asn Tyr Thr Glu Ile Arg Val Asp Glu Ser Glu Lys
675 680 685

Thr Thr Lys Ser Phe Ser Ala Gly Pro Val Met Ser Gln Gly Pro Ser
690 695 700

Val Thr Asp Leu Glu Met Pro His Tyr Ser Thr Phe Ala Tyr Phe Pro
705 710 715 720

Thr Glu Val Thr Pro His Ala Phe Thr Pro Ser Ser Arg Gln Gln Asp
725 730 735

Leu Val Ser Thr Val Asn Val Val Tyr Ser Gln Thr Thr Gln Pro Val
740 745 750

Tyr Asn Gly Glu Thr Pro Leu Gln Pro Ser Tyr Ser Ser Glu Val Phe
755 760 765

Pro Leu Val Thr Pro Leu Leu Leu Asp Asn Gln Ile Leu Asn Thr Thr
770 775 780

Pro Ala Ala Ser Ser Ser Asp Ser Ala Leu His Ala Thr Pro Val Phe
785 790 795 800

Pro Ser Val Asp Val Ser Phe Glu Ser Ile Leu Ser Ser Tyr Asp Gly
805 810 815

Ala Pro Leu Leu Pro Phe Ser Ser Ala Ser Phe Ser Ser Glu Leu Phe
820 825 830

Arg His Leu His Thr Val Ser Gln Ile Leu Pro Gln Val Thr Ser Ala
835 840 845

Thr Glu Ser Asp Lys Val Pro Leu His Ala Ser Leu Pro Val Ala Gly
850 855 860

Gly Asp Leu Leu Leu Glu Pro Ser Leu Ala Gln Tyr Ser Asp Val Leu
865 870 875 880

Ser Thr Thr His Ala Ala Ser Glu Thr Leu Glu Phe Gly Ser Glu Ser
885 890 895

Gly Val Leu Tyr Lys Thr Leu Met Phe Ser Gln Val Glu Pro Pro Ser
900 905 910

Ser Asp Ala Met Met His Ala Arg Ser Ser Gly Pro Glu Pro Ser Tyr
915 920 925

Ala Leu Ser Asp Asn Glu Gly Ser Gln His Ile Phe Thr Val Ser Tyr
930 935 940

Ser Ser Ala Ile Pro Val His Asp Ser Val Gly Val Thr Tyr Gln Gly
945 950 955 960

Ser Leu Phe Ser Gly Pro Ser His Ile Pro Ile Pro Lys Ser Ser Leu
965 970 975

Ile Thr Pro Thr Ala Ser Leu Leu Gln Pro Thr His Ala Leu Ser Gly
980 985 990

Asp Gly Glu Trp Ser Gly Ala Ser Ser Asp Ser Glu Phe Leu Leu Pro
995 1000 1005

Asp Thr Asp Gly Leu Thr Ala Leu Asn Ile Ser Ser Pro Val Ser
1010 1015 1020

Val Ala Glu Phe Thr Tyr Thr Ser Val Phe Gly Asp Asp Asn
1025 1030 1035

Lys Ala Leu Ser Lys Ser Glu Ile Ile Tyr Gly Asn Glu Thr Glu
1040 1045 1050

Leu Gln Ile Pro Ser Phe Asn Glu Met Val Tyr Pro Ser Glu Ser
1055 1060 1065

Thr Val Met Pro Asn Met Tyr Asp Asn Val Asn Lys Leu Asn Ala

1070 1075 1080

Ser Leu Gln Glu Thr Ser Val Ser Ile Ser Ser Thr Lys Gly Met
1085 1090 1095

Phe Pro Gly Ser Leu Ala His Thr Thr Thr Lys Val Phe Asp His
1100 1105 1110

Glu Ile Ser Gln Val Pro Glu Asn Asn Phe Ser Val Gln Pro Thr
1115 1120 1125

His Thr Val Ser Gln Ala Ser Gly Asp Thr Ser Leu Lys Pro Val
1130 1135 1140

Leu Ser Ala Asn Ser Glu Pro Ala Ser Ser Asp Pro Ala Ser Ser
1145 1150 1155

Glu Met Leu Ser Pro Ser Thr Gln Leu Leu Phe Tyr Glu Thr Ser
1160 1165 1170

Ala Ser Phe Ser Thr Glu Val Leu Leu Gln Pro Ser Phe Gln Ala
1175 1180 1185

Ser Asp Val Asp Thr Leu Ile Lys Thr Val Leu Pro Ala Val Pro
1190 1195 1200

Ser Asp Pro Ile Leu Val Glu Thr Pro Lys Val Asp Lys Ile Ser
1205 1210 1215

Ser Thr Met Ile His Leu Ile Val Ser Asn Ser Ala Ser Ser Glu
1220 1225 1230

Asn Met Leu His Ser Thr Ser Val Pro Val Phe Asp Val Ser Pro
1235 1240 1245

Thr Ser His Met His Ser Ala Ser Leu Gln Gly Leu Thr Ile Ser
1250 1255 1260

Tyr Ala Ser Glu Lys Tyr Glu Pro Val Leu Leu Lys Ser Glu Ser
1265 1270 1275

Ser His Gln Val Val Pro Ser Leu Tyr Ser Asn Asp Glu Leu Phe
1280 1285 1290

Gln Thr Ala Asn Leu Glu Ile Asn Gln Ala His Pro Pro Lys Gly
1295 1300 1305

Arg His Val Phe Ala Thr Pro Val Leu Ser Ile Asp Glu Pro Leu
1310 1315 1320

Asn Thr Leu Ile Asn Lys Ieu Ile His Ser Asp Glu Ile Leu Thr
1325 1330 1335

Ser Thr Lys Ser Ser Val Thr Gly Lys Val Phe Ala Gly Ile Pro
1340 1345 1350

Thr Val Ala Ser Asp Thr Phe Val Ser Thr Asp His Ser Val Pro
1355 1360 1365

Ile Gly Asn Gly His Val Ala Ile Thr Ala Val Ser Pro His Arg
1370 1375 1380

Asp Gly Ser Val Thr Ser Thr Lys Leu Leu Phe Pro Ser Lys Ala
1385 1390 1395

Thr Ser Glu Leu Ser His Ser Ala Lys Ser Asp Ala Gly Leu Val
1400 1405 1410

Gly Gly Gly Glu Asp Gly Asp Thr Asp Asp Asp Gly Asp Asp Asp
1415 1420 1425

Asp Asp Arg Asp Ser Asp Gly Leu Ser Ile His Lys Cys Met Ser
1430 1435 1440

Cys Ser Ser Tyr Arg Glu Ser Gln Glu Lys Val Met Asn Asp Ser
1445 1450 1455

Asp Thr His Glu Asn Ser Leu Met Asp Gln Asn Asn Pro Ile Ser
1460 1465 1470

Tyr Ser Leu Ser Glu Asn Ser Glu Glu Asp Asn Arg Val Thr Ser
1475 1480 1485

Val Ser Ser Asp Ser Gln Thr Gly Met Asp Arg Ser Pro Gly Lys
1490 1495 1500

Ser Pro Ser Ala Asn Gly Leu Ser Gln Lys His Asn Asp Gly Lys
1505 1510 1515

Glu Glu Asn Asp Ile Gln Thr Gly Ser Ala Leu Leu Pro Leu Ser
1520 1525 1530

Pro Glu Ser Lys Ala Trp Ala Val Leu Thr Ser Asp Glu Glu Ser
1535 1540 1545

Gly Ser Gly Gln Gly Thr Ser Asp Ser Leu Asn Glu Asn Glu Thr
1550 1555 1560

Ser Thr Asp Phe Ser Phe Ala Asp Thr Asn Glu Lys Asp Ala Asp
1565 1570 1575

Gly Ile Leu Ala Ala Gly Asp Ser Glu Ile Thr Pro Gly Phe Pro
1580 1585 1590

Gln Ser Pro Thr Ser Ser Val Thr Ser Glu Asn Ser Glu Val Phe
1595 1600 1605

His Val Ser Glu Ala Glu Ala Ser Asn Ser Ser His Glu Ser Arg
1610 1615 1620

Ile Gly Leu Ala Glu Gly Leu Glu Ser Glu Lys Lys Ala Val Ile
1625 1630 1635

Pro Leu Val Ile Val Ser Ala Leu Thr Phe Ile Cys Leu Val Val
1640 1645 1650

Leu Val Gly Ile Leu Ile Tyr Trp Arg Lys Cys Phe Gln Thr Ala
 1655 1660 1665

His Phe Tyr Leu Glu Asp Ser Thr Ser Pro Arg Val Ile Ser Thr
 1670 1675 1680

Pro Pro Thr Pro Ile Phe Pro Ile Ser Asp Thr Glu Glu Val Leu
 1685 1690 1695

Pro Gly Leu Arg Tyr Tyr Asp Glu Gln Leu Gln Pro Pro Glu Gln
 1700 1705 1710

Gln Ala Gln Glu Ser Ile His Lys Tyr Arg Cys Leu
 1715 1720 1725

<210> 89.

<211> 2307

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 89

Met Arg Ile Leu Lys Arg Phe Leu Ala Cys Ile Gln Leu Leu Cys Val
 1 5 10 15

Cys Arg Leu Asp Trp Ala Asn Gly Tyr Tyr Arg Gln Gln Arg Lys Leu
 20 25 30

Val Glu Glu Ile Gly Trp Ser Tyr Thr Gly Ala Leu Asn Gln Lys Asn
 35 40 45

Trp Gly Lys Lys Tyr Pro Thr Cys Asn Ser Pro Lys Gln Ser Pro Ile
 50 55 60

Asn Ile Asp Glu Asp Leu Thr Gln Val Asn Val Asn Leu Lys Lys Leu
 65 70 75 80

Lys Phe Gln Gly Trp Asp Lys Thr Ser Leu Glu Asn Thr Phe Ile His
 85 90 95

Asn Thr Gly Lys Thr Val Glu Ile Asn Leu Thr Asn Asp Tyr Arg Val
 100 105 110

Ser Gly Gly Val Ser Glu Met Val Phe Lys Ala Ser Lys Ile Thr Phe
 115 120 125

His Trp Gly Lys Cys Asn Met Ser Ser Asp Gly Ser Glu His Ser Leu
 130 135 140

Glu Gly Gln Lys Phe Pro Leu Glu Met Gln Ile Tyr Cys Phe Asp Ala
 145 150 155 160

Asp Arg Phe Ser Ser Phe Glu Glu Ala Val Lys Gly Lys Gly Lys Leu
 165 170 175

Arg Ala Leu Ser Ile Leu Phe Glu Val Gly Thr Glu Glu Asn Leu Asp
 180 185 190

Phe Lys Ala Ile Ile Asp Gly Val Glu Ser Val Ser Arg Phe Gly Lys
195 200 205

Gln Ala Ala Leu Asp Pro Phe Ile Leu Leu Asn Leu Leu Pro Asn Ser
210 215 220

Thr Asp Lys Tyr Tyr Ile Tyr Asn Gly Ser Leu Thr Ser Pro Pro Cys
225 230 235 240

Thr Asp Thr Val Asp Trp Ile Val Phe Lys Asp Thr Val Ser Ile Ser
245 250 255

Glu Ser Gln Leu Ala Val Phe Cys Glu Val Leu Thr Met Gln Gln Ser
260 265 270

Gly Tyr Val Met Leu Met Asp Tyr Leu Gln Asn Asn Phe Arg Glu Gln
275 280 285

Gln Tyr Lys Phe Ser Arg Gln Val Phe Ser Ser Tyr Thr Gly Lys Glu
290 295 300

Glu Ile His Glu Ala Val Cys Ser Ser Glu Pro Glu Asn Val Gln Ala
305 310 315 320

Asp Pro Glu Asn Tyr Thr Ser Leu Leu Val Thr Trp Glu Arg Pro Arg
325 330 335

Val Val Tyr Asp Thr Met Ile Glu Lys Phe Ala Val Leu Tyr Gln Gln
340 345 350

Leu Asp Gly Glu Asp Gln Thr Lys His Glu Phe Leu Thr Asp Gly Tyr
355 360 365

Gln Asp Leu Gly Ala Ile Leu Asn Asn Leu Leu Pro Asn Met Ser Tyr
370 375 380

Val Leu Gln Ile Val Ala Ile Cys Thr Asn Gly Leu Tyr Gly Lys Tyr
385 390 395 400

Ser Asp Gln Leu Ile Val Asp Met Pro Thr Asp Asn Pro Glu Leu Asp
405 410 415

Leu Phe Pro Glu Leu Ile Gly Thr Glu Glu Ile Ile Lys Glu Glu Glu
420 425 430

Glu Gly Lys Asp Ile Glu Glu Gly Ala Ile Val Asn Pro Gly Arg Asp
435 440 445

Ser Ala Thr Asn Gln Ile Arg Lys Lys Glu Pro Gln Ile Ser Thr Thr
450 455 460

Thr His Tyr Asn Arg Ile Gly Thr Lys Tyr Asn Glu Ala Lys Thr Asn
465 470 475 480

Arg Ser Pro Thr Arg Gly Ser Glu Phe Ser Gly Lys Gly Asp Val Pro
485 490 495

Asn Thr Ser Leu Asn Ser Thr Ser Gln Pro Val Thr Lys Leu Ala Thr
 500 505 510

Glu Lys Asp Ile Ser Leu Thr Ser Gln Thr Val Thr Glu Leu Pro Pro
 515 520 525

His Thr Val Glu Gly Thr Ser Ala Ser Leu Asn Asp Gly Ser Lys Thr
 530 535 540

Val Leu Arg Ser Pro His Met Asn Leu Ser Gly Thr Ala Glu Ser Leu
 545 550 555 560

Asn Thr Val Ser Ile Thr Glu Tyr Glu Glu Ser Leu Leu Thr Ser
 565 570 575

Phe Lys Leu Asp Thr Gly Ala Glu Asp Ser Ser Gly Ser Ser Pro Ala
 580 585 590

Thr Ser Ala Ile Pro Phe Ile Ser Glu Asn Ile Ser Gln Gly Tyr Ile
 595 600 605

Phe Ser Ser Glu Asn Pro Glu Thr Ile Thr Tyr Asp Val Leu Ile Pro
 610 615 620

Glu Ser Ala Arg Asn Ala Ser Glu Asp Ser Thr Ser Ser Gly Ser Glu
 625 630 635 640

Glu Ser Leu Lys Asp Pro Ser Met Glu Gly Asn Val Trp Phe Pro Ser
 645 650 655

Ser Thr Asp Ile Thr Ala Gln Pro Asp Val Gly Ser Gly Arg Glu Ser
 660 665 670

Phe Leu Gln Thr Asn Tyr Thr Glu Ile Arg Val Asp Glu Ser Glu Lys
 675 680 685

Thr Thr Lys Ser Phe Ser Ala Gly Pro Val Met Ser Gln Gly Pro Ser
 690 695 700

Val Thr Asp Leu Glu Met Pro His Tyr Ser Thr Phe Ala Tyr Phe Pro
 705 710 715 720

Thr Glu Val Thr Pro His Ala Phe Thr Pro Ser Ser Arg Gln Gln Asp
 725 730 735

Leu Val Ser Thr Val Asn Val Val Tyr Ser Gln Thr Thr Gln Pro Val
 740 745 750

Tyr Asn Gly Glu Thr Pro Leu Gln Pro Ser Tyr Ser Ser Glu Val Phe
 755 760 765

Pro Leu Val Thr Pro Leu Leu Asp Asn Gln Ile Leu Asn Thr Thr
 770 775 780

Pro Ala Ala Ser Ser Ser Asp Ser Ala Leu His Ala Thr Pro Val Phe
 785 790 795 800

Pro Ser Val Asp Val Ser Phe Glu Ser Ile Leu Ser Ser Tyr Asp Gly
805 810 815

Ala Pro Leu Leu Pro Phe Ser Ser Ala Ser Phe Ser Ser Glu Leu Phe
820 825 830

Arg His Leu His Thr Val Ser Gln Ile Leu Pro Gln Val Thr Ser Ala
835 840 845

Thr Glu Ser Asp Lys Val Pro Leu His Ala Ser Leu Pro Val Ala Gly
850 855 860

Gly Asp Leu Leu Leu Glu Pro Ser Leu Ala Gln Tyr Ser Asp Val Leu
865 870 875 880

Ser Thr Thr His Ala Ala Ser Glu Thr Leu Glu Phe Gly Ser Glu Ser
885 890 895

Gly Val Leu Tyr Lys Thr Leu Met Phe Ser Gln Val Glu Pro Pro Ser
900 905 910

Ser Asp Ala Met Met His Ala Arg Ser Ser Gly Pro Glu Pro Ser Tyr
915 920 925

Ala Leu Ser Asp Asn Glu Gly Ser Gln His Ile Phe Thr Val Ser Tyr
930 935 940

Ser Ser Ala Ile Pro Val His Asp Ser Val Gly Val Thr Tyr Gln Gly
945 950 955 960

Ser Leu Phe Ser Gly Pro Ser His Ile Pro Ile Pro Lys Ser Ser Leu
965 970 975

Ile Thr Pro Thr Ala Ser Leu Leu Gln Pro Thr His Ala Leu Ser Gly
980 985 990

Asp Gly Glu Trp Ser Gly Ala Ser Ser Asp Ser Glu Phe Leu Leu Pro
995 1000 1005

Asp Thr Asp Gly Leu Thr Ala Leu Asn Ile Ser Ser Pro Val Ser
1010 1015 1020

Val Ala Glu Phe Thr Tyr Thr Ser Val Phe Gly Asp Asp Asn
1025 1030 1035

Lys Ala Leu Ser Lys Ser Glu Ile Ile Tyr Gly Asn Glu Thr Glu
1040 1045 1050

Leu Gln Ile Pro Ser Phe Asn Glu Met Val Tyr Pro Ser Glu Ser
1055 1060 1065

Thr Val Met Pro Asn Met Tyr Asp Asn Val Asn Lys Leu Asn Ala
1070 1075 1080

Ser Leu Gln Glu Thr Ser Val Ser Ile Ser Ser Thr Lys Gly Met
1085 1090 1095

Phe Pro Gly Ser Leu Ala His Thr Thr Thr Lys Val Phe Asp His

1100 1105 1110
Glu Ile Ser Gln Val Pro Glu Asn Asn Phe Ser Val Gln Pro Thr
1115 1120 1125

His Thr Val Ser Gln Ala Ser Gly Asp Thr Ser Leu Lys Pro Val
1130 1135 1140

Leu Ser Ala Asn Ser Glu Pro Ala Ser Ser Asp Pro Ala Ser Ser
1145 1150 1155

Glu Met Leu Ser Pro Ser Thr Gln Leu Leu Phe Tyr Glu Thr Ser
1160 1165 1170

Ala Ser Phe Ser Thr Glu Val Leu Leu Gln Pro Ser Phe Gln Ala
1175 1180 1185

Ser Asp Val Asp Thr Leu Leu Lys Thr Val Leu Pro Ala Val Pro
1190 1195 1200

Ser Asp Pro Ile Leu Val Glu Thr Pro Lys Val Asp Lys Ile Ser
1205 1210 1215

Ser Thr Met Leu His Leu Ile Val Ser Asn Ser Ala Ser Ser Glu
1220 1225 1230

Asn Met Leu His Ser Thr Ser Val Pro Val Phe Asp Val Ser Pro
1235 1240 1245

Thr Ser His Met His Ser Ala Ser Leu Gln Gly Leu Thr Ile Ser
1250 1255 1260

Tyr Ala Ser Glu Lys Tyr Glu Pro Val Leu Leu Lys Ser Glu Ser
1265 1270 1275

Ser His Gln Val Val Pro Ser Leu Tyr Ser Asn Asp Glu Leu Phe
1280 1285 1290

Gln Thr Ala Asn Leu Glu Ile Asn Gln Ala His Pro Pro Lys Gly
1295 1300 1305

Arg His Val Phe Ala Thr Pro Val Leu Ser Ile Asp Glu Pro Leu
1310 1315 1320

Asn Thr Leu Ile Asn Lys Leu Ile His Ser Asp Glu Ile Leu Thr
1325 1330 1335

Ser Thr Lys Ser Ser Val Thr Gly Lys Val Phe Ala Gly Ile Pro
1340 1345 1350

Thr Val Ala Ser Asp Thr Phe Val Ser Thr Asp His Ser Val Pro
1355 1360 1365

Ile Gly Asn Gly His Val Ala Ile Thr Ala Val Ser Pro His Arg
1370 1375 1380

Asp Gly Ser Val Thr Ser Thr Lys Leu Leu Phe Pro Ser Lys Ala
1385 1390 1395

Thr Ser Glu Leu Ser His Ser Ala Lys Ser Asp Ala Gly Leu Val
1400 1405 1410

Gly Gly Gly Glu Asp Gly Asp Thr Asp Asp Asp Gly Asp Asp Asp
1415 1420 1425

Asp Asp Arg Asp Ser Asp Gly Leu Ser Ile His Lys Cys Met Ser
1430 1435 1440

Cys Ser Ser Tyr Arg Glu Ser Gln Glu Lys Val Met Asn Asp Ser
1445 1450 1455

Asp Thr His Glu Asn Ser Leu Met Asp Gln Asn Asn Pro Ile Ser
1460 1465 1470

Tyr Ser Leu Ser Glu Asn Ser Glu Glu Asp Asn Arg Val Thr Ser
1475 1480 1485

Val Ser Ser Asp Ser Gln Thr Gly Met Asp Arg Ser Pro Gly Lys
1490 1495 1500

Ser Pro Ser Ala Asn Gly Leu Ser Gln Lys His Asn Asp Gly Lys
1505 1510 1515

Glu Glu Asn Asp Ile Gln Thr Gly Ser Ala Leu Leu Pro Leu Ser
1520 1525 1530

Pro Glu Ser Lys Ala Trp Ala Val Leu Thr Ser Asp Glu Glu Ser
1535 1540 1545

Gly Ser Gly Gln Gly Thr Ser Asp Ser Leu Asn Glu Asn Glu Thr
1550 1555 1560

Ser Thr Asp Phe Ser Phe Ala Asp Thr Asn Glu Lys Asp Ala Asp
1565 1570 1575

Gly Ile Leu Ala Ala Gly Asp Ser Glu Ile Thr Pro Gly Phe Pro
1580 1585 1590

Gln Ser Pro Thr Ser Ser Val Thr Ser Glu Asn Ser Glu Val Phe
1595 1600 1605

His Val Ser Glu Ala Glu Ala Ser Asn Ser Ser His Glu Ser Arg
1610 1615 1620

Ile Gly Leu Ala Glu Gly Leu Glu Ser Glu Lys Lys Ala Val Ile
1625 1630 1635

Pro Leu Val Ile Val Ser Ala Leu Thr Phe Ile Cys Leu Val Val
1640 1645 1650

Leu Val Gly Ile Leu Ile Tyr Trp Arg Lys Cys Phe Gln Thr Ala
1655 1660 1665

His Phe Tyr Leu Glu Asp Ser Thr Ser Pro Arg Val Ile Ser Thr
1670 1675 1680

Pro Pro Thr Pro Ile Phe Pro Ile Ser Asp Asp Val Gly Ala Ile
1685 1690 1695

Pro Ile Lys His Phe Pro Lys His Val Ala Asp Leu His Ala Ser
1700 1705 1710

Ser Gly Phe Thr Glu Glu Phe Glu Glu Val Gln Ser Cys Thr Val
1715 1720 1725

Asp Leu Gly Ile Thr Ala Asp Ser Ser Asn His Pro Asp Asn Lys
1730 1735 1740

His Lys Asn Arg Tyr Ile Asn Ile Val Ala Tyr Asp His Ser Arg
1745 1750 1755

Val Lys Leu Ala Gln Leu Ala Glu Lys Asp Gly Lys Leu Thr Asp
1760 1765 1770

Tyr Ile Asn Ala Asn Tyr Val Asp Gly Tyr Asn Arg Pro Lys Ala
1775 1780 1785

Tyr Ile Ala Ala Gln Gly Pro Leu Lys Ser Thr Ala Glu Asp Phe
1790 1795 1800

Trp Arg Met Ile Trp Glu His Asn Val Glu Val Ile Val Met Ile
1805 1810 1815

Thr Asn Leu Val Glu Lys Gly Arg Arg Lys Cys Asp Gln Tyr Trp
1820 1825 1830

Pro Ala Asp Gly Ser Glu Glu Tyr Gly Asn Phe Leu Val Thr Gln
1835 1840 1845

Lys Ser Val Gln Val Leu Ala Tyr Tyr Thr Val Arg Asn Phe Thr
1850 1855 1860

Leu Arg Asn Thr Lys Ile Lys Lys Gly Ser Gln Lys Gly Arg Pro
1865 1870 1875

Ser Gly Arg Val Val Thr Gln Tyr His Tyr Thr Gln Trp Pro Asp
1880 1885 1890

Met Gly Val Pro Glu Tyr Ser Leu Pro Val Leu Thr Phe Val Arg
1895 1900 1905

Lys Ala Ala Tyr Ala Lys Arg His Ala Val Gly Pro Val Val Val
1910 1915 1920

His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Val Leu
1925 1930 1935

Asp Ser Met Leu Gln Gln Ile Gln His Glu Gly Thr Val Asn Ile
1940 1945 1950

Phe Gly Phe Leu Lys His Ile Arg Ser Gln Arg Asn Tyr Leu Val
1955 1960 1965

Gln Thr Glu Glu Gln Tyr Val Phe Ile His Asp Thr Leu Val Glu
1970 1975 1980

Ala Ile Leu Ser Lys Glu Thr Glu Val Leu Asp Ser His Ile His
1985 1990 1995

Ala Tyr Val Asn Ala Leu Leu Ile Pro Gly Pro Ala Gly Lys Thr
2000 2005 2010

Lys Leu Glu Lys Gln Phe Gln Leu Leu Ser Gln Ser Asn Ile Gln
2015 2020 2025

Gln Ser Asp Tyr Ser Ala Ala Leu Lys Gln Cys Asn Arg Glu Lys
2030 2035 2040

Asn Arg Thr Ser Ser Ile Ile Pro Val Glu Arg Ser Arg Val Gly
2045 2050 2055

Ile Ser Ser Leu Ser Gly Glu Gly Thr Asp Tyr Ile Asn Ala Ser
2060 2065 2070

Tyr Ile Met Gly Tyr Tyr Gln Ser Asn Glu Phe Ile Ile Thr Gln
2075 2080 2085

His Pro Leu Leu His Thr Ile Lys Asp Phe Trp Arg Met Ile Trp
2090 2095 2100

Asp His Asn Ala Gln Leu Val Val Met Ile Pro Asp Gly Gln Asn
2105 2110 2115

Met Ala Glu Asp Glu Phe Val Tyr Trp Pro Asn Lys Asp Glu Pro
2120 2125 2130

Ile Asn Cys Glu Ser Phe Lys Val Thr Leu Met Ala Glu Glu His
2135 2140 2145

Lys Cys Leu Ser Asn Glu Glu Lys Leu Ile Ile Gln Asp Phe Ile
2150 2155 2160

Leu Glu Ala Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe
2165 2170 2175

Gln Cys Pro Lys Trp Pro Asn Pro Asp Ser Pro Ile Ser Lys Thr
2180 2185 2190

Phe Glu Leu Ile Ser Val Ile Lys Glu Glu Ala Ala Asn Arg Asp
2195 2200 2205

Gly Pro Met Ile Val His Asp Glu His Gly Gly Val Thr Ala Gly
2210 2215 2220

Thr Phe Cys Ala Leu Thr Thr Leu Met His Gln Leu Glu Lys Glu
2225 2230 2235

Asn Ser Val Asp Val Tyr Gln Val Ala Lys Met Ile Asn Leu Met
2240 2245 2250

Arg Pro Gly Val Phe Ala Asp Ile Glu Gln Tyr Gln Phe Leu Tyr

2255

2260

2265

Lys Val Ile Leu Ser Leu Val Ser Thr Arg Gln Glu Glu Asn Pro
 2270 2275 2280

Ser Thr Ser Leu Asp Ser Asn Gly Ala Ala Leu Pro Asp Gly Asn
 2285 2290 2295

Ile Ala Glu Ser Leu Glu Ser Leu Val
 2300 2305

<210> 90.

<211> 1976

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 90

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Cys Arg Leu Asp Trp Ala Asn Gly Tyr Tyr Arg Gln Gln Arg Lys Leu
 20 25 30

Val Glu Glu Ile Gly Trp Ser Tyr Thr Gly Ala Leu Asn Gln Lys Asn
 35 40 45

Trp Gly Lys Lys Tyr Pro Thr Cys Asn Ser Pro Lys Gln Ser Pro Ile
 50 55 60

Asn Ile Asp Glu Asp Leu Thr Gln Val Asn Val Asn Leu Lys Lys Leu
 65 70 75 80

Lys Phe Gln Gly Trp Asp Lys Thr Ser Leu Glu Asn Thr Phe Ile His
 85 90 95

Asn Thr Gly Lys Thr Val Glu Ile Asn Leu Thr Asn Asp Tyr Arg Val
 100 105 110

Ser Gly Gly Val Ser Glu Met Val Phe Lys Ala Ser Lys Ile Thr Phe
 115 120 125

His Trp Gly Lys Cys Asn Met Ser Ser Asp Gly Ser Glu His Ser Leu
 130 135 140

Glu Gly Gln Lys Phe Pro Leu Glu Met Gln Ile Tyr Cys Phe Asp Ala
 145 150 155 160

Asp Arg Phe Ser Ser Phe Glu Glu Ala Val Lys Gly Lys Gly Lys Leu
 165 170 175

Arg Ala Leu Ser Ile Leu Phe Glu Val Gly Thr Glu Glu Asn Leu Asp
 180 185 190

Phe Lys Ala Ile Ile Asp Gly Val Glu Ser Val Ser Arg Phe Gly Lys
 195 200 205

Gln Ala Ala Leu Asp Pro Phe Ile Leu Leu Asn Leu Leu Pro Asn Ser
210 215 220

Thr Asp Lys Tyr Tyr Ile Tyr Asn Gly Ser Leu Thr Ser Pro Pro Cys
225 230 235 240

Thr Asp Thr Val Asp Trp Ile Val Phe Lys Asp Thr Val Ser Ile Ser
245 250 255

Glu Ser Gln Leu Ala Val Phe Cys Glu Val Leu Thr Met Gln Gln Ser
260 265 270

Gly Tyr Val Met Leu Met Asp Tyr Leu Gln Asn Asn Phe Arg Glu Gln
275 280 285

Gln Tyr Lys Phe Ser Arg Gln Val Phe Ser Ser Tyr Thr Gly Lys Glu
290 295 300

Glu Ile His Glu Ala Val Cys Ser Ser Glu Pro Glu Asn Val Gln Ala
305 310 315 320

Asp Pro Glu Asn Tyr Thr Ser Leu Leu Val Thr Trp Glu Arg Pro Arg
325 330 335

Val Val Tyr Asp Thr Met Ile Glu Lys Phe Ala Val Leu Tyr Gln Gln
340 345 350

Leu Asp Gly Glu Asp Gln Thr Lys His Glu Phe Leu Thr Asp Gly Tyr
355 360 365

Gln Asp Leu Gly Ala Ile Leu Asn Asn Leu Leu Pro Asn Met Ser Tyr
370 375 380

Val Leu Gln Ile Val Ala Ile Cys Thr Asn Gly Leu Tyr Gly Lys Tyr
385 390 395 400

Ser Asp Gln Leu Ile Val Asp Met Pro Thr Asp Asn Pro Glu Leu Asp
405 410 415

Leu Phe Pro Glu Leu Ile Gly Thr Glu Glu Ile Ile Lys Glu Glu Glu
420 425 430

Glu Gly Lys Asp Ile Glu Glu Gly Ala Ile Val Asn Pro Gly Arg Asp
435 440 445

Ser Ala Thr Asn Gln Ile Arg Lys Lys Glu Pro Gln Ile Ser Thr Thr
450 455 460

Thr His Tyr Asn Arg Ile Gly Thr Lys Tyr Asn Glu Ala Lys Thr Asn
465 470 475 480

Arg Ser Pro Thr Arg Gly Ser Glu Phe Ser Gly Lys Gly Asp Val Pro
485 490 495

Asn Thr Ser Leu Asn Ser Thr Ser Gln Pro Val Thr Lys Leu Ala Thr
500 505 510

Glu Lys Asp Ile Ser Leu Thr Ser Gln Thr Val Thr Glu Leu Pro Pro

515 520 525

His Thr Val Glu Gly Thr Ser Ala Ser Leu Asn Asp Gly Ser Lys Thr
530 535 540

Val Leu Arg Ser Pro His Met Asn Leu Ser Gly Thr Ala Glu Ser Leu
545 550 555 560

Asn Thr Val Ser Ile Thr Glu Tyr Glu Glu Ser Leu Leu Thr Ser
565 570 575

Phe Lys Leu Asp Thr Gly Ala Glu Asp Ser Ser Gly Ser Ser Pro Ala
580 585 590

Thr Ser Ala Ile Pro Phe Ile Ser Glu Asn Ile Ser Gln Gly Tyr Ile
595 600 605

Phe Ser Ser Glu Asn Pro Glu Thr Ile Thr Tyr Asp Val Leu Ile Pro
610 615 620

Glu Ser Ala Arg Asn Ala Ser Glu Asp Ser Thr Ser Ser Gly Ser Glu
625 630 635 640

Glu Ser Leu Lys Asp Pro Ser Met Glu Gly Asn Val Trp Phe Pro Ser
645 650 655

Ser Thr Asp Ile Thr Ala Gln Pro Asp Val Gly Ser Gly Arg Glu Ser
660 665 670

Phe Leu Gln Thr Asn Tyr Thr Glu Ile Arg Val Asp Glu Ser Glu Lys
675 680 685

Thr Thr Lys Ser Phe Ser Ala Gly Pro Val Met Ser Gln Gly Pro Ser
690 695 700

Val Thr Asp Leu Glu Met Pro His Tyr Ser Thr Phe Ala Tyr Phe Pro
705 710 715 720

Thr Glu Val Thr Pro His Ala Phe Thr Pro Ser Ser Arg Gln Gln Asp
725 730 735

Leu Val Ser Thr Val Asn Val Val Tyr Ser Gln Thr Thr Gln Pro Val
740 745 750

Tyr Asn Gly Glu Thr Pro Leu Gln Pro Ser Tyr Ser Ser Glu Val Phe
755 760 765

Pro Leu Val Thr Pro Leu Leu Asp Asn Gln Ile Leu Asn Thr Thr
770 775 780

Pro Ala Ala Ser Ser Ser Asp Ser Ala Leu His Ala Thr Pro Val Phe
785 790 795 800

Pro Ser Val Asp Val Ser Phe Glu Ser Ile Leu Ser Ser Tyr Asp Gly
805 810 815

Ala Pro Leu Leu Pro Phe Ser Ser Ala Ser Phe Ser Ser Glu Leu Phe
820 825 830

Arg His Ieu His Thr Val Ser Gln Ile Leu Pro Gln Val Thr Ser Ala
835 840 845

Thr Glu Ser Asp Lys Val Pro Leu His Ala Ser Leu Pro Val Ala Gly
850 855 860

Gly Asp Leu Leu Leu Glu Pro Ser Leu Ala Gln Tyr Ser Asp Val Leu
865 870 875 880

Ser Thr Thr His Ala Ala Ser Glu Thr Leu Glu Phe Gly Ser Glu Ser
885 890 895

Gly Val Leu Tyr Lys Thr Leu Met Phe Ser Gln Val Glu Pro Pro Ser
900 905 910

Ser Asp Ala Met Met His Ala Arg Ser Ser Gly Pro Glu Pro Ser Tyr
915 920 925

Ala Leu Ser Asp Asn Glu Gly Ser Gln His Ile Phe Thr Val Ser Tyr
930 935 940

Ser Ser Ala Ile Pro Val His Asp Ser Val Gly Val Thr Tyr Gln Gly
945 950 955 960

Ser Leu Phe Ser Gly Pro Ser His Ile Pro Ile Pro Lys Ser Ser Leu
965 970 975

Ile Thr Pro Thr Ala Ser Leu Leu Gln Pro Thr His Ala Leu Ser Gly
980 985 990

Asp Gly Glu Trp Ser Gly Ala Ser Ser Asp Ser Glu Phe Leu Leu Pro
995 1000 1005

Asp Thr Asp Gly Ieu Thr Ala Leu Asn Ile Ser Ser Pro Val Ser
1010 1015 1020

Val Ala Glu Phe Thr Tyr Thr Thr Ser Val Phe Gly Asp Asp Asn
1025 1030 1035

Lys Ala Leu Ser Lys Ser Glu Ile Ile Tyr Gly Asn Glu Thr Glu
1040 1045 1050

Leu Gln Ile Pro Ser Phe Asn Glu Met Val Tyr Pro Ser Glu Ser
1055 1060 1065

Thr Val Met Pro Asn Met Tyr Asp Asn Val Asn Lys Leu Asn Ala
1070 1075 1080

Ser Leu Gln Glu Thr Ser Val Ser Ile Ser Ser Thr Lys Gly Met
1085 1090 1095

Phe Pro Gly Ser Leu Ala His Thr Thr Thr Lys Val Phe Asp His
1100 1105 1110

Glu Ile Ser Gln Val Pro Glu Asn Asn Phe Ser Val Gln Pro Thr
1115 1120 1125

His Thr Val Ser Gln Ala Ser Gly Asp Thr Ser Leu Lys Pro Val
1130 1135 1140

Leu Ser Ala Asn Ser Glu Pro Ala Ser Ser Asp Pro Ala Ser Ser
1145 1150 1155

Glu Met Leu Ser Pro Ser Thr Gln Leu Leu Phe Tyr Glu Thr Ser
1160 1165 1170

Ala Ser Phe Ser Thr Glu Val Leu Leu Gln Pro Ser Phe Gln Ala
1175 1180 1185

Ser Asp Val Asp Thr Leu Leu Lys Thr Val Leu Pro Ala Val Pro
1190 1195 1200

Ser Asp Pro Ile Leu Val Glu Thr Pro Lys Val Asp Lys Ile Ser
1205 1210 1215

Ser Thr Met Leu His Leu Ile Val Ser Asn Ser Ala Ser Ser Glu
1220 1225 1230

Asn Met Leu His Ser Thr Ser Val Pro Val Phe Asp Val Ser Pro
1235 1240 1245

Thr Ser His Met His Ser Ala Ser Leu Gln Gly Leu Thr Ile Ser
1250 1255 1260

Tyr Ala Ser Glu Lys Tyr Glu Pro Val Leu Leu Lys Ser Glu Ser
1265 1270 1275

Ser His Gln Val Val Pro Ser Leu Tyr Ser Asn Asp Glu Leu Phe
1280 1285 1290

Gln Thr Ala Asn Leu Glu Ile Asn Gln Ala His Pro Pro Lys Gly
1295 1300 1305

Arg His Val Phe Ala Thr Pro Val Leu Ser Ile Asp Glu Pro Leu
1310 1315 1320

Asn Thr Leu Ile Asn Lys Leu Ile His Ser Asp Glu Ile Leu Thr
1325 1330 1335

Ser Thr Lys Ser Ser Val Thr Gly Lys Val Phe Ala Gly Ile Pro
1340 1345 1350

Thr Val Ala Ser Asp Thr Phe Val Ser Thr Asp His Ser Val Pro
1355 1360 1365

Ile Gly Asn Gly His Val Ala Ile Thr Ala Val Ser Pro His Arg
1370 1375 1380

Asp Gly Ser Val Thr Ser Thr Lys Leu Leu Phe Pro Ser Lys Ala
1385 1390 1395

Thr Ser Glu Leu Ser His Ser Ala Lys Ser Asp Ala Gly Leu Val
1400 1405 1410

Gly Gly Gly Glu Asp Gly Asp Thr Asp Asp Asp Gly Asp Asp Asp
 1415 1420 1425

 Asp Asp Arg Asp Ser Asp Gly Leu Ser Ile His Lys Cys Met Ser
 1430 1435 1440

 Cys Ser Ser Tyr Arg Glu Ser Gln Glu Lys Val Met Asn Asp Ser
 1445 1450 1455

 Asp Thr His Glu Asn Ser Leu Met Asp Gln Asn Asn Pro Ile Ser
 1460 1465 1470

 Tyr Ser Leu Ser Glu Asn Ser Glu Glu Asp Asn Arg Val Thr Ser
 1475 1480 1485

 Val Ser Ser Asp Ser Gln Thr Gly Met Asp Arg Ser Pro Gly Lys
 1490 1495 1500

 Ser Pro Ser Ala Asn Gly Leu Ser Gln Lys His Asn Asp Gly Lys
 1505 1510 1515

 Glu Glu Asn Asp Ile Gln Thr Gly Ser Ala Leu Leu Pro Leu Ser
 1520 1525 1530

 Pro Glu Ser Lys Ala Trp Ala Val Leu Thr Ser Asp Glu Glu Ser
 1535 1540 1545

 Gly Ser Gly Gln Gly Thr Ser Asp Ser Leu Asn Glu Asn Glu Thr
 1550 1555 1560

 Ser Thr Asp Phe Ser Phe Ala Asp Thr Asn Glu Lys Asp Ala Asp
 1565 1570 1575

 Gly Ile Leu Ala Ala Gly Asp Ser Glu Ile Thr Pro Gly Phe Pro
 1580 1585 1590

 Gln Ser Pro Thr Ser Ser Val Thr Ser Glu Asn Ser Glu Val Phe
 1595 1600 1605

 His Val Ser Glu Ala Glu Ala Ser Asn Ser Ser His Glu Ser Arg
 1610 1615 1620

 Ile Gly Leu Ala Glu Gly Leu Glu Ser Glu Lys Lys Ala Val Ile
 1625 1630 1635

 Pro Leu Val Ile Val Ser Ala Leu Thr Phe Ile Cys Leu Val Val
 1640 1645 1650

 Leu Val Gly Ile Leu Ile Tyr Trp Arg Lys Cys Phe Gln Thr Ala
 1655 1660 1665

 His Phe Tyr Leu Glu Asp Ser Thr Ser Pro Arg Val Ile Ser Thr
 1670 1675 1680

 Pro Pro Thr Pro Ile Phe Pro Ile Ser Asp Asp Val Gly Ala Ile
 1685 1690 1695

 Pro Ile Lys His Phe Pro Lys His Val Ala Asp Leu His Ala Ser

1700 1705 1710

Ser Gly Phe Thr Glu Glu Phe Glu Thr Leu Lys Glu Phe Tyr Gln
1715 1720 1725

Glu Val Gln Ser Cys Thr Val Asp Leu Gly Ile Thr Ala Asp Ser
1730 1735 1740

Ser Asn His Pro Asp Asn Lys His Lys Asn Arg Tyr Ile Asn Ile
1745 1750 1755

Val Ala Tyr Asp His Ser Arg Val Lys Leu Ala Gln Leu Ala Glu
1760 1765 1770

Lys Asp Gly Lys Leu Thr Asp Tyr Ile Asn Ala Asn Tyr Val Asp
1775 1780 1785

Gly Tyr Asn Arg Pro Lys Ala Tyr Ile Ala Ala Gln Gly Pro Leu
1790 1795 1800

Lys Ser Thr Ala Glu Asp Phe Trp Arg Met Ile Trp Glu His Asn
1805 1810 1815

Val Glu Val Ile Val Met Ile Thr Asn Leu Val Glu Lys Gly Arg
1820 1825 1830

Arg Lys Cys Asp Gln Tyr Trp Pro Ala Asp Gly Ser Glu Glu Tyr
1835 1840 1845

Gly Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val Leu Ala Tyr
1850 1855 1860

Tyr Thr Val Arg Asn Phe Thr Leu Arg Asn Thr Lys Ile Lys Lys
1865 1870 1875

Gly Ser Gln Lys Gly Arg Pro Ser Gly Arg Val Val Thr Gln Tyr
1880 1885 1890

His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu Tyr Ser Leu
1895 1900 1905

Pro Val Leu Thr Phe Val Arg Lys Ala Ala Tyr Ala Lys Arg His
1910 1915 1920

Ala Val Gly Pro Val Val Val His Cys Arg Ser Asn Met Ser Ser
1925 1930 1935

Phe Met Ile His Trp Leu Arg Pro Tyr Leu Val Lys Lys Leu Arg
1940 1945 1950

Cys Trp Thr Val Ile Phe Met Pro Met Leu Met His Ser Ser Phe
1955 1960 1965

Leu Asp Gln Gln Ala Lys Gln Ser
1970 1975

<210> 91
<211> 1758

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 91

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Glu Ser Lys Ala Ser Ser His Ser Val Ser Ile Gln Trp Arg Ile Leu
35 40 45

Gly Ser Pro Cys Asn Phe Ser Leu Ile Tyr Ser Ser Asp Thr Leu Gly
50 55 60

Ala Ala Leu Cys Pro Thr Phe Arg Ile Asp Asn Thr Thr Tyr Gly Cys
65 70 75 80

Asn Leu Gln Asp Leu Gln Ala Gly Thr Ile Tyr Asn Phe Lys Ile Ile
85 90 95

Ser Leu Asp Glu Glu Arg Thr Val Val Leu Gln Thr Asp Pro Leu Pro
100 105 110

Pro Ala Arg Phe Gly Val Ser Lys Glu Lys Thr Thr Ser Thr Gly Leu
115 120 125

His Val Trp Trp Thr Pro Ser Ser Gly Lys Val Thr Ser Tyr Glu Val
130 135 140

Gln Leu Phe Asp Glu Asn Asn Gln Lys Ile Gln Gly Val Gln Ile Gln
145 150 155 160

Glu Ser Thr Ser Trp Asn Glu Tyr Thr Phe Phe Asn Leu Thr Ala Gly
165 170 175

Ser Lys Tyr Asn Ile Ala Ile Thr Ala Val Ser Gly Gly Lys Arg Ser
180 185 190

Phe Ser Val Tyr Thr Asn Gly Ser Thr Val Pro Ser Pro Val Lys Asp
195 200 205

Ile Gly Ile Ser Thr Lys Ala Asn Ser Leu Leu Ile Ser Trp Ser His
210 215 220

Gly Ser Gly Asn Val Glu Arg Tyr Arg Leu Met Leu Met Asp Lys Gly
225 230 235 240

Ile Leu Val His Gly Gly Val Val Asp Lys His Ala Thr Ser Tyr Ala
245 250 255

Phe His Gly Leu Ser Pro Gly Tyr Leu Tyr Asn Leu Thr Val Met Thr
260 265 270

Glu Ala Ala Gly Leu Gln Asn Tyr Arg Trp Lys Leu Val Arg Thr Ala

275 280 285

Pro Met Glu Val Ser Asn Leu Lys Val Thr Asn Asp Gly Ser Leu Thr
290 295 300

Ser Leu Lys Val Lys Trp Gln Arg Pro Pro Gly Asn Val Asp Ser Tyr
305 310 315 320

Asn Ile Thr Leu Ser His Lys Gly Thr Ile Lys Glu Ser Arg Val Leu
325 330 335

Ala Pro Trp Ile Thr Glu Thr His Phe Lys Glu Leu Val Pro Gly Arg
340 345 350

Leu Tyr Gln Val Thr Val Ser Cys Val Ser Gly Glu Leu Ser Ala Gln
355 360 365

Lys Met Ala Val Gly Arg Thr Phe Pro Asp Lys Val Ala Asn Leu Glu
370 375 380

Ala Asn Asn Asn Gly Arg Met Arg Ser Leu Val Val Ser Trp Ser Pro
385 390 395 400

Pro Ala Gly Asp Trp Glu Gln Tyr Arg Ile Leu Leu Phe Asn Asp Ser
405 410 415

Val Val Leu Leu Asn Ile Thr Val Gly Lys Glu Glu Thr Gln Tyr Val
420 425 430

Met Asp Asp Thr Gly Leu Val Pro Gly Arg Gln Tyr Glu Val Glu Val
435 440 445

Ile Val Glu Ser Gly Asn Leu Lys Asn Ser Glu Arg Cys Gln Gly Arg
450 455 460

Thr Val Pro Leu Ala Val Leu Gln Leu Arg Val Lys His Ala Asn Glu
465 470 475 480

Thr Ser Leu Ser Ile Met Trp Gln Thr Pro Val Ala Glu Trp Glu Lys
485 490 495

Tyr Ile Ile Ser Leu Ala Asp Arg Asp Leu Leu Leu Ile His Lys Ser
500 505 510

Leu Ser Lys Asp Ala Lys Glu Phe Thr Phe Thr Asp Leu Val Pro Gly
515 520 525

Arg Lys Tyr Met Ala Thr Val Thr Ser Ile Ser Gly Asp Leu Lys Asn
530 535 540

Ser Ser Ser Val Lys Gly Arg Thr Val Pro Ala Gln Val Thr Asp Leu
545 550 555 560

His Val Ala Asn Gln Gly Met Thr Ser Ser Leu Phe Thr Asn Trp Thr
565 570 575

Gln Ala Gln Gly Asp Val Glu Phe Tyr Gln Val Leu Leu Ile His Glu
580 585 590

Asn Val Val Ile Lys Asn Glu Ser Ile Ser Ser Glu Thr Ser Arg Tyr
595 600 605

Ser Phe His Ser Leu Lys Ser Gly Ser Leu Tyr Ser Val Val Val Thr
610 615 620

Thr Val Ser Gly Gly Ile Ser Ser Arg Gln Val Val Val Glu Gly Arg
625 630 635 640

Thr Val Pro Ser Ser Val Ser Gly Val Thr Val Asn Asn Ser Gly Arg
645 650 655

Asn Asp Tyr Leu Ser Val Ser Trp Leu Val Ala Pro Gly Asp Val Asp
660 665 670

Asn Tyr Glu Val Thr Ile Ser His Asp Gly Lys Val Val Gln Ser Leu
675 680 685

Val Ile Ala Lys Ser Val Arg Glu Cys Ser Phe Ser Ser Leu Thr Pro
690 695 700

Gly Arg Leu Tyr Thr Val Thr Ile Thr Arg Ser Gly Lys Tyr Glu
705 710 715 720

Asn His Ser Phe Ser Gln Glu Arg Thr Val Pro Asp Lys Val Gln Gly
725 730 735

Val Ser Val Ser Asn Ser Ala Arg Ser Asp Tyr Leu Arg Val Ser Trp
740 745 750

Val His Ala Thr Gly Asp Phe Asp His Tyr Glu Val Thr Ile Lys Asn
755 760 765

Lys Asn Asn Phe Ile Gln Thr Lys Ser Ile Pro Lys Ser Glu Asn Glu
770 775 780

Cys Val Phe Val Gln Leu Val Pro Gly Arg Leu Tyr Ser Val Thr Val
785 790 795 800

Thr Thr Lys Ser Gly Gln Tyr Glu Ala Asn Glu Gln Gly Asn Gly Arg
805 810 815

Thr Ile Pro Glu Pro Val Lys Asp Leu Thr Leu Arg Asn Arg Ser Thr
820 825 830

Glu Asp Leu His Val Thr Trp Ser Gly Ala Asn Gly Asp Val Asp Gln
835 840 845

Tyr Glu Ile Gln Leu Leu Phe Asn Asp Met Lys Val Phe Pro Pro Phe
850 855 860

His Leu Val Asn Thr Ala Thr Glu Tyr Arg Phe Thr Ser Leu Thr Pro
865 870 875 880

Gly Arg Gln Tyr Lys Ile Leu Val Leu Thr Ile Ser Gly Asp Val Gln
885 890 895

Gln Ser Ala Phe Ile Glu Gly Phe Thr Val Pro Ser Ala Val Lys Asn
900 905 910

Ile His Ile Ser Pro Asn Gly Ala Thr Asp Ser Leu Thr Val Asn Trp
915 920 925

Thr Pro Gly Gly Asp Val Asp Ser Tyr Thr Val Ser Ala Phe Arg
930 935 940

His Ser Gln Lys Val Asp Ser Gln Thr Ile Pro Lys His Val Phe Glu
945 950 955 960

His Thr Phe His Arg Leu Glu Ala Gly Glu Gln Tyr Gln Ile Met Ile
965 970 975

Ala Ser Val Ser Gly Ser Leu Lys Asn Gln Ile Asn Val Val Gly Arg
980 985 990

Thr Val Pro Ala Ser Val Gln Gly Val Ile Ala Asp Asn Ala Tyr Ser
995 1000 1005

Ser Tyr Ser Leu Ile Val Ser Trp Gln Lys Ala Ala Gly Val Ala
1010 1015 1020

Glu Arg Tyr Asp Ile Leu Leu Leu Thr Glu Asn Gly Ile Leu Leu
1025 1030 1035

Arg Asn Thr Ser Glu Pro Ala Thr Thr Lys Gln His Lys Phe Glu
1040 1045 1050

Asp Leu Thr Pro Gly Lys Lys Tyr Lys Ile Gln Ile Leu Thr Val
1055 1060 1065

Ser Gly Gly Ile Phe Ser Lys Glu Ala Gln Thr Glu Gly Arg Thr
1070 1075 1080

Val Pro Ala Ala Val Thr Asp Leu Arg Ile Thr Glu Asn Ser Thr
1085 1090 1095

Arg His Leu Ser Phe Arg Trp Thr Ala Ser Glu Gly Glu Leu Ser
1100 1105 1110

Trp Tyr Asn Ile Phe Leu Tyr Asn Pro Asp Gly Asn Leu Gln Glu
1115 1120 1125

Arg Ala Gln Val Asp Pro Leu Val Gln Ser Phe Ser Phe Gln Asn
1130 1135 1140

Leu Leu Gln Gly Arg Met Tyr Lys Met Val Ile Val Thr His Ser
1145 1150 1155

Gly Glu Leu Ser Asn Glu Ser Phe Ile Phe Gly Arg Thr Val Pro
1160 1165 1170

Ala Ser Val Ser His Leu Arg Gly Ser Asn Arg Asn Thr Thr Asp
1175 1180 1185

Ser Leu Trp Phe Asn Trp Ser Pro Ala Ser Gly Asp Phe Asp Phe
1190 1195 1200

Tyr Glu Leu Ile Leu Tyr Asn Pro Asn Gly Thr Lys Lys Glu Asn
1205 1210 1215

Trp Lys Asp Lys Asp Leu Thr Glu Trp Arg Phe Gln Gly Leu Val
1220 1225 1230

Pro Gly Arg Lys Tyr Val Leu Trp Val Val Thr His Ser Gly Asp
1235 1240 1245

Leu Ser Asn Lys Val Thr Ala Glu Ser Arg Thr Ala Pro Ser Pro
1250 1255 1260

Pro Ser Leu Met Ser Phe Ala Asp Ile Ala Asn Thr Ser Leu Ala
1265 1270 1275

Ile Thr Trp Lys Gly Pro Pro Asp Trp Thr Asp Tyr Asn Asp Phe
1280 1285 1290

Glu Leu Gln Trp Leu Pro Arg Asp Ala Leu Thr Val Phe Asn Pro
1295 1300 1305

Tyr Asn Asn Arg Lys Ser Glu Gly Arg Ile Val Tyr Gly Leu Arg
1310 1315 1320

Pro Gly Arg Ser Tyr Gln Phe Asp Val Lys Thr Val Ser Gly Asp
1325 1330 1335

Ser Trp Lys Thr Tyr Ser Lys Pro Ile Phe Gly Ser Val Arg Thr
1340 1345 1350

Lys Pro Asp Lys Ile Gln Asn Leu His Cys Arg Pro Gln Asn Ser
1355 1360 1365

Thr Ala Ile Ala Cys Ser Trp Ile Pro Pro Asp Ser Asp Phe Asp
1370 1375 1380

Gly Tyr Ser Ile Glu Cys Arg Lys Met Asp Thr Gln Glu Val Glu
1385 1390 1395

Phe Ser Arg Lys Leu Glu Lys Glu Lys Ser Leu Leu Asn Ile Met
1400 1405 1410

Met Leu Val Pro His Lys Arg Tyr Leu Val Ser Ile Lys Val Gln
1415 1420 1425

Ser Ala Gly Met Thr Ser Glu Val Val Glu Asp Ser Thr Ile Thr
1430 1435 1440

Met Ile Asp Arg Pro Pro Pro Pro Pro His Ile Arg Val Asn
1445 1450 1455

Glu Lys Asp Val Leu Ile Ser Lys Ser Ser Ile Asn Phe Thr Val
1460 1465 1470

Asn Cys Ser Trp Phe Ser Asp Thr Asn Gly Ala Val Lys Tyr Phe

1475	1480	1485
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Thr Val Val Val Arg Glu Ala Asp Gly Ser Asp Glu Leu Lys Pro
 1490 1495 1500

Glu Gln Gln His Pro Leu Pro Ser Tyr Leu Glu Tyr Arg His Asn
 1505 1510 1515

Ala Ser Ile Arg Val Tyr Gln Thr Asn Tyr Phe Ala Ser Lys Cys
 1520 1525 1530

Ala Glu Asn Pro Asn Ser Asn Ser Lys Ser Phe Asn Ile Lys Leu
 1535 1540 1545

Gly Ala Glu Met Glu Ser Leu Gly Gly Lys Arg Asp Pro Thr Gln
 1550 1555 1560

Gln Lys Phe Cys Asp Gly Pro Leu Lys Pro His Thr Ala Tyr Arg
 1565 1570 1575

Ile Ser Ile Arg Ala Phe Thr Gln Leu Phe Asp Glu Asp Leu Lys
 1580 1585 1590

Glu Phe Thr Lys Pro Leu Tyr Ser Asp Thr Phe Phe Ser Leu Pro
 1595 1600 1605

Ile Thr Thr Glu Ser Glu Pro Leu Phe Gly Ala Ile Glu Gly Val
 1610 1615 1620

Ser Ala Gly Leu Phe Leu Ile Gly Met Leu Val Ala Val Val Ala
 1625 1630 1635

Leu Leu Ile Cys Arg Gln Lys Val Ser His Gly Arg Glu Arg Pro
 1640 1645 1650

Ser Ala Arg Leu Ser Ile Arg Arg Asp Arg Pro Leu Ser Val His
 1655 1660 1665

Leu Asn Leu Gly Gln Lys Gly Asn Arg Lys Thr Ser Cys Pro Ile
 1670 1675 1680

Lys Ile Asn Gln Phe Glu Gly His Phe Met Lys Leu Gln Ala Asp
 1685 1690 1695

Ser Asn Tyr Leu Leu Ser Lys Glu Tyr Glu Glu Leu Lys Asp Val
 1700 1705 1710

Gly Arg Asn Gln Ser Cys Asp Ile Ala Leu Leu Pro Glu Asn Arg
 1715 1720 1725

Gly Lys Asn Arg Tyr Asn Asn Ile Leu Pro Trp Gln Gln Leu Gln
 1730 1735 1740

Lys Arg Ile His Cys His Ser Gly Thr Ala Ser Trp His Gln Gly
 1745 1750 1755

<210> 92
 <211> 286

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 92

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu
1 5 10 15

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg
20 25 30

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
35 40 45

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
50 55 60

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser
65 70 75 80

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
85 90 95

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val
100 105 110

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys
115 120 125

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
130 135 140

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr
145 150 155 160

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg
165 170 175

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
180 185 190

Leu Arg Asn Asp Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro
195 200 205

Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe
210 215 220

Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Tyr Val
225 230 235 240

Ala Arg Glu Arg Glu Arg Val Ser Arg Ser Val Ile Val Ala Cys Ile
245 250 255

Asn Thr Val Thr Phe Val His Trp Leu Val Thr Val His Val Cys Phe
260 265 270

Ile Asn Glu Ala Ala Leu Asn Lys Phe Ile Phe Cys Leu Glu

275 280 285

<210> 93
<211> 423
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 93

Met Arg Gly Ala Arg Gly Ala Trp Asp Phe Leu Cys Val Leu Leu
1 5 10 15

Leu Leu Arg Val Gln Thr Gly Ser Ser Gln Pro Ser Val Ser Pro Gly
20 25 30

Glu Pro Ser Pro Pro Ser Ile His Pro Gly Lys Ser Asp Leu Ile Val
35 40 45

Arg Val Gly Asp Glu Ile Arg Leu Leu Cys Thr Asp Pro Gly Phe Val
50 55 60

Lys Trp Thr Phe Glu Ile Leu Asp Glu Thr Asn Glu Asn Lys Gln Asn
65 70 75 80

Glu Trp Ile Thr Glu Ala Glu Ala Thr Asn Thr Gly Lys Tyr Thr
85 90 95

Cys Thr Asn Lys His Gly Leu Ser Asn Ser Ile Tyr Val Phe Val Arg
100 105 110

Asp Pro Ala Lys Leu Phe Leu Val Asp Arg Ser Leu Tyr Gly Lys Glu
115 120 125

Asp Asn Asp Thr Leu Val Arg Cys Pro Leu Thr Asp Pro Glu Val Thr
130 135 140

Asn Tyr Ser Leu Lys Gly Cys Gln Gly Lys Pro Leu Pro Lys Asp Leu
145 150 155 160

Arg Phe Ile Pro Asp Pro Lys Ala Gly Ile Met Ile Lys Ser Val Lys
165 170 175

Arg Ala Tyr His Arg Leu Cys Leu His Cys Ser Val Asp Gln Glu Gly
180 185 190

Lys Ser Val Leu Ser Glu Lys Phe Ile Leu Lys Val Arg Pro Ala Phe
195 200 205

Lys Ala Val Pro Val Val Ser Val Ser Iys Ala Ser Tyr Leu Leu Arg
210 215 220

Glu Gly Glu Glu Phe Thr Val Thr Cys Thr Ile Lys Asp Val Ser Ser
225 230 235 240

Ser Val Tyr Ser Thr Trp Lys Arg Glu Asn Ser Gln Thr Lys Leu Gln
245 250 255

Glu Lys Tyr Asn Ser Trp His His Gly Asp Phe Asn Tyr Glu Arg Gln
 260 265 270

Ala Thr Leu Thr Ile Ser Ser Ala Arg Val Asn Asp Ser Gly Val Phe
 275 280 285

Met Cys Tyr Ala Asn Asn Thr Phe Gly Ser Ala Asn Val Thr Thr Thr
 290 295 300

Leu Glu Val Val Asp Lys Gly Phe Ile Asn Ile Phe Pro Met Ile Asn
 305 310 315 320

Thr Thr Val Phe Val Asn Asp Gly Glu Asn Val Asp Leu Ile Val Glu
 325 330 335

Tyr Glu Ala Phe Pro Lys Pro Glu His Gln Gln Trp Ile Tyr Met Asn
 340 345 350

Arg Thr Phe Thr Asp Lys Trp Glu Asp Tyr Pro Lys Ser Glu Asn Glu
 355 360 365

Ser Asn Ile Arg Tyr Val Ser Glu Leu His Leu Thr Arg Leu Lys Gly
 370 375 380

Thr Glu Gly Gly Thr Tyr Thr Phe Leu Val Ser Asn Ser Asp Val Asn
 385 390 395 400

Ala Ala Ile Ala Phe Asn Val Tyr Val Asn Asn Ala Leu Leu Tyr
 405 410 415

Cys Gln Trp Met Cys Arg His
 420

<210> 94

<211> 673

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 94

Met Arg Gly Ala Arg Gly Ala Trp Asp Phe Leu Cys Val Leu Leu
 1 5 10 15

Leu Leu Arg Val Gln Thr Gly Ser Ser Gln Pro Ser Val Ser Pro Gly
 20 25 30

Glu Pro Ser Pro Pro Ser Ile His Pro Gly Lys Ser Asp Leu Ile Val
 35 40 45

Arg Val Gly Asp Glu Ile Arg Leu Leu Cys Thr Asp Pro Gly Phe Val
 50 55 60

Lys Trp Thr Phe Glu Ile Leu Asp Glu Thr Asn Glu Asn Lys Gln Asn
 65 70 75 80

Glu Trp Ile Thr Glu Lys Ala Glu Ala Thr Asn Thr Gly Lys Tyr Thr
 85 90 95

Cys Thr Asn Lys His Gly Leu Ser Asn Ser Ile Tyr Val Phe Val Arg
100 105 110

Asp Pro Ala Lys Leu Phe Leu Val Asp Arg Ser Leu Tyr Gly Lys Glu
115 120 125

Asp Asn Asp Thr Leu Val Arg Cys Pro Leu Thr Asp Pro Glu Val Thr
130 135 140

Asn Tyr Ser Leu Lys Gly Cys Gln Gly Lys Pro Leu Pro Lys Asp Leu
145 150 155 160

Arg Phe Ile Pro Asp Pro Lys Ala Gly Ile Met Ile Lys Ser Val Lys
165 170 175

Arg Ala Tyr His Arg Leu Cys Leu His Cys Ser Val Asp Gln Glu Gly
180 185 190

Lys Ser Val Leu Ser Glu Lys Phe Ile Leu Lys Val Arg Pro Ala Phe
195 200 205

Lys Ala Val Pro Val Val Ser Val Ser Lys Ala Ser Tyr Leu Leu Arg
210 215 220

Glu Gly Glu Glu Phe Thr Val Thr Cys Thr Ile Lys Asp Val Ser Ser
225 230 235 240

Ser Val Tyr Ser Thr Trp Lys Arg Glu Asn Ser Gln Thr Lys Leu Gln
245 250 255

Glu Lys Tyr Asn Ser Trp His His Gly Asp Phe Asn Tyr Glu Arg Gln
260 265 270

Ala Thr Leu Thr Ile Ser Ser Ala Arg Val Asn Asp Ser Gly Val Phe
275 280 285

Met Cys Tyr Ala Asn Asn Thr Phe Gly Ser Ala Asn Val Thr Thr Thr
290 295 300

Leu Glu Val Val Asp Lys Gly Phe Ile Asn Ile Phe Pro Met Ile Asn
305 310 315 320

Thr Thr Val Phe Val Asn Asp Gly Glu Asn Val Asp Leu Ile Val Glu
325 330 335

Tyr Glu Ala Phe Pro Lys Pro Glu His Gln Gln Trp Ile Tyr Met Asn
340 345 350

Arg Thr Phe Thr Asp Lys Trp Glu Asp Tyr Pro Lys Ser Glu Asn Glu
355 360 365

Ser Asn Ile Arg Tyr Val Ser Glu Leu His Leu Thr Arg Leu Lys Gly
370 375 380

Thr Glu Gly Gly Thr Tyr Thr Phe Leu Val Ser Asn Ser Asp Val Asn
385 390 395 400

Ala Ala Ile Ala Phe Asn Val Tyr Val Asn Thr Lys Pro Glu Ile Leu
405 410 415

Thr Tyr Asp Arg Leu Val Asn Gly Met Leu Gln Cys Val Ala Ala Gly
420 425 430

Phe Pro Glu Pro Thr Ile Asp Trp Tyr Phe Cys Pro Gly Thr Glu Gln
435 440 445

Arg Cys Ser Ala Ser Val Leu Pro Val Asp Val Gln Thr Leu Asn Ser
450 455 460

Ser Gly Pro Pro Phe Gly Lys Leu Val Val Gln Ser Ser Ile Asp Ser
465 470 475 480

Ser Ala Phe Lys His Asn Gly Thr Val Glu Cys Lys Ala Tyr Asn Asp
485 490 495

Val Gly Lys Thr Ser Ala Tyr Phe Asn Phe Ala Phe Lys Gly Asn Asn
500 505 510

Lys Glu Gln Ile His Pro His Thr Leu Phe Thr Pro Leu Leu Ile Gly
515 520 525

Phe Val Ile Val Ala Gly Met Met Cys Ile Ile Val Met Ile Leu Thr
530 535 540

Tyr Lys Tyr Leu Gln Lys Pro Met Tyr Glu Val Gln Trp Lys Val Val
545 550 555 560

Glu Glu Ile Asn Gly Asn Asn Tyr Val Tyr Ile Asp Pro Thr Gln Leu
565 570 575

Pro Tyr Asp His Lys Trp Glu Phe Pro Arg Asn Arg Leu Ser Phe Gly
580 585 590

Lys Thr Leu Gly Ala Gly Ala Phe Gly Lys Val Val Glu Ala Thr Ala
595 600 605

Tyr Gly Leu Ile Lys Ser Asp Ala Ala Met Thr Val Ala Val Lys Met
610 615 620

Leu Lys Pro Ser Ala His Leu Thr Glu Arg Glu Ala Leu Met Ser Glu
625 630 635 640

Leu Lys Val Leu Ser Tyr Leu Gly Asn His Met Asn Ile Val Asn Leu
645 650 655

Leu Gly Ala Cys Thr Ile Gly Ala Ala Ile Val Leu Met Ser Thr Trp
660 665 670

Thr

- <210> 95
- <211> 225
- <212> PRT
- <213> Artificial sequence

Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
 20 25 30

Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
 35 40 45

Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
 50 55 60

Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
 65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
 85 90 95

Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
 100 105 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
 115 120 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Gly Pro Pro Cys
 130 135 140

His Glu Val Cys Lys Gly Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys
 145 150 155 160

Gln Thr Leu Thr Lys Thr Ile Cys Ala Pro Gln Cys Asn Gly His Cys
 165 170 175

Phe Gly Pro Asn Pro Asn Gln Cys Cys His Asp Glu Cys Ala Gly Gly
 180 185 190

Cys Ser Gly Pro Gln Asp Thr Asp Cys Phe Ala Cys Arg His Phe Asn
 195 200 205

Asp Ser Gly Ala Cys Val Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn
 210 215 220

Lys Leu Thr Phe Gln Leu Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr
 225 230 235 240

Gly Gly Val Cys Val Ala Ser Cys Pro His Asn Phe Val Val Asp Gln
 245 250 255

Thr Ser Cys Val Arg Ala Cys Pro Pro Asp Lys Met Glu Val Asp Lys
 260 265 270

Asn Gly Leu Lys Met Cys Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala
 275 280 285

Cys Glu Gly Thr Gly Ser Gly Ser Arg Phe Gln Thr Val Asp Ser Ser
 290 295 300

Asn Ile Asp Gly Phe Val Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp
 305 310 315 320

Phe Leu Ile Thr Gly Leu Asn Gly Asp Pro Trp His Lys Ile Pro Ala
 325 330 335

Leu Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr
 340 345 350

Gly Tyr Leu Asn Ile Gln Ser Trp Pro Pro His Met His Asn Phe Ser
 355 360 365

Val Phe Ser Asn Leu Thr Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg
 370 375 380

Gly Phe Ser Leu Leu Ile Met Lys Asn Leu Asn Val Thr Ser Leu Gly
 385 390 395 400

Phe Arg Ser Leu Lys Glu Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala
 405 410 415

Asn Arg Gln Leu Cys Tyr His His Ser Leu Asn Trp Thr Lys Val Leu
 420 425 430

Arg Gly Pro Thr Glu Glu Arg Leu Asp Ile Lys His Asn Arg Pro Arg
 435 440 445

Arg Asp Cys Val Ala Glu Gly Lys Val Cys Asp Pro Leu Cys Ser Ser
 450 455 460

Gly Gly Cys Trp Gly Pro Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn
 465 470 475 480

Tyr Ser Arg Gly Gly Val Cys Val Thr His Cys Asn Phe Leu Asn Gly
 485 490 495

Glu Pro Arg Glu Phe Ala His Glu Ala Glu Cys Phe Ser Cys His Pro
 500 505 510

Glu Cys Gln Pro Met Glu Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser
 515 520 525

Asp Thr Cys Ala Gln Cys Ala His Phe Arg Asp Gly Pro His Cys Val
 530 535 540

Ser Ser Cys Pro His Gly Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys
 545 550 555 560

Tyr Pro Asp Val Glu Asn Glu Cys Arg Pro Cys His Glu Asn Cys Thr
 565 570 575

Gln Gly Cys Lys Gly Pro Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu
 580 585 590

Val Leu Ile Gly Lys Thr His Leu Thr Met Ala Leu Thr Val Ile Ala
 595 600 605

Gly Leu Val Val Ile Phe Met Met Leu Gly Gly Thr Phe Leu Tyr Trp
 610 615 620

Arg Gly Arg Arg Ile Gln Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu
625 630 635 640

Arg Gly Glu Ser Ile Glu Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys
645 650 655

Val Leu Ala Arg Ile Phe Lys Glu Thr Glu Leu Arg Lys Leu Lys Val
660 665 670

Leu Gly Ser Gly Val Phe Gly Thr Val His Lys Gly Val Trp Ile Pro
675 680 685

Glu Gly Glu Ser Ile Lys Ile Pro Val Cys Ile Lys Val Ile Glu Asp
690 695 700

Lys Ser Gly Arg Gln Ser Phe Gln Ala Val Thr Asp His Met Leu Ala
705 710 715 720

Ile Gly Ser Leu Asp His Ala His Ile Val Arg Leu Leu Gly Leu Cys
725 730 735

Pro Gly Ser Ser Leu Gln Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser
740 745 750

Leu Leu Asp His Val Arg Gln His Arg Gly Ala Leu Gly Pro Gln Leu
755 760 765

Leu Leu Asn Trp Gly Val Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu
770 775 780

Glu His Gly Met Val His Arg Asn Leu Ala Ala Arg Asn Val Leu Leu
785 790 795 800

Lys Ser Pro Ser Gln Val Gln Val Ala Asp Phe Gly Val Ala Asp Leu
805 810 815

Leu Pro Pro Asp Asp Lys Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro
820 825 830

Ile Lys Trp Met Ala Leu Glu Ser Ile His Phe Gly Lys Tyr Thr His
835 840 845

Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr
850 855 860 865

Phe Gly Ala Glu Pro Tyr Ala Gly Leu Arg Leu Ala Glu Val Pro Asp
865 870 875 880

Leu Leu Glu Lys Gly Glu Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile
885 890 895

Asp Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp Glu Asn Ile
900 905 910

Arg Pro Thr Phe Lys Glu Leu Ala Asn Glu Phe Thr Arg Met Ala Arg
915 920 925

Asp Pro Pro Arg Tyr Leu Val Ile Lys Arg Glu Ser Gly Pro Gly Ile

930 . . . 935 . . . 940

Ala Pro Gly Pro Glu Pro His Gly Leu Thr Asn Lys Lys Leu Glu Glu
945 950 955 960

Val Glu Leu Glu Pro Glu Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu
965 970 975

Glu Asp Asn Leu Ala Thr Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro
980 985 990

Val Gly Thr Leu Asn Arg Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro
995 1000 1005

Ser Ser Gly Tyr Met Pro Met Asn Gln Gly Asn Leu Gly Glu Ser
1010 1015 1020

Cys Gln Glu Ser Ala Val Ser Gly Ser Ser Glu Arg Cys Pro Arg
1025 1030 1035

Pro Val Ser Leu His Pro Met Pro Arg Gly Cys Leu Ala Ser Glu
1040 1045 1050

Ser Ser Glu Gly His Val Thr Gly Ser Glu Ala Glu Leu Gln Glu
1055 1060 1065

Lys Val Ser Met Cys Arg Ser Arg Ser Arg Ser Pro Arg
1070 1075 1080

Pro Arg Gly Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu Leu
1085 1090 1095

Thr Pro Val Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp
1100 1105 1110

Val Asn Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro
1115 1120 1125

Ser Ser Arg Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val
1130 1135 1140

Leu Gly Thr Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met
1145 1150 1155

Asn Arg Arg Arg Arg His Ser Pro Pro His Pro Pro Arg Pro Ser
1160 1165 1170

Ser Leu Glu Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp
1175 1180 1185

Leu Ser Ala Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu His Pro
1190 1195 1200

Val Pro Ile Met Pro Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr
1205 1210 1215

Glu Tyr Met Asn Arg Gln Arg Asp Gly Gly Gly Pro Gly Gly Asp
1220 1225 1230

Tyr Ala Ala Met Gly Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu
 1235 1240 1245

Glu Met Arg Ala Phe Gln Gly Pro Gly His Gln Ala Pro His Val
 1250 1255 1260

His Tyr Ala Arg Leu Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp
 1265 1270 1275

Ser Ala Phe Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe Pro
 1280 1285 1290

Lys Ala Asn Ala Gln Arg Thr
 1295 1300

<210> 97

<211> 569

<212> PRT

<213> Artificial séquence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 97

Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu
 1 5 10 15

Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
 20 25 30

Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
 35 40 45

Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
 50 55 60

Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
 65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
 85 90 95

Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
 100 105 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
 115 120 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
 130 135 140

Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
 145 150 155 160

Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
 165 170 175

Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly

180	185	190
Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr		
195	200	205
Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn		
210	215	220
Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp		
225	230	235
Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val		
245	250	255
Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu		
260	265	270
Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala		
275	280	285
Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala		
290	295	300
Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys		
305	310	315
320		
Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser		
325	330	335
Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val		
340	345	350
Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu		
355	360	365
Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu		
370	375	380
Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln		
385	390	395
400		
Ser Trp Pro Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr		
405	410	415
Thr Ile Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile		
420	425	430
Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu		
435	440	445
Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr		
450	455	460
His His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu		
465	470	475
480		
Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu		
485	490	495

Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro
500 505 510

Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val
515 520 525

Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala
530 535 540

His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu
545 550 555 560

Gly Thr Ala Thr Cys Asn Gly Ser Val
565

<210> 98

<211> 13'02

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 98

Met Arg Ala Asn Asp Ala Leu Gin Val Leu Gly Leu Leu Phe Ser Leu
1 5 10 15.

Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
20 25 30

Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
35 40 45

Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60

Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
65 70 75 80

Arg Glu Val Thr Gly Tyr Val Ile Val Ala Met Asn Glu Phe Ser Thr
85 90 95

Leu Pro Ile Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
100 105 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
115 120 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
130 135 140

Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
145 150 155 160

Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
165 170 175

Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly

180

185

190

Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
195 200 205

Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
210 215 220

Gln Cys Cys His Asp Glu Cys Ala Gly Cys Ser Gly Pro Gln Asp
225 230 235 240

Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
245 250 255

Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
260 265 270

Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
275 280 285

Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
290 295 300

Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
305 310 315 320

Glu Pro Cys Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser
325 330 335

Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val
340 345 350

Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
355 360 365

Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu
370 375 380

Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln
385 390 395 400

Ser Trp Pro Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr
405 410 415

Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Ile
420 425 430

Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu
435 440 445

Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr
450 455 460

His His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu
465 470 475 480

Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu
485 490 495

Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro
500 505 510

Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val
515 520 525

Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala
530 535 540

His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu
545 550 555 560

Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys
565 570 575

Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly
580 585 590

Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn
595 600 605

Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro
610 615 620

Glu Leu Gln Asp Cys Leu Gly Gln Thr Ile Val Leu Ile Gly Lys Thr
625 630 635 640

His Leu Thr Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe
645 650 655

Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln
660 665 670

Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Gly Val Trp
675 680 685

Ile Pro Glu Gly Glu Ser Ile Lys Ile Pro Val Cys Ile Lys Val Ile
690 695 700

Glu Asp Lys Ser Gly Arg Gln Ser Phe Gln Ala Val Thr Asp His Met
705 710 715 720

Leu Ala Ile Gly Ser Leu Asp His Ala His Ile Val Arg Leu Leu Gly
725 730 735

Leu Cys Pro Gly Ser Ser Leu Gln Leu Val Thr Gln Tyr Leu Pro Leu
740 745 750

Gly Ser Leu Leu Asp His Val Arg Gln His Arg Gly Ala Leu Gly Pro
755 760 765

Gln Leu Leu Leu Asn Trp Gly Val Gln Ile Ala Lys Gly Met Tyr Tyr
770 775 780

Leu Glu Glu His Gly Met Val His Arg Asn Leu Ala Ala Arg Asn Val
785 790 795 800

Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala Asp Phe Gly Val Ala
805 810 815

Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu Tyr Ser Glu Ala Lys
820 825 830

Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile His Phe Gly Lys Tyr
835 840 845

Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu
850 855 860

Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu Arg Leu Ala Glu Val
865 870 875 880

Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala Gln Pro Gln Ile Cys
885 890 895

Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp Glu
900 905 910

Asn Ile Arg Pro Thr Phe Lys Glu Leu Ala Asn Glu Phe Thr Arg Met
915 920 925

Ala Arg Asp Pro Pro Arg Tyr Leu Val Ile Lys Arg Glu Ser Gly Pro
930 935 940

Gly Ile Ala Pro Gly Pro Glu Pro His Gly Leu Thr Asn Lys Lys Leu
945 950 955 960

Glu Glu Val Glu Leu Glu Pro Glu Leu Asp Leu Asp Leu Asp Leu Glu
965 970 975

Ala Glu Glu Asp Asn Leu Ala Thr Thr Thr Leu Gly Ser Ala Leu Ser
980 985 990

Leu Pro Val Gly Thr Leu Asn Arg Pro Arg Gly Ser Gln Ser Leu Leu
995 1000 1005

Ser Pro Ser Ser Gly Tyr Met Pro Met Asn Gln Gly Asn Leu Gly
1010 1015 1020

Glu Ser Cys Gln Glu Ser Ala Val Ser Gly Ser Ser Glu Arg Cys
1025 1030 1035

Pro Arg Pro Val Ser Leu His Pro Met Pro Arg Gly Cys Leu Ala
1040 1045 1050

Ser Glu Ser Ser Glu Gly His Val Thr Gly Ser Glu Ala Glu Leu
1055 1060 1065

Gln Glu Lys Val Ser Met Cys Arg Ser Arg Ser Arg Ser Arg Ser
1070 1075 1080

Pro Arg Pro Arg Gly Asp Ser Ala Tyr His Ser Gln Arg His Ser
1085 1090 1095

Leu Leu Thr Pro Val Thr Pro Ieu Ser Pro Pro Gly Leu Glu Glu
 1100 1105 1110

Glu Asp Val Asn Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly
 1115 1120 1125

Thr Pro Ser Ser Arg Glu Gly Thr Leu Ser Ser Val Gly Leu Ser
 1130 1135 1140

Ser Val Leu Gly Thr Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu
 1145 1150 1155

Tyr Met Asn Arg Arg Arg Arg His Ser Pro Pro His Pro Pro Arg
 1160 1165 1170

Pro Ser Ser Leu Glu Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly
 1175 1180 1185

Ser Asp Leu Ser Ala Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu
 1190 1195 1200

His Pro Val Pro Ile Met Pro Thr Ala Gly Thr Thr Pro Asp Glu
 1205 1210 1215

Asp Tyr Glu Tyr Met Asn Arg Gln Arg Asp Gly Gly Gly Pro Gly
 1220 1225 1230

Gly Asp Tyr Ala Ala Met Gly Ala Cys Pro Ala Ser Glu Gln Gly
 1235 1240 1245

Tyr Glu Glu Met Arg Ala Phe Gln Gly Pro Gly His Gln Ala Pro
 1250 1255 1260

His Val His Tyr Ala Arg Leu Lys Thr Leu Arg Ser Leu Glu Ala
 1265 1270 1275

Thr Asp Ser Ala Phe Asp Asn Pro Asp Tyr Trp His Ser Arg Leu
 1280 1285 1290

Phe Pro Lys Ala Asn Ala Gln Arg Thr
 1295 1300

<210> 99

<211> 619

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 99

Met Lys Pro Ala Thr Gly Leu Trp Val Trp Val Ser Leu Leu Val Ala
 1 5 10 15

Ala Gly Thr Val Gln Pro Ser Asp Ser Gln Ser Val Cys Ala Gly Thr
 20 25 30

Glu Asn Lys Leu Ser Ser Leu Ser Asp Leu Glu Gln Gln Tyr Arg Ala
 35 40 45

Leu Arg Lys Tyr Tyr Glu Asn Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60

Ile Thr Ser Ile Glu His Asn Arg Asp Leu Ser Phe Leu Arg Ser Val
65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Leu Asn Gln Phe Arg Tyr
85 90 95

Leu Pro Leu Glu Asn Leu Arg Ile Ile Arg Gly Thr Lys Leu Tyr Glu
100 105 110

Asp Arg Tyr Ala Leu Ala Ile Phe Leu Asn Tyr Arg Lys Asp Gly Asn
115 120 125

Phe Gly Leu Gln Glu Leu Gly Leu Lys Asn Leu Thr Glu Ile Leu Asn
130 135 140

Gly Gly Val Tyr Val Asp Gln Asn Lys Phe Leu Cys Tyr Ala Asp Thr
145 150 155 160

Ile His Trp Asp Ile Val Arg Asn Pro Trp Pro Ser Asn Leu Thr
165 170 175

Leu Val Ser Thr Asn Gly Ser Ser Gly Cys Gly Arg Cys His Lys Ser
180 185 190

Cys Thr Gly Arg Cys Trp Gly Pro Thr Glu Asn His Cys Gln Thr Leu
195 200 205

Thr Arg Thr Val Cys Ala Glu Gln Cys Asp Gly Arg Cys Tyr Gly Pro
210 215 220

Tyr Val Ser Asp Cys Cys His Arg Glu Cys Ala Gly Gly Cys Ser Gly
225 230 235 240

Pro Lys Asp Thr Asp Cys Phe Ala Cys Met Asn Phe Asn Asp Ser Gly
245 250 255

Ala Cys Val Thr Gln Cys Pro Gln Thr Phe Val Tyr Asn Pro Thr Thr
260 265 270

Phe Gln Leu Glu His Asn Phe Asn Ala Lys Tyr Thr Tyr Gly Ala Phe
275 280 285

Cys Val Lys Lys Cys Pro His Asn Phe Val Val Asp Ser Ser Ser Cys
290 295 300

Val Arg Ala Cys Pro Ser Ser Lys Met Glu Val Glu Glu Asn Gly Ile
305 310 315 320

Lys Met Cys Lys Pro Cys Thr Asp Ile Cys Pro Lys Ala Cys Asp Gly
325 330 335

Ile Gly Thr Gly Ser Leu Met Ser Ala Gln Thr Val Asp Ser Ser Asn
340 345 350

Ile Asp Lys Phe Ile Asn Cys Thr Lys Ile Asn Gly Asn Leu Ile Phe
355 360 365

Leu Val Thr Gly Ile His Gly Asp Pro Tyr Asn Ala Ile Glu Ala Ile
370 375 380

Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly
385 390 395 400

Phe Leu Asn Ile Gln Ser Trp Pro Pro Asn Met Thr Asp Phe Ser Val
405 410 415

Phe Ser Asn Leu Val Thr Ile Gly Gly Arg Val Leu Tyr Ser Gly Leu
420 425 430

Ser Leu Leu Ile Leu Lys Gln Gln Gly Ile Thr Ser Leu Gln Phe Gln
435 440 445

Ser Leu Lys Glu Ile Ser Ala Gly Asn Ile Tyr Ile Thr Asp Asn Ser
450 455 460 465

Asn Leu Cys Tyr Tyr His Thr Ile Asn Trp Thr Thr Leu Phe Ser Thr
465 470 475 480

Ile Asn Gln Arg Ile Val Ile Arg Asp Asn Arg Lys Ala Glu Asn Cys
485 490 495

Thr Ala Glu Gly Met Val Cys Asn His Leu Cys Ser Ser Asp Gly Cys
500 505 510

Trp Gly Pro Gly Pro Asp Gln Cys Leu Ser Cys Arg Arg Phe Ser Arg
515 520 525

Gly Arg Ile Cys Ile Glu Ser Cys Asn Leu Tyr Asp Gly Val Leu Thr
530 535 540

Thr Val Gln Ser Ala Leu Ile Leu Lys Met Ala Gln Thr Val Trp Lys
545 550 555 560

Asn Val Gln Met Ala Tyr Arg Gly Gln Thr Val Ser Phe Ser Ser Met
565 570 575

Leu Ile Gln Ile Gly Ser Ala Thr His Ala Ile Gln Thr Ala Pro Lys
580 585 590

Gly Val Thr Val Pro Leu Val Met Thr Ala Phe Thr His Gly Arg Ala
595 600 605

Ile Pro Leu Tyr His Asn Met Leu Glu Leu Pro
610 615

<210> 100

<211> 1283

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 100

Met Lys Pro Ala Thr Gly Leu Trp Val Trp Val Ser Leu Leu Val Ala
1 5 10 15

Ala Gly Thr Val Gln Pro Ser Asp Ser Gln Ser Val Cys Ala Gly Thr
20 25 30

Glu Asn Lys Leu Ser Ser Leu Ser Asp Leu Glu Gln Gln Tyr Arg Ala
35 40 45

Leu Arg Lys Tyr Tyr Glu Asn Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60

Ile Thr Ser Ile Glu His Asn Arg Asp Leu Ser Phe Leu Arg Ser Val
65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Leu Asn Gln Phe Arg Tyr
85 90 95

Leu Pro Leu Glu Asn Leu Arg Ile Ile Arg Gly Thr Lys Leu Tyr Glu
100 105 110

Asp Arg Tyr Ala Leu Ala Ile Phe Leu Asn Tyr Arg Lys Asp Gly Asn
115 120 125

Phe Gly Leu Gln Glu Leu Gly Leu Lys Asn Leu Thr Glu Ile Leu Asn
130 135 140

Gly Gly Val Tyr Val Asp Gln Asn Lys Phe Leu Cys Tyr Ala Asp Thr
145 150 155 160

Ile His Trp Gln Asp Ile Val Arg Asn Pro Trp Pro Ser Asn Leu Thr
165 170 175

Leu Val Ser Thr Asn Gly Ser Ser Gly Cys Gly Arg Cys His Lys Ser
180 185 190

Cys Thr Gly Arg Cys Trp Gly Pro Thr Glu Asn His Cys Gln Thr Leu
195 200 205

Thr Arg Thr Val Cys Ala Glu Gln Cys Asp Gly Arg Cys Tyr Gly Pro
210 215 220

Tyr Val Ser Asp Cys Cys His Arg Glu Cys Ala Gly Gly Cys Ser Gly
225 230 235 240

Pro Lys Asp Thr Asp Cys Phe Ala Cys Met Asn Phe Asn Asp Ser Gly
245 250 255

Ala Cys Val Thr Gln Cys Pro Gln Thr Phe Val Tyr Asn Pro Thr Thr
260 265 270

Phe Gln Leu Glu His Asn Phe Asn Ala Lys Tyr Thr Tyr Gly Ala Phe
275 280 285

Cys Val Lys Lys Cys Pro His Asn Phe Val Val Asp Ser Ser Ser Cys
290 295 300

Val Arg Ala Cys Pro Ser Ser Lys Met Glu Val Glu Asn Gly Ile
 305 310 315 320

Lys Met Cys Lys Pro Cys Thr Asp Ile Cys Pro Lys Ala Cys Asp Gly
 325 330 335

Ile Gly Thr Gly Ser Leu Met Ser Ala Gln Thr Val Asp Ser Ser Asn
 340 345 350

Ile Asp Lys Phe Ile Asn Cys Thr Lys Ile Asn Gly Asn Leu Ile Phe
 355 360 365

Leu Val Thr Gly Ile His Gly Asp Pro Tyr Asn Ala Ile Glu Ala Ile
 370 375 380

Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly
 385 390 395 400

Phe Leu Asn Ile Gln Ser Trp Pro Pro Asn Met Thr Asp Phe Ser Val
 405 410 415

Phe Ser Asn Leu Val Thr Ile Gly Gly Arg Val Leu Tyr Ser Gly Leu
 420 425 430

Ser Leu Leu Ile Leu Lys Gln Gln Gly Ile Thr Ser Leu Gln Phe Gln
 435 440 445

Ser Leu Lys Glu Ile Ser Ala Gly Asn Ile Tyr Ile Thr Asp Asn Ser
 450 455 460

Asn Leu Cys Tyr Tyr His Thr Ile Asn Trp Thr Thr Leu Phe Ser Thr
 465 470 475 480

Ile Asn Gln Arg Ile Val Ile Arg Asp Asn Arg Lys Ala Glu Asn Cys
 485 490 495

Thr Ala Glu Gly Met Val Cys Asn His Leu Cys Ser Ser Asp Gly Cys
 500 505 510

Trp Gly Pro Gly Pro Asp Gln Cys Leu Ser Cys Arg Arg Phe Ser Arg
 515 520 525

Gly Arg Ile Cys Ile Glu Ser Cys Asn Leu Tyr Asp Gly Glu Phe Arg
 530 535 540

Glu Phe Glu Asn Gly Ser Ile Cys Val Glu Cys Asp Pro Gln Cys Glu
 545 550 555 560

Lys Met Glu Asp Gly Leu Leu Thr Cys His Gly Pro Gly Pro Asp Asn
 565 570 575

Cys Thr Lys Cys Ser His Phe Lys Asp Gly Pro Asn Cys Val Glu Lys
 580 585 590

Cys Pro Asp Gly Leu Gln Gly Ala Asn Ser Phe Ile Phe Lys Tyr Ala
 595 600 605

Asp Pro Asp Arg Glu Cys His Pro Cys His Pro Asn Cys Thr Gln Gly

610 615 620

Thr Pro Leu Ile Ala Ala Gly Val Ile Gly Gly Leu Phe Ile Leu Val
625 630 635 640

Ile Val Gly Leu Thr Phe Ala Val Tyr Val Arg Arg Lys Ser Ile Lys
645 650 655

Lys Lys Arg Ala Leu Arg Arg Phe Leu Glu Thr Glu Leu Val Glu Pro
660 665 670

Leu Thr Pro Ser Gly Thr Ala Pro Asn Gln Ala Gln Leu Arg Ile Leu
675 680 685

Lys Glu Thr Glu Leu Lys Arg Val Lys Val Leu Gly Ser Gly Ala Phe
690 695 700

Gly Thr Val Tyr Lys Gly Ile Trp Val Pro Glu Gly Glu Thr Val Lys
705 710 715 720

Ile Pro Val Ala Ile Lys Ile Leu Asn Glu Thr Thr Gly Pro Lys Ala
725 730 735

Asn Val Glu Phe Met Asp Glu Ala Leu Ile Met Ala Ser Met Asp His
740 745 750

Pro His Leu Val Arg Leu Leu Gly Val Cys Leu Ser Pro Thr Ile Gln
755 760 765

Leu Val Thr Gln Leu Met Pro His Gly Cys Leu Leu Glu Tyr Val His
770 775 780

Glu His Lys Asp Asn Ile Gly Ser Gln Leu Leu Asn Trp Cys Val
785 790 795 800

Gln Ile Ala Lys Gly Met Met Tyr Leu Glu Glu Arg Arg Leu Val His
805 810 815

Arg Asp Leu Ala Ala Arg Asp Val Leu Val Lys Ser Pro Asn His Val
820 825 830

Lys Ile Thr Asp Phe Gly Leu Ala Arg Leu Leu Glu Gly Asp Glu Lys
835 840 845

Glu Tyr Asn Ala Asp Gly Gly Lys Met Pro Ile Lys Trp Met Ala Leu
850 855 860

Glu Cys Ile His Tyr Arg Lys Phe Thr His Gln Ser Asp Val Trp Ser
865 870 875 880

Tyr Gly Val Thr Ile Trp Glu Leu Met Thr Phe Gly Gly Lys Pro Tyr
885 890 895

Asp Gly Ile Pro Thr Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu
900 905 910

Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Val Met
915 920 925